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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:54:34 ; Search time 479.47 Seconds

(without alignments)
8828.602 Million cell updates/sec

Title: US-09-763-978B-1

Perfect score: 2587

Sequence: 1 ggaagcgacgagcgagcgcgc.....tgatataatatacttctt 2587

Scoring table: IDENTITY_NUC

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*

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6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 2565 | 99.1 | 2627 | 3 | US-09-404-879A-391 |
| 2 | 2565 | 99.1 | 2627 | 4 | US-09-667-857-391 |
| 3 | 1543 | 59.6 | 1567 | 3 | US-09-404-879A-74 |
| 4 | 1543 | 59.6 | 1567 | 4 | US-09-338-933-74 |
| 5 | 1543 | 59.6 | 1567 | 4 | US-09-215-681-74 |
| 6 | 1543 | 59.6 | 1567 | 4 | US-09-215-681-74 |
| 7 | 1543 | 59.6 | 1567 | 4 | US-09-667-857-74 |
| 8 | 958.8 | 37.1 | 1046 | 4 | US-09-799-451-332 |
| 9 | 532.2 | 20.6 | 541 | 3 | US-09-404-879A-28 |
| 10 | 532.2 | 20.6 | 541 | 4 | US-09-338-933-28 |
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| 13 | 532.2 | 20.6 | 541 | 4 | US-09-667-857-28 |
| 14 | 448.2 | 17.3 | 461 | 3 | US-09-404-879A-27 |
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| 16 | 448.2 | 17.3 | 461 | 4 | US-09-215-681-27 |
| 17 | 448.2 | 17.3 | 461 | 4 | US-09-215-681-27 |
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| 19 | 412 | 15.9 | 695 | 3 | US-09-667-857-27 |
| 20 | 412 | 15.9 | 695 | 3 | US-09-040-984-15 |
| 21 | 412 | 15.9 | 695 | 3 | US-09-123-912-15 |
| 22 | 412 | 15.9 | 695 | 4 | US-09-643-597-15 |
| 23 | 412 | 15.9 | 695 | 4 | US-09-480-884A-15 |
| 24 | 412 | 15.9 | 695 | 4 | US-09-542-615A-15 |
| 25 | 412 | 15.9 | 695 | 4 | US-09-606-421B-15 |
| 26 | 412 | 15.9 | 695 | 4 | US-09-221-107-15 |
| 27 | 412 | 15.9 | 695 | 4 | US-09-466-396A-15 |

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| 28 | 412 | 15.9 | 695 | 4 | US-09-630-940B-15 | Sequence 15, Appl |
| 29 | 412 | 15.9 | 695 | 4 | US-09-285-479-15 | Sequence 15, Appl |
| 30 | 320 | 12.4 | 335 | 4 | US-09-513-999C-30680 | Sequence 30680, A |
| 31 | 74 | 2.9 | 247299 | 4 | US-09-949-016-17590 | Sequence 17590, A |
| 32 | 72.6 | 2.8 | 59828 | 4 | US-09-949-016-16238 | Sequence 16238, A |
| 33 | 70.6 | 2.7 | 10610 | 4 | US-09-949-016-15967 | Sequence 15967, A |
| 34 | 70.2 | 2.7 | 132438 | 4 | US-09-949-016-14349 | Sequence 14349, A |
| 35 | 70.2 | 2.7 | 132438 | 4 | US-09-949-016-14350 | Sequence 14350, A |
| 36 | 70.2 | 2.7 | 151089 | 4 | US-09-949-016-14348 | Sequence 14348, A |
| 37 | 70.2 | 2.7 | 524032 | 4 | US-09-949-016-16328 | Sequence 16328, A |
| 38 | 70.2 | 2.7 | 524032 | 4 | US-09-949-016-16329 | Sequence 16329, A |
| 39 | 70.2 | 2.7 | 524032 | 4 | US-09-949-016-16330 | Sequence 16330, A |
| 40 | 70.2 | 2.7 | 524032 | 4 | US-09-949-016-16331 | Sequence 16331, A |
| 41 | 70.2 | 2.7 | 529885 | 4 | US-09-949-016-14340 | Sequence 14340, A |
| 42 | 70.2 | 2.7 | 529885 | 4 | US-09-949-016-14341 | Sequence 14341, A |
| 43 | 70.2 | 2.7 | 529885 | 4 | US-09-949-016-14342 | Sequence 14342, A |
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| 45 | 70.2 | 2.7 | 529885 | 4 | US-09-949-016-14344 | Sequence 14344, A |

ALIGNMENTS

| | | | | | |
|------------------------------------------------------------------|-----|---------------------------------------------------------|-----|--|--|
| RESULT 1 | | | | | |
| US-09-404-879A-391 | | | | | |
| Sequence 391, Application US/09404879A | | | | | |
| Patent No. 6468346 | | | | | |
| GENERAL INFORMATION: | | | | | |
| APPLICANT: Mitcham, Jennifer L. | | | | | |
| APPLICANT: King, Gordon E. | | | | | |
| APPLICANT: Algate, Paul A. | | | | | |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND | | | | | |
| FILE REFERENCE: 210121.462C2 | | | | | |
| CURRENT APPLICATION NUMBER: US/09/404,879A | | | | | |
| CURRENT FILING DATE: 1999-09-24 | | | | | |
| NUMBER OF SEQ ID NOS: 393 | | | | | |
| SOFTWARE: FASTSEQ for Windows Version 3.0 | | | | | |
| SEQ ID NO 391 | | | | | |
| LENGTH: 2627 | | | | | |
| TYPE: DNA | | | | | |
| ORGANISM: Homo sapiens | | | | | |
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| Best Local Similarity 100.0%; Pred. No. 0; | | | | | |
| Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1; | | | | | |
| QY | 12 | GGAGCTCAGTCAGCAGTACCCAGTACGCGGAGACCTTCCCGACGATGGCTTCC | 71 | | |
| DB | 33 | GGAGCTCAGTCAGCAGTACCCAGTACGCGGAGACCTTCCCGACGATGGCTTCC | 92 | | |
| QY | 72 | TGGGAGATCTCTTCTGAGCATTAATGATCATCTTAATTTGCTGAGCAATG | 131 | | |
| DB | 93 | TGGGAGATCTCTTCTGAGCATTAATGATCATCTTAATTTGCTGAGCAATG | 152 | | |
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| DB | 153 | CAGTATCTTGGCTTGTATTTTACGAGACATCTTCATCAGTATCTTGTGCT | 212 | | |
| QY | 192 | CAGCTGGGAACCTTGGGAGATGGAATCTGAGCGCATTTTGAACCTGACATCAAC | 251 | | |
| DB | 213 | CAGCTGGGAACCTTGGGAGATGGAATCTGAGCGCATTTTGAACCTGACATCAAC | 272 | | |
| QY | 252 | TTTCTGATTCGTATACATGCTGGAAGAGGTGTTTAACTGCTGATGATTTCA | 311 | | |
| DB | 273 | TTTCTGATTCGTATACATGCTGGAAGAGGTGTTTAACTGCTGATGATTTCA | 332 | | |
| QY | 312 | AAGAAGCAAGATGAGCTGTCGAGCAGGATGAATTTTCAGAGCCGGAACAGTGT | 371 | | |
| DB | 333 | AAGAAGCAAGATGAGCTGTCGAGCAGGATGAATTTTCAGAGCCGGAACAGTGT | 392 | | |
| QY | 372 | TTCGTATCAAGTATGATTTGCAATTCCTTTGGCGCTGAAGAAACGTCAATCAGAG | 431 | | |

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Db 393 TTGGATCAATGATAGTTGGCAATGCTCTTTGGGCTGAAAAACGTGCAACTCAGC 452
Oy 432 ATGCTGGCACTTACAAATGTTATATCATCTTTAAAGGCAAGGGAAATGCTAACTTG 491
Db 453 ATGCTGGCACTTACAAATGTTATATCATCTTTAAAGGCAAGGGAAATGCTAACTTG 512
Oy 492 AGTATAAACTGAGCTTCAGCATGCGGGAAGTGAATGTGACTATATGTCAGCTGAG 551
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Db 1713 TGTCATCACAAGCTCTGAGGCTTCTCTTTCATCTGCGAGGACAGCTAAGACCTCAGT 1772
Oy 1752 TTTCAATAGCATCTAGACAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGG 1811
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Oy 1812 GGAATGTCTGAAGACATTTTGTGTTACTCATATGAGGAGTGAAGAGATACAGTGTCTA 1871
Db 1833 GGAATGTCTGAAGACATTTTGTGTTACTCATATGAGGAGTGAAGAGATACAGTGTCTA 1892
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Db 1893 CTACCAACTAGTGAATAAAGGCAAGGAGTGTGCTCAACTCTTACCATGTACAGAGAGCT 1952
Oy 1932 CTCCCATTTACACCTACCCCAATCCGAAGTGTCAACTGTGACAGACTAAGAAACCTGCT 1991
Db 1953 CTCCCATTTACACCTACCCCAATCCGAAGTGTCAACTGTGACAGACTAAGAAACCTGCT 2012
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Db 2553 AGAAACGATTTTATGATGCTGATCTGTTCAAGAGATGATTAATATACCTTCTCT 2609
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RESULT 2
US-09-667-857-391
; Sequence 391, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Aigale, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-667-857-391

Query Match      99.1%; Score 2565; DB 4; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB      93  TGGGGGAGATCCCTTCTGGAGATATTTAGCANTCATTTCTGGGCTGGAGCAATTG 152
QY      132  CACTCATCATTTGGCTTGTGATTTTCAGGGAGACACTTCATCAGATCACTACTGTGCGCT 191
DB      153  CACTCATCATTTGGCTTGTGATTTTCAGGGAGACACTTCATCAGATCACTACTGTGCGCT 212
QY      192  CAGCTGGGAACTTTGGGAGATGGAATCTGAGCTGCATTTTGAACCTGACATCAAC 251
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DB      333  AAGAAGGCAAAAGATGAGCTGTGGAGAGAGATGAAATGTTCAAGGCGCGGACAGAGTGT 392
QY      372  TTGCTGATCAAGTATGATTTGGCAATGCTCTTTTGGCGCTGAAAACGTGCAACTCAAG 431
DB      393  TTGCTGATCAAGTATGATTTGGCAATGCTCTTTTGGCGCTGAAAACGTGCAACTCAAG 452
QY      432  ATGCTGGCACTCAAAATGTTATATATCACTCTTAAAGGCAAGGGGAAATGCTAACTTGG 491
DB      453  ATGCTGGCACTCAAAATGTTATATATCACTCTTAAAGGCAAGGGGAAATGCTAACTTGG 512
QY      492  AGTATTAATACTGAGGCTTTCAGCATGCGGAGATGATGATGATGATTAATGCCAGCTCAG 551
DB      513  AGTATTAATACTGAGGCTTTCAGCATGCGGAGATGATGATGATGATTAATGCCAGCTCAG 572
QY      552  AGACCTTGGCGGTGAGGCTTCCCGATGTTTCCCGCAAGCCCAAGTGTCTGCGCATCCC 611
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QY      672  AGAATGTGACATGAAAGTGTGTCTGTCTCTACATGTTACGATCAACAACACTACT 731
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QY      732  CCTGTATGATTTGAAAATGACATTTGCCAAGCAACAGGGATATCAAAAGTACAGAACTCG 791
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QY      792  AGATCAAAAGGCGAGTACCTACAGCTGCTTAACTCAAGGCTTCTGTGTCTCTT 851
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QY      852  CTTTCTTTGCCATCAGCTGGGCACTTCTGCTCTCAGCCCTTAAGCTGATGCTAAATTAAT 911
DB      873  CTTTCTTTGCCATCAGCTGGGCACTTCTGCTCTCAGCCCTTAAGCTGATGCTAAATTAAT 932
QY      912  GTGCTTGGCCCAAAAAAAGCATGCAAAATGCTTTTACAACAGGATCTACAGAACTAT 971
DB      933  GTGCTTGGCCCAAAAAAAGCATGCAAAATGCTTTTACAACAGGATCTACAGAACTAT 992
QY      972  TTCACCAACAGATATGACCTAGTTTATATTTCTGGAGGAAATGAATTCAATCTAGAA 1031
DB      993  TTCACCAACAGATATGACCTAGTTTATATTTCTGGAGGAAATGAATTCAATCTAGAA 1052
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DB      1053  GTCTGAGTGTGACAAACAAGACCAAGAAACAAAAAGCCAAAGACAGAGGCTCAAT 1112
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DB      1113  ATGAACAATATTAATTTATCTTCAAGAATATTTAGAAATTTGGGAAATTAATTTCAATGTA 1172
QY      1152  ACTAGACAAGTGTGTTAAGATGATPAAGTAAATGACCTGAGACAAATGATGATCCCCAG 1211
DB      1173  ACTAGACAAGTGTGTTAAGATGATPAAGTAAATGACCTGAGACAAATGATGATCCCCAG 1232
QY      1212  ATCTCAGGAGACCTCCCTGCTGTGACCTGAGGAGTGAAGAGACAGATATGTCATGTT 1271
DB      1233  ATCTCAGGAGACCTCCCTGCTGTGACCTGAGGAGTGAAGAGACAGATATGTCATGTT 1292
QY      1272  CTTTGTCTCTGAATTTTATGATTAATGTCGTGAATGTTGCTCTGAGGAAGCCCTCGGAA 1331
DB      1293  CTTTGTCTCTGAATTTTATGATTAATGTCGTGAATGTTGCTCTGAGGAAGCCCTCGGAA 1352
QY      1332  AGTCTATCCCAATATTCACATCTTATATTCACAAATTTAAGCTGTAGTATGACCTTA 1391
DB      1353  AGTCTATCCCAATATTCACATCTTATATTCACAAATTTAAGCTGTAGTATGACCTTA 1412
QY      1392  AGACGCTGTAAATTTGACTGCACTTTCGCAACTCAAGGAGGCGCTGCAATTTTATGATGGGT 1451
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QY      1452  CAAATATTTCACTTTTATGATGCTTCCAAAGTGTCTTGTCTTCTTCCCACTGACA 1511
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QY      1632  GATGATGTTCAATCCGTAATGCTTCCAGGAGAAAGACCTTTCACCTTGACATATATGATTA 1691
DB      1653  GATGATGTTCAATCCGTAATGCTTCCAGGAGAAAGACCTTTCACCTTGACATATATGATTA 1712
QY      1692  TGTGATCAACAAGCTGAGGCTTCTCTTTCATCTGCTGAGACAGTAAACCTCACT 1751
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Db 900 TACGAGACGTCTCCCACTTCAACTACCAATCCGAAGTCTCACTGTGTGACAGACTAG 959
Qy 1982 AAACCTGTTTTGAGTAGAAAAAGGCTGTGAAAAGAGGGAGCCAACTCTGTCTGT 2041
Db 960 AAACCTGTTTTGAGTAGAAAAAGGCTGTGAAAAGAGGGAGCCAACTCTGTCTGT 1019
Qy 2042 T-CTCATTAGTCAATTTGCAATTAAGCAATTTCTCTTTGGCTGTGCTCAAGCAG 2100
Db 1020 TCTTCACATTAGTCAATTTGCAATTAAGCAATTTCTCTTTGGCTGTGCTCAAGCAG 1079
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Db 1080 AGAGCCAGAACTATCGGGGACCAAGATTAACATCTCTGAGTAACAGAGTTGCAAGG 1139
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Db 1380 TGAAGCCTTGAAGATTAAGTCTTGAAGAAGAAATCTTTGTTTCAACCCCTTCC 1439
Qy 2461 ACACTCTCATGTGTAACTGCTTCTGAGACCTTGAAGCAGGCTGATATTAAC 2520
Db 1440 ACACTCTCATGTGTAACTGCTTCTGAGACCTTGAAGCAGGCTGATATTAAC 1499
Qy 2521 ATGTGTATTAAGAACTGATTTTGAAGTTCTGATCTTGAAGAAATTAATTAATAC 2580
Db 1500 ATGTGTATTAAGAACTGATTTTGAAGTTCTGATCTTGAAGAAATTAATTAATAC 1559
Qy 2581 ATTTTCT 2587
Db 1560 ATTTTCT 1566

RESULT 4
US-09-338-933-74
Sequence 74, Application US/09338933
Patent No. 6488931
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon B.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338, 933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: Pabseq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
ORGANISM: Homo sapien
US-09-338-933-74

Query Match 59.6%; Score 1543; DB 4; Length 1567;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1022 ATATCTAGAGTCTGAGTAGCAAAACAGACAGAAACAAAGAACCAAGCAG 1081

Db 1 ATATCTAGAGTCTGAGTAGCAAAACAGACAGAAACAAAGAACCAAGCAG 60
Qy 1082 AGGCTCAATATGACAAAGATTAATCTATCTTCAAAAGACATATTAAGTTGGAAATTA 1141
Db 61 AGGCTCAATATGACAAAGATTAATCTATCTTCAAAAGACATATTAAGTTGGAAATTA 120
Qy 1142 ATTCATGTGACATGACAAAGTGTGTAAGAGATTAAGTAAATGACCGTGGACAGT 1201
Db 121 ATTCATGTGACATGACAAAGTGTGTAAGAGATTAAGTAAATGACCGTGGACAGT 180
Qy 1202 GCATCCCAAGATCTGAGGACCTCCCTGCTGTGACCTGAGGAGTGAAGAGACAGAT 1261
Db 181 GCATCCCAAGATCTGAGGACCTCCCTGCTGTGACCTGAGGAGTGAAGAGACAGAT 240
Qy 1262 AGTGAATGTTCTTGTCTGTGAATTTTGAATATATGTGCTGAATGTGTGAGAA 1321
Db 241 AGTGAATGTTCTTGTCTGTGAATTTTGAATATATGTGCTGAATGTGTGAGAA 300
Qy 1322 GCCCTGGAAAGTCTATCCCAATATCCAACTTATATTCACAAATTAAGCTGAT 1381
Db 301 GCCCTGGAAAGTCTATCCCAATATCCAACTTATATTCACAAATTAAGCTGAT 360
Qy 1382 ATGTACCTTAAGAGCGCTGATATTTGACCTGCACTTGCACACTGAGGGCGGCTGANTTT 1441
Db 361 ATGTACCTTAAGAGCGCTGATATTTGACCTGCACTTGCACACTGAGGGCGGCTGANTTT 420
Qy 1442 AGTAATGGGTCAATGATTCATTTTATGATGCTTCAAGGTCCTTGTCTTCTTC 1501
Db 421 AGTAATGGGTCAATGATTCATTTTATGATGCTTCAAGGTCCTTGTCTTCTTC 480
Qy 1502 CCACTGACAAATGCGCAAGTTGAGAAAAATGATCTAATTTTGAAGATTAACAGACAGT 1561
Db 481 CCACTGACAAATGCGCAAGTTGAGAAAAATGATCTAATTTTGAAGATTAACAGACAGT 540
Qy 1562 CGGCGACACGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1621
Db 541 CGGCGACACGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Qy 1622 TTAATTTCTGATGATGTTTATCCGTGAATGTCGAGGAGGACCTTTCACCTTGACTA 1681
Db 601 TTAATTTCTGATGATGTTTATCCGTGAATGTCGAGGAGGACCTTTCACCTTGACTA 660
Qy 1682 TATGCAATATGATCAACAGCTGAGGCTTCTCTTCCATCTCTGCTGAGACGCTA 1741
Db 661 TATGCAATATGATCAACAGCTGAGGCTTCTCTTCCATCTCTGCTGAGACGCTA 720
Qy 1742 AGACCTCAATTTCAATAGCATCTAGAGAGTGGAGTCAAGCTGAGGCTGATTTTCCGCC 1801
Db 721 AGACCTCAATTTCAATAGCATCTAGAGAGTGGAGTCAAGCTGAGGCTGATTTTCCGCC 780
Qy 1802 CATCTCCGGGGAATGCTGAAGACAAATTTTGTATCTTCAATGAGGAGTGAAGAGA 1861
Db 781 CATCTCCGGGGAATGCTGAAGACAAATTTTGTATCTTCAATGAGGAGTGAAGAGA 839
Qy 1862 TACAGTCTACTACCACTAGTGGATTAAGGCGGAGGATGCTCTCACTCTTACAG 1921
Db 840 TACAGTCTACTACCACTAGTGGATTAAGGCGGAGGATGCTCTCACTCTTACAG 899
Qy 1922 TACAGGACGTCTCCCATTAACAATCCCAATCCGAATCCGAATCCGAATCCGAATCCGA 1981
Db 900 TACAGGACGTCTCCCATTAACAATCCCAATCCGAATCCGAATCCGAATCCGAATCCGA 959
Qy 1982 AAACCTGTTTTGAGTAGAAAAAGGCTGTGAAAAGAGGGAGCCAACTCTGTCTGT 2041
Db 960 AAACCTGTTTTGAGTAGAAAAAGGCTGTGAAAAGAGGGAGCCAACTCTGTCTGT 1019
Qy 2042 T-CTCATTAGTCAATTTGCAATTAAGCAATTTCTCTTTGGCTGTGCTCAAGCAG 2100
Db 1020 TCTTCACATTAGTCAATTTGCAATTAAGCAATTTCTCTTTGGCTGTGCTCAAGCAG 1079
Qy 2101 AGAGCCAGAACTATCGGGGACCAAGATTAACATCTCTGAGTAACAGAGTTGCAAGG 2160

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Db      1080 AGAGCCAGAACTCTATCGGGCAACAGATACATCTCTCAGTAAACAGATTGACAAAGC 1139
Oy      2161 CTATGGAAATGCGCTGATGGATTAATCTTCACTTTGAGCTTCAAGTTTCTTCCCT 2220
Db      1140 CTATGGAAATGCGCTGATGGATTAATCTTCACTTTGAGCTTCAAGTTTCTTCCCT 1199
Oy      2221 TCATTCACCCCTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAAGTTT 2280
Db      1200 TCATTCACCCCTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAAGTTT 1259
Oy      2281 CTATTCCTGAATTTAGATCTCCAGACCCCTTCTGGCCCAATTCAAATTAAGCAACAA 2340
Db      1260 CTATTCCTGAATTTAGATCTCCAGACCCCTTCTGGCCCAATTCAAATTAAGCAACAA 1319
Oy      2341 CATATACCTTCCATGAAGCAACAGACTTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCC 2400
Db      1320 CATATACCTTCCATGAAGCAACAGACTTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCC 1379
Oy      2401 TGAGGCTTGAAGAAATGAAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCC 2460
Db      1380 TGAGGCTTGAAGAAATGAAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCC 1439
Oy      2461 AACCTTCATGTTAATGAACACTGCTTCTGGAAGCTTGAAGCAAGCTGATTAATAC 2520
Db      1440 AACCTTCATGTTAATGAACACTGCTTCTGGAAGCTTGAAGCAAGCTGATTAATAC 1499
Oy      2521 ATGTTGTTATGAAGAACTGATTTTGAAGTTCTGATTCGTTCAAGATGATTAATATAC 2580
Db      1500 ATGTTGTTATGAAGAACTGATTTTGAAGTTCTGATTCGTTCAAGATGATTAATATAC 1559
Oy      2581 ATTTCCT 2587
Db      1560 ATTTCCT 1566

RESULT 5
US-09-215-681-74
; Sequence 74, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-215-681-74

Query Match      59.6%; Score 1543; DB 4; Length 1567;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
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Db      181 GCATCCCAAGATCTCAGGACCTCCCTGCTGCACTGGGGAGTAGAGACAGAT 240
Oy      1262 AGTGATGCTTGTGCTCTGAATTTTATGTAATGCTGTAATGTTGCTGAGAA 1321
Db      241 AGTGATGCTTGTGCTCTGAATTTTATGTAATGCTGTAATGTTGCTGAGAA 300
Oy      1322 GCCCTGGAAGTCTATCCAAATATCCAACTTAATTTCAAAATTAAGCTAGT 1381
Db      301 GCCCTGGAAGTCTATCCAAATATCCAACTTAATTTCAAAATTAAGCTAGT 360
Oy      1382 ATGATCCCTAAGACGCTGTAATGATCTGCACTTCCGAATCTCAGGGGCTGATTTT 1441
Db      361 ATGATCCCTAAGACGCTGTAATGATCTGCACTTCCGAATCTCAGGGGCTGATTTT 420
Oy      1442 AGTATGGGTCAAAATGATTCCTTTTATGATGCTTCCAAAGGCTTGGCTTCTTC 1501
Db      421 AGTATGGGTCAAAATGATTCCTTTTATGATGCTTCCAAAGGCTTGGCTTCTTC 480
Oy      1502 CCAACTGA CAATGCAAAATGAGAAATGATCATATTTTATGATTAACAGACAGT 1561
Db      481 CCAACTGA CAATGCAAAATGAGAAATGATCATATTTTATGATTAACAGACAGT 540
Oy      1562 CGGCGACACCGATTTTATTAATTAACCTGACACTTCTTTTAAACAAATGCGGCT 1621
Db      541 CGGCGACACCGATTTTATTAATTAACCTGACACTTCTTTTAAACAAATGCGGCT 600
Oy      1622 TTATTTCTCAGATGATGTTCAATCCGCTGATGATGATCCAGGGAAGACCTTCACTGATTA 1681
Db      601 TTATTTCTCAGATGATGTTCAATCCGCTGATGATGATCCAGGGAAGACCTTCACTGATTA 660
Oy      1682 TATGGCATTAATGTCATCAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACGTA 1741
Db      661 TATGGCATTAATGTCATCAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACGTA 720
Oy      1742 AGACTCAGTTTTCATATGATCTTAGAGACATGAGGACCTACCTGGGGTGAATTTGCCCCC 1801
Db      721 AGACTCAGTTTTCATATGATCTTAGAGACATGAGGACCTACCTGGGGTGAATTTGCCCCC 780
Oy      1802 CATCTCCGGGGGAATGCTGAAGACAAATTTTGGTTTAACTCATGAGGAGTAGAGAGA 1861
Db      781 CATCTCCGGGGGAATGCTGAAGACAAATTTTGGTTTAACTCATGAGGAGTAGAGAGA 839
Oy      1862 TACAGTGTACTACCACTAGATGATTAAGGCAAGGATGCTGCTCAACTCTTCACTAGT 1921
Db      840 TACAGTGTACTACCACTAGATGATTAAGGCAAGGATGCTGCTCAACTCTTCACTAGT 899
Oy      1922 TACAGGAGTCTCCCATTTAACAATCCCAATCCGAATGTCATGCTGTGACGACTAG 1981
Db      900 TACAGGAGTCTCCCATTTAACAATCCCAATCCGAATGTCATGCTGTGACGACTAG 959
Oy      1982 AAACCTGTTTGTAGTAGAAAGGGCTGGAAGAGGGAGCCAAATCTGCTGCT 2041
Db      960 AAACCTGTTTGTAGTAGAAAGGGCTGGAAGAGGGAGCCAAATCTGCTGCT 1019
Oy      2042 T-CTCACTTAATGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 2100
Db      1020 TCTTCACATTAATGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1079
Oy      2101 AGAGCCAAATCTTATCGGGCAACAGATTAATCTTCACTGATGAACAGATTGACAAAGC 2160
Db      1080 AGAGCCAAATCTTATCGGGCAACAGATTAATCTTCACTGATGAACAGATTGACAAAGC 1139
Oy      2161 CTATGGAAATGCGCTGATGGATTAATCTTCACTTTGAGCTTCAAGTTTCTTCCCT 2220
Db      1140 CTATGGAAATGCGCTGATGGATTAATCTTCACTTTGAGCTTCAAGTTTCTTCCCT 1199
Oy      2221 TCATTCACCCCTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAAGTTT 2280
Db      1200 TCATTCACCCCTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAAGTTT 1259
Oy      2281 CTATTCCTGAATTTAGATCTCCAGACCTTCTGGCCCAATTCAAATTAAGCAACAA 2340
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Db 1260 CTTACTGTGATTTAGATCTCCAGACCCTTCCTGCGCACATTTCAATTAAGCAACAA 1319
Qy 2341 CATATACCTCCATGAGACACACACATTTTGAAGCAAGCAATGACTGTTAAAT 2400
Db 1320 CATATACCTCCATGAGACACACACATTTTGAAGCAAGCAATGACTGTTAAAT 1379
Qy 2401 TGAGGCTTGAGGATGAGCTTTGAAGAAAGAAATGATTTGTTCCAGCCCTTCCC 2460
Db 1380 TGAGGCTTGAGGATGAGCTTTGAAGAAAGAAATGATTTGTTCCAGCCCTTCCC 1439
Qy 2461 ACACTCTTCATGTTTAAACCACTGCTTCTGACCTTGAAGCCAGGTGATGTATAC 2520
Db 1440 ACACTCTTCATGTTTAAACCACTGCTTCTGACCTTGAAGCCAGGTGATGTATAC 1499
Qy 2521 ATGTGTTATGAAACCTGATTTTAAAGTTTCTGATCTTCAAGGAATGATTAATATAC 2580
Db 1500 ATGTGTTATGAAACCTGATTTTAAAGTTTCTGATCTTCAAGGAATGATTAATATAC 1559
Qy 2581 ATTTTCT 2587
Db 1560 ATTTTCT 1566

RESULT 6
US-09-216-003A-74
Sequence 74, Application US/09216003A
Patent No. 6670463
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
FILE REFERENCE: 210121.462
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: Patencin Ver. 2.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
ORGANISM: Homo sapiens
US-09-216-003A-74

Query Match 59.6%; Score 1543; DB 4; Length 1567;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1022 ATATCTAGAAGTCTGAGTGAAGCAACAAAGCAAGAAACAAAGCAAGCAAGCA 1081
Db 1 ATATCTAGAAGTCTGAGTGAAGCAACAAAGCAAGAAACAAAGCAAGCAAGCAAGCA 60
Qy 1082 AGGCTCCATATGAAACAAGATAATCTATCTTCAAGACATATTAAGAGTTGGAAAAAT 1141
Db 61 AGGCTCCATATGAAACAAGATAATCTATCTTCAAGACATATTAAGAGTTGGAAAAAT 120
Qy 1142 ATTCATGTGAACAGCAAGTGTGTTAAGTGTATAGTAAATGCACTGAGACAACT 1201
Db 121 ATTCATGTGAACAGCAAGTGTGTTAAGTGTATAGTAAATGCACTGAGACAACT 180
Qy 1202 GCATCCCAAGATCTCAGGAGCTCCCTCTCTCTGACCTGGGAGTGAAGAGACAGAT 1261
Db 181 GCATCCCAAGATCTCAGGAGCTCCCTCTCTCTGACCTGGGAGTGAAGAGACAGAT 240
Qy 1262 AGTGCAATGTTCTTGTCTGAAATTTTATGATATGCTGTAATGTTGCTCTGAGAA 1321
Db 241 AGTGCAATGTTCTTGTCTGAAATTTTATGATATGCTGTAATGTTGCTCTGAGAA 300
Qy 1322 GCGGCTTGAAAGTCTATCCCAATATCCATCTTATATCCAAATTAAGCTGATG 1381
Db 301 GCGGCTTGAAAGTCTATCCCAATATCCCAATCTTATATCCAAATTAAGCTGATG 360
Qy 1382 ATGTACCTTAAGAGCTGTATATGACTGCACTTGCACACTCAGGGGCGGCTGCAATTT 1441
Db 1441 ATGTACCTTAAGAGCTGTATATGACTGCACTTGCACACTCAGGGGCGGCTGCAATTT 1441

Db 361 ATGTACCTTAAGAGCTGTATATGACTGCACTTGCACACTCAGGGGCGGCTGCAATTT 420
Qy 1442 AGTAATGGGTCAAAATGATTCATCTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTC 1501
Db 421 AGTAATGGGTCAAAATGATTCATCTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTC 480
Qy 1502 CCAACTGACAAATGCAAAAGTTGAGAAAAATGATCAATATTTTAAAGATTAACAGACAGT 1561
Db 481 CCAACTGACAAATGCAAAAGTTGAGAAAAATGATCAATATTTTAAAGATTAACAGACAGT 540
Qy 1562 CCGGCAACCGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1621
Db 541 CCGGCAACCGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Qy 1622 TTAATTTCTGAGATGATGCTTCCGGAATGCTTCCGGAATGCTTCCGGAATGCTTCC 1681
Db 601 TTAATTTCTGAGATGATGCTTCCGGAATGCTTCCGGAATGCTTCCGGAATGCTTCC 660
Qy 1682 TATGCAATATGTCATCAACAGCTGAGGCTTCTCTTCCATCTCTGCGTGAAGCTTA 1741
Db 661 TATGCAATATGTCATCAACAGCTGAGGCTTCTCTTCCATCTCTGCGTGAAGCTTA 720
Qy 1742 AGACTCAGTTTCAATTAAGATCTAGAGAGTGAAGCTGAGGCTGAGTGAATTCGCCCC 1801
Db 721 AGACTCAGTTTCAATTAAGATCTAGAGAGTGAAGCTGAGGCTGAGTGAATTCGCCCC 780
Qy 1802 CATCTCCGGGGGAATGCTGGAAGACAAATTTGTTTCTCTCATGAGGAGTGAAGAGGA 1861
Db 781 CATCTCCGGGGGAATGCTGGAAGACAAATTTT-GTATCTCTCATGAGGAGTGAAGAGGA 839
Qy 1862 TACAGTCTACTACCAACTAGTGAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1921
Db 840 TACAGTCTACTACCAACTAGTGAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 899
Qy 1922 TACAGGAGTCTCCCATTAACAATCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAG 1981
Db 900 TACAGGAGTCTCCCATTAACAATCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAG 959
Qy 1982 AAAACCTGTTTGAATGAGAAAGGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2041
Db 960 AAAACCTGTTTGAATGAGAAAGGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1019
Qy 2042 T-CTCATTAGCATTTGCAATTAAGCAATTCGTCTTCTTGGCTGCTGCTGAGCAGAG 2100
Db 1020 TCTCTCATTTAGCATTTGCAATTAAGCAATTCGTCTTCTTGGCTGCTGCTGAGCAGAG 1079
Qy 2101 AGAGCCAGAACTTATCGGCAACAGGATTAATCTCTCAGTGAACAGAGTTGACAAAGC 2160
Db 1080 AGAGCCAGAACTTATCGGCAACAGGATTAATCTCTCAGTGAACAGAGTTGACAAAGC 1139
Qy 2161 CTATGGGAAATGCTGATGAGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCT 2220
Db 1140 CTATGGGAAATGCTGATGAGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCT 1199
Qy 2221 TCATTTCAACCTGCAAGGCAAGTCTGTAAGGAAATGCTGAGTCTTCAAGCTTCAAG 2280
Db 1200 TCATTTCAACCTGCAAGGCAAGTCTGTAAGGAAATGCTGAGTCTTCAAGCTTCAAG 1259
Qy 2281 CTTACTCTGAATTTAGATCTCAGACCTTCTGAGCAATTAATTAAGCAACAA 2340
Db 1260 CTTACTCTGAATTTAGATCTCAGACCTTCTGAGCAATTAATTAAGCAACAA 1319
Qy 2341 CATATACCTTCAATGAGACACACACATTTTGAAGCAAGCAATGACTGTTGAAT 2400
Db 1320 CATATACCTTCAATGAGACACACACATTTTGAAGCAAGCAATGACTGTTGAAT 1379
Qy 2401 TGAGGCTTGAGGATGAGCTTTGAAGAAAGAAATATCTTGTTCAGCCCTTCCC 2460
Db 1380 TGAGGCTTGAGGATGAGCTTTGAAGAAAGAAATATCTTGTTCAGCCCTTCCC 1439
Qy 2461 ACACTCTTCATGTTTAAACCACTGCTTCTGACCTTGAAGCCAGGTGATGTATAC 2520
Db 1440 ACACTCTTCATGTTTAAACCACTGCTTCTGACCTTGAAGCCAGGTGATGTATAC 1499

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RESULT 7
US-09-667-857-74
; Sequence 74, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.46205
; CURRENT APPLICATION NUMBER: US/09/667,857
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-667-857-74

Query Match      59.6%; Score 1543; DB 4; Length 1567;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY      1022 ATATCTAGAGTCTGAGTGAAGCAACAGACCAAGAAACAAAGAACCCAAAGCAGA 1081
DB      1 ATATCTAGAGTCTGAGTGAAGCAACAGACCAAGAAACAAAGAACCCAAAGCAGA 60
QY      1082 AGGCTCCAAATAGAACAAATTAATCTCTCAAGACATATTAAGTTGGAAAAATA 1141
DB      61 AGGCTCCAAATAGAACAAATTAATCTCTCAAGACATATTAAGTTGGAAAAATA 120
QY      1142 ATTCAATGTAAGTGAAGCAAGTGTGTAAGAGTGAATGAATGAATGCACTGGAGACAGT 1201
DB      121 ATTCAATGTAAGTGAAGCAAGTGTGTAAGAGTGAATGAATGAATGCACTGGAGACAGT 180
QY      1202 GCATCCCAAGATCTCAAGGACCTCCCTGCTGTCACTGGAGAGTGAAGAGACAGAT 1261
DB      181 GCATCCCAAGATCTCAAGGACCTCCCTGCTGTCACTGGAGAGTGAAGAGACAGAT 240
QY      1262 AATGATATGTTCTTGTCTGTGAATTTTATATATGCTGAATATGTTGCTCTGAGGA 1321
DB      241 AATGATATGTTCTTGTCTGTGAATTTTATATATGCTGAATATGTTGCTCTGAGGA 300
QY      1322 GCCCTGGAAGTCTATCCCAATATTCACATCTTATTCACAAATTAAGCTGTAGT 1381
DB      301 GCCCTGGAAGTCTATCCCAATATTCACATCTTATTCACAAATTAAGCTGTAGT 360
QY      1382 ATGTAACCTTAAGACGCTGTAAATGAAGTCACTTGGCAAGTCAAGGGGCGGCTGATTT 1441
DB      361 ATGTAACCTTAAGACGCTGTAAATGAAGTCACTTGGCAAGTCAAGGGGCGGCTGATTT 420
QY      1442 AGTATGGGTCAAAATGATTCATTTTATGATGCTTCCAAAGGTGCTTGGCTTCTCTTC 1501
DB      421 AGTATGGGTCAAAATGATTCATTTTATGATGCTTCCAAAGGTGCTTGGCTTCTCTTC 480
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QY      1502 CCAACTGACAAATGCGCAAGTTGAGAAAAATGATCATTAATTTTATGATTAACAGACAGT 1561
DB      481 CCAACTGACAAATGCGCAAGTTGAGAAAAATGATCATTAATTTTATGATTAACAGACAGT 540
QY      1562 CGGCGACACCGATTTTATTAATTAACCTGACACCTCTTTTAAACAAACAAATGCGGGT 1621
DB      541 CGGCGACACCGATTTTATTAATTAACCTGACACCTCTTTTAAACAAACAAATGCGGGT 600
QY      1622 TTATTTCTAGATGATGTTCAATCCGTGAATGTCAGAGGAAGACCTTTCACTTGAAGTA 1681
DB      601 TTATTTCTAGATGATGTTCAATCCGTGAATGTCAGAGGAAGACCTTTCACTTGAAGTA 660
QY      1682 TATGCAATTAATGATCAACAAAGCTGAGGCTTCTCTTTCATCTGCGTGAACAGTA 1741
DB      661 TATGCAATTAATGATCAACAAAGCTGAGGCTTCTCTTTCATCTGCGTGAACAGTA 720
QY      1742 AGACTCACTTTTCAATGACATCTAGACAGTGGGACCTCAGCTGGGGTGAATTTGCCCCC 1801
DB      721 AGACTCACTTTTCAATGACATCTAGACAGTGGGACCTCAGCTGGGGTGAATTTGCCCCC 780
QY      1802 CATCTCGGGGGGAATGTCGAAGCAATTTTGTACTCAATGAGGAGTGAAGAGGA 1861
DB      781 CATCTCGGGGGGAATGTCGAAGCAATTTTGTACTCAATGAGGAGTGAAGAGGA 839
QY      1862 TACAGTGTACTACCACTAGTGAATTAAGGCGCAGAGTGTCTCTCAACCTTCAACATG 1921
DB      840 TACAGTGTACTACCACTAGTGAATTAAGGCGCAGAGTGTCTCTCAACCTTCAACATG 899
QY      1922 TACAGAGTGTCTCCCATTAACATCAACCAATCCGAAATGTCACCTGTGACAGCTAAG 1981
DB      900 TACAGAGTGTCTCCCATTAACATCAACCAATCCGAAATGTCACCTGTGACAGCTAAG 959
QY      1982 AAACCTGATTTTGAAGTGAAGAAAGGCGCTGGAAGAGGGAGCCAAATCTGCTGCT 2041
DB      960 AAACCTGATTTTGAAGTGAAGAAAGGCGCTGGAAGAGGGAGCCAAATCTGCTGCT 1019
QY      2042 TCTCACTATGATCAATGGAACAAATTAAGCATTTCTCTTGTGCTGCTCTCAGACAG 2100
DB      1020 TCTCACTATGATCAATGGAACAAATTAAGCATTTCTCTTGTGCTGCTCTCAGACAG 1079
QY      2101 AGAGCCAAAGCTCTATCGGGGACCGAGTAACATCTCACTGAACAGAGTTGACAAAGG 2160
DB      1080 AGAGCCAAAGCTCTATCGGGGACCGAGTAACATCTCACTGAACAGAGTTGACAAAGG 1139
QY      2161 CTATGGAAGATGCGCTGATGGGATTTCTTCAAGCTTGTGAGCTTGAATTTCTTCCCT 2220
DB      1140 CTATGGAAGATGCGCTGATGGGATTTCTTCAAGCTTGTGAGCTTGAATTTCTTCCCT 1199
QY      2221 TCATTTCTA CCGTGAAGGCAAGTTCTGTGAAGAAATGCTGAAGTTCTAGCTCAGGTTTT 2280
DB      1200 TCATTTCTA CCGTGAAGGCAAGTTCTGTGAAGAAATGCTGAAGTTCTAGCTCAGGTTTT 1259
QY      2281 CTTACTCTGAATTTATGATCTCAAGACCTTCTGCGCCCAATTCAAATTAAGGCAACAA 2340
DB      1260 CTTACTCTGAATTTATGATCTCAAGACCTTCTGCGCCCAATTCAAATTAAGGCAACAA 1319
QY      2341 CATATACCTTCATGAAGACACACAGACTTTTGAACAAAGCAATGAAGTCTGTAAT 2400
DB      1320 CATATACCTTCATGAAGACACACAGACTTTTGAACAAAGCAATGAAGTCTGTAAT 1379
QY      2401 TGAGGCTTTGAAGATGAAGCTTTGAAGAAAGAAATCTTTGTTTCCAGCCCCCTTCCC 2460
DB      1380 TGAGGCTTTGAAGATGAAGCTTTGAAGAAAGAAATCTTTGTTTCCAGCCCCCTTCCC 1439
QY      2461 ACACCTTCATGTTGTTAAACCACTGCTTCTGAGACCTTGAAGCCAGGTAAGTATTAAC 2520
DB      1440 ACACCTTCATGTTGTTAAACCACTGCTTCTGAGACCTTGAAGCCAGGTAAGTATTAAC 1499
QY      2521 ATGTTGTTATGAAGAAAGATTTTGAAGTTCGATCGTTCAAGAGATGAATTAATATAC 2580
DB      1500 ATGTTGTTATGAAGAAAGATTTTGAAGTTCGATCGTTCAAGAGATGAATTAATATAC 1559
QY      2581 ATTTCTT 2587
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Db      61 TATGAAACAAGATAATCTATCTTCAAAAGACATATTGAGATGGGAAATAATTCATGTG 120
Qy      1151 AACTAGACAAGTGTCTTAAGAGTGAATTAATAATGCACTGAGACAAAGTGCATCCCA 1210
Db      121 AACTAGACAAGTGTCTTAAGAGTGAATTAATAATGCACTGAGACAAAGTGCATCCCA 180
Qy      1211 GATCTCAGGAGACTCCCTGCTGCTGCACTGAGGAGTGAAGAGCAGATAGTGCATGT 1270
Db      181 GATCTCAGGAGACTCCCTGCTGCTGCACTGAGGAGTGAAGAGCAGATAGTGCATGT 240
Qy      1271 TCTTTGCTCTGAATTTTAAATTGATTATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 1330
Db      241 TCTTTGCTCTGAATTTTAAATTGATTATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 300
Qy      1331 AAGTCTATCCCAACAATATCCATCTTAATTCACAATAATTAAGCTGTATGTAACCT 1390
Db      301 AAGTCTATCCCAACAATATCCATCTTAATTCACAATAATTAAGCTGTATGTAACCT 360
Qy      1391 AAGAGCGTCTAATTGACTGCACTTCGCACTCAGGGGCGGCTGCATTTTATGTAATGG 1450
Db      361 AAGAGCGTCTAATTGACTGCACTTCGCACTCAGGGGCGGCTGCATTTTATGTAATGG 420
Qy      1451 TCAATGATTCACCTTTTATGATGCTTCCAAAGTGCTTGGCTTCTTCCCACTGAC 1510
Db      421 TCAATGATTCACCTTTTATGATGCTTCCAAAGTGCTTGGCTTCTTCCCACTGAC 480
Qy      1511 AATGCGCAAGTTGAGAAAAATGATCATATTTTATGCAATTAACAGAGCAGTGGGAGAC 1570
Db      481 AATGCGCAAGTTGAGAAAAATGATCATATTTTATGCAATTAACAGAGCAGTGGGAGAC 540
Qy      1571 C 1571
Db      541 C 541
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RESULT 10
US-09-763-978b-1
; Sequence 28, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-763-978b-1
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Query Match      20.6%; Score 532.2; DB 4; Length 541;
Best Local Similarity 98.7%; Pred. No. 2.6e-150;
Matches 534; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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Qy      1031 AGCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAAGAGGCTCCAA 1090
Db      1 AGCTGAGTGAAGCAAAAGAGCAAGAAACAAARRAGAGCCAAAAGAGGCTCCAA 60
Qy      1091 TATGAACAAGTATCTATCTTCAAAAGCATTTTGAAGTTGGGAAAAATATTCATGTG 1150
Db      61 TATGAACAAGTATCTATCTTCAAAAGCATATTGAAGTTGGGAAAAATATTCATGTG 120
Qy      1151 AACTAGACAAGTGTCTTAAGAGTGAATTAATAATGCACTGAGACAAAGTGCATCCCA 1210
Db      121 AACTAGACAAGTGTCTTAAGAGTGAATTAATAATGCACTGAGACAAAGTGCATCCCA 180
Qy      1211 GATCTCAGGAGACTCCCTGCTGCTGCACTGAGGAGTGAAGAGCAGATAGTGCATGT 1270
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Db      181 GATCTCAGGAGACTCCCTGCTGCTGCACTGAGGAGTGAAGAGCAGATAGTGCATGT 240
Qy      1271 TCTTTGCTCTGAATTTTAAATTGATTATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 1330
Db      241 TCTTTGCTCTGAATTTTAAATTGATTATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 300
Qy      1331 AAGTCTATCCCAACAATATCCATCTTAATTCACAATAATTAAGCTGTATGTAACCT 1390
Db      301 AAGTCTATCCCAACAATATCCATCTTAATTCACAATAATTAAGCTGTATGTAACCT 360
Qy      1391 AAGAGCGTCTAATTGACTGCACTTCGCACTCAGGGGCGGCTGCATTTTATGTAATGG 1450
Db      361 AAGAGCGTCTAATTGACTGCACTTCGCACTCAGGGGCGGCTGCATTTTATGTAATGG 420
Qy      1451 TCAATGATTCACCTTTTATGATGCTTCCAAAGTGCTTGGCTTCTTCCCACTGAC 1510
Db      421 TCAATGATTCACCTTTTATGATGCTTCCAAAGTGCTTGGCTTCTTCCCACTGAC 480
Qy      1511 AATGCGCAAGTTGAGAAAAATGATCATATTTTATGCAATTAACAGAGCAGTGGGAGAC 1570
Db      481 AATGCGCAAGTTGAGAAAAATGATCATATTTTATGCAATTAACAGAGCAGTGGGAGAC 540
Qy      1571 C 1571
Db      541 C 541
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RESULT 11
US-09-763-978b-1
; Sequence 28, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Rudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-763-978b-1
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Query Match      20.6%; Score 532.2; DB 4; Length 541;
Best Local Similarity 98.7%; Pred. No. 2.6e-150;
Matches 534; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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Qy      1031 AGCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAAGAGGCTCCAA 1090
Db      1 AGCTGAGTGAAGCAAAAGAGCAAGAAACAAARRAGAGCCAAAAGAGGCTCCAA 60
Qy      1091 TATGAACAAGTATCTATCTTCAAAAGCATATTGAAGTTGGGAAAAATATTCATGTG 1150
Db      61 TATGAACAAGTATCTATCTTCAAAAGCATATTGAAGTTGGGAAAAATATTCATGTG 120
Qy      1151 AACTAGACAAGTGTCTTAAGAGTGAATTAATAATGCACTGAGACAAAGTGCATCCCA 1210
Db      121 AACTAGACAAGTGTCTTAAGAGTGAATTAATAATGCACTGAGACAAAGTGCATCCCA 180
Qy      1211 GATCTCAGGAGACTCCCTGCTGCTGCACTGAGGAGTGAAGAGCAGATAGTGCATGT 1270
Db      181 GATCTCAGGAGACTCCCTGCTGCTGCACTGAGGAGTGAAGAGCAGATAGTGCATGT 240
Qy      1271 TCTTTGCTCTGAATTTTAAATTGATTATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 1330
Db      241 TCTTTGCTCTGAATTTTAAATTGATTATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 300
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[illegible]

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RESULT 14
US-09-404-879A-27/C
Sequence 27, Application US/09404879A
Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITL OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121,462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(461)
OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-27

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|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 17.3% | Score 448.2; | DB 3; | Length 461; |
| Best Local Similarity | 99.1%; | Pred. No. 6.2e-125; | | |
| Matches 458; | Conservative 2; | Mismatches 1; | Indels 1; | Gaps 1; |

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RESULT 15 US-09-338-933-27/C
; Sequence 27, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-338-933-27

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|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 17.3% | Score 448.2; | DB 4; | Length 461; |
| Best Local Similarity | 99.1%; | Pred. No. 6.2e-125; | | |
| Matches 458; | Conservative 2; | Mismatches 1; | Indels 1; | Gaps 1; |

Search completed: May 31, 2005, 00:28:50
Job time : 485.47 secs

100.0%; Score 2587; DB 6; Length 2587;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAAGGACGGGAGCTCCACTCAGCCGATGCCGATACCGTGGAACTTCCCCAGC 60
Db 1 GGAAGGACGGGAGCTCCACTCAGCCGATGCCGATACCGTGGAACTTCCCCAGC 60
QY 61 CATTGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATTAATAGCATCATTAATCTGSC 120
Db 61 CATTGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATTAATAGCATCATTAATCTGSC 120
QY 121 TGGAGCAATTTGCACTCATCATTTGGCTTTGGTATTTTCAAGGAGACACTCCATCAGACTAC 180
Db 121 TGGAGCAATTTGCACTCATCATTTGGCTTTGGTATTTTCAAGGAGACACTCCATCAGACTAC 180
QY 181 TACTGTCCCTCAGCTGGGAGACATTTGGGAGAGATGGAAATCTGAGCTGCATTTTGAAC 240
Db 181 TACTGTCCCTCAGCTGGGAGACATTTGGGAGAGATGGAAATCTGAGCTGCATTTTGAAC 240
QY 241 TGAACATCAAACTTTCTGATATGTGTATACATGGCTGGAAGAAAGTGTGAGCTTGT 300
Db 241 TGAACATCAAACTTTCTGATATGTGTATACATGGCTGGAAGAAAGTGTGAGCTTGT 300
QY 301 CCATGAGTTCAAGAAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAAGAGCCG 360
Db 301 CCATGAGTTCAAGAAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAAGAGCCG 360
QY 361 GACAGAGTGTGTTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGCGCTGAAAAACGT 420
Db 361 GACAGAGTGTGTTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGCGCTGAAAAACGT 420
QY 421 GCAACCTCAGAGATGCTGGACCTCAAAATGTTATATCATCACTTCAAGGCAAGGGAA 480
Db 421 GCAACCTCAGAGATGCTGGACCTCAAAATGTTATATCATCACTTCAAGGCAAGGGAA 480
QY 481 TGTAACTCTTGAATATAACTGAGACCTTCAGCATGCCGAAAGTGAATGTGACTATTA 540
Db 481 TGTAACTCTTGAATATAACTGAGACCTTCAGCATGCCGAAAGTGAATGTGACTATTA 540
QY 541 TGGCACTCAGAGACCTTGGCGGTGTAGAGCTCCCGATGTTCCCGACCCCAAGTGT 600
Db 541 TGGCACTCAGAGACCTTGGCGGTGTAGAGCTCCCGATGTTCCCGACCCCAAGTGT 600
QY 601 CTGGGATCCCAAGTTGACCAAGGAGCAAACTTCTGGAAAGTCTCAATGTTACGATCA 660
Db 601 CTGGGATCCCAAGTTGACCAAGGAGCAAACTTCTGGAAAGTCTCAATGTTACGATCA 660
QY 661 GCTGAACCTGTGAAGATGTACCAATGAAGGTTGTCTGTCTTACAAATGTTACGATCA 720
Db 661 GCTGAACCTGTGAAGATGTACCAATGAAGGTTGTGTGTCTTACAAATGTTACGATCA 720
QY 721 CAACACATCTCTGTATATGTAATAATGACATTTGCCAAGCAAGAGGAGATATCAAACT 780
Db 721 CAACACATCTCTGTATATGTAATAATGACATTTGCCAAGCAAGAGGAGATATCAAACT 780
QY 781 GACAGAAATGAGATCAAAAGGCGAGTACCTACAGCTGCTAACTCAAAAGCTTCTCT 840
Db 781 GACAGAAATGAGATCAAAAGGCGAGTACCTACAGCTGCTAACTCAAAAGCTTCTCT 840
QY 841 GTGTGCTCTTCTTCTTTCCTTCCATCAGCTGGGCACTTCTGCTCAGCCCTTAAGT 900
Db 841 GTGTGCTCTTCTTCTTTCCTTCCATCAGCTGGGCACTTCTGCTCAGCCCTTAAGT 900
QY 901 GCTAAATATATGCTCTTGGCCCAAAAAGCATGCAATGTTTCAACAGGAGATC 960
Db 901 GCTAAATATATGCTCTTGGCCCAAAAAGCATGCAATGTTTCAACAGGAGATC 960
QY 961 TACAGAACTATTTCAACAGATATGAGCTTATATTTCTGGAGGAAATGAAT 1020
Db 961 TACAGAACTATTTCAACAGATATGAGCTTATATTTCTGGAGGAAATGAAT 1020
QY 1021 CATATCTAGAACTGTGAGTGAACAACAGCAAGAAACAAAAGCAAAAGCAG 1080
Db 1021 CATATCTAGAACTGTGAGTGAACAACAGCAAGAAACAAAAGCAAAAGCAG 1080
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Db 1021 CATATCTAGAACTGTGAGTGAACAACAGCAAGAAACAAAAGCAAAAGCAG 1080
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Db 1081 AAGGCTCCAAATATGAAACAAGATTAATCTATCTTCAAGAACATATTAGAAAGTTGGAAAT 1140
QY 1141 AATTCATGTGAACCTAGCAAGTGTGTAAAGTGAATGAATGAATGCACTGAGACAAAG 1200
Db 1141 AATTCATGTGAACCTAGCAAGTGTGTAAAGTGAATGAATGAATGCACTGAGACAAAG 1200
QY 1201 TGCATCCCAAGATCTCAGAGACCTCCCTGCTGTCACTGGGAGAGTGAAGACAGAGA 1260
Db 1201 TGCATCCCAAGATCTCAGAGACCTCCCTGCTGTCACTGGGAGAGTGAAGACAGAGA 1260
QY 1261 TAGTCAGTGTCTTGTCTGGAATTTTATGTAATGTCGTGAATGTGCTGAGAGA 1320
Db 1261 TAGTCAGTGTCTTGTCTGGAATTTTATGTAATGTCGTGAATGTGCTGAGAGA 1320
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Db 1321 AGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTAG 1380
QY 1381 TATGTACCTTAAGACGCTGTCTAATTTGACTGCCAATCTGCAACTCAGGGGCGGCTGCATTT 1440
Db 1381 TATGTACCTTAAGACGCTGTCTAATTTGACTGCCAATCTGCAACTCAGGGGCGGCTGCATTT 1440
QY 1441 TAGTAATGGGTCAAAATGATCACTTTTATGATGCTTCAAAAGGTCCTTGCTCTCTT 1500
Db 1441 TAGTAATGGGTCAAAATGATCACTTTTATGATGCTTCAAAAGGTCCTTGCTCTCTT 1500
QY 1501 CCCAATGACAAATGCCAAAGTTGAGAAAAATGATCATTAATTTTATGATTAACAGAGCAG 1560
Db 1501 CCCAATGACAAATGCCAAAGTTGAGAAAAATGATCATTAATTTTATGATTAACAGAGCAG 1560
QY 1561 TGGGCAACAGGATTTTAAATTAACAGACCTTCTTTTAAACAAACAAATGCGGG 1620
Db 1561 TGGGCAACAGGATTTTAAATTAACAGACCTTCTTTTAAACAAACAAATGCGGG 1620
QY 1621 TTTATTTCTCAGATGATGTCATCCGTGAATGTCAGAGAGGACCTTTCACCTTGACT 1680
Db 1621 TTTATTTCTCAGATGATGTCATCCGTGAATGTCAGAGAGGACCTTTCACCTTGACT 1680
QY 1681 ATATGCAATTAATGTCATCAAAAGCTCTGAGGCTTCTCTTTCATCTGCTGTGACAGCT 1740
Db 1681 ATATGCAATTAATGTCATCAAAAGCTCTGAGGCTTCTCTTTCATCTGCTGTGACAGCT 1740
QY 1741 AAGACCTCAGTTTCAATATGATCTAGAGCAGTGGGAATCAGCTGGGTGATTTTCCGCC 1800
Db 1741 AAGACCTCAGTTTCAATATGATCTAGAGCAGTGGGAATCAGCTGGGTGATTTTCCGCC 1800
QY 1801 CCATCTCGGGGGGAATGTCTGAAACAATTTTGTGTTACTCAATGAGGAGATGAGAGAG 1860
Db 1801 CCATCTCGGGGGGAATGTCTGAAACAATTTTGTGTTACTCAATGAGGAGATGAGAGAG 1860
QY 1861 ATACAGTCTACTCAACAACTAGTGAATGAAGGCCAGGATGCTGTCAACCTCTTACCAT 1920
Db 1861 ATACAGTCTACTCAACAACTAGTGAATGAAGGCCAGGATGCTGTCAACCTCTTACCAT 1920
QY 1921 GTACAGAGCTGTCCCAATTAACACTACCCCAATCCGAAGTGTCAACTGTGTGACAGACTPA 1980
Db 1921 GTACAGAGCTGTCCCAATTAACACTACCCCAATCCGAAGTGTCAACTGTGTGACAGACTPA 1980
QY 1981 GAAACCTGTTTGTAGTGAAGAAAGGGCTGGAAGAGAGGGAGCCCAAAATCTGTCTGC 2040
Db 1981 GAAACCTGTTTGTAGTGAAGAAAGGGCTGGAAGAGAGGGAGCCCAAAATCTGTCTGC 2040
QY 2041 TTCTCAGATTAAGTCAATTTGCAAAATAGCAATTCGTCTTGTGCTGCTCCTCAGACAG 2100
Db 2041 TTCTCAGATTAAGTCAATTTGCAAAATAGCAATTCGTCTTGTGCTGCTCCTCAGACAG 2100
QY 2101 AGAGCCAGAACTCTATCGGGGACCGAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGC 2160
Db 2101 AGAGCCAGAACTCTATCGGGGACCGAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGC 2160
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| | | | | | | | |
|------------|--------------------------------------------------------------------------|----------------------------------------------------------------|------------|-----------------|--|--|--|
| OY | 2161 | CTATGGGAATAGCCCTGATGGGATTATCTTCAAGCTTGTTGACCTTCTAAGTTCTTTCCCT | 2220 | | | | |
| Db | 2161 | CTATGGGAATAGCCCTGATGGGATTATCTTCAAGCTTGTTGACCTTCTAAGTTCTTTCCCT | 2220 | | | | |
| OY | 2221 | TCATTCTACCCCTGCAAGCCAAAGTTCTGTAAAGAGAAATGCTGAGTTCTAGCTCAGGTTT | 2280 | | | | |
| Db | 2221 | TCATTCTACCCCTGCAAGCCAAAGTTCTGTAAAGAGAAATGCTGAGTTCTAGCTCAGGTTT | 2280 | | | | |
| OY | 2281 | CTTACTCTGAATTAGATCTCCAGACCCCTTCCGTGGCCAAATTCAAATTAAAGCAACAA | 2340 | | | | |
| Db | 2281 | CTTACTCTGAATTAGATCTCCAGACCCCTTCCGTGGCCAAATTCAAATTAAAGCAACAA | 2340 | | | | |
| OY | 2341 | CATATACCTTCCATCAAGCAACACACAGCTTTGAAACCAAGACAAATGACTGCTGAAT | 2400 | | | | |
| Db | 2341 | CATATACCTTCCATCAAGCAACACACAGCTTTGAAACCAAGACAAATGACTGCTGAAT | 2400 | | | | |
| OY | 2401 | TGAGGCCCTTGAGAGATGAAGCTTTGAAAGAAAGATCTTGTGTTCCAGGCCCTTCCC | 2460 | | | | |
| Db | 2401 | TGAGGCCCTTGAGAGATGAAGCTTTGAAAGAAAGATCTTGTGTTCCAGGCCCTTCCC | 2460 | | | | |
| OY | 2461 | ACACTCTTCATGTGTAAACAACCTGCTTCTTGACCTTGAAGCAACGGTGACTGTATTAC | 2520 | | | | |
| Db | 2461 | ACACTCTTCATGTGTAAACAACCTGCTTCTTGACCTTGAAGCAACGGTGACTGTATTAC | 2520 | | | | |
| OY | 2521 | ATGTGTTATATGAAAACTGATTTTGAAGATTCCTGATCCTTCAAGAGAAATGATTAATATAC | 2580 | | | | |
| Db | 2521 | ATGTGTTATATGAAAACTGATTTTGAAGATTCCTGATCCTTCAAGAGAAATGATTAATATAC | 2580 | | | | |
| OY | 2581 | ATTTCCT 2587 | | | | | |
| Db | 2581 | ATTTCCT 2587 | | | | | |
| RESULT 2 | BD265002 | 2627 bp | DNA linear | PAT 17-JUN-2003 | | | |
| LOCUS | BD265002 | | | | | | |
| DEFINITION | Compositions and methods for the therapy and diagnosis of ovarian | | | | | | |
| ACCESSION | BD265002 | | | | | | |
| VERSION | BD265002.1 | GI:33074770 | | | | | |
| KEYWORDS | JP 2002532093-A/387. | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | | |
| ORGANISM | Homo sapiens | | | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | | | |
| TITLE | 1 (baaes 1 to 2627) | | | | | | |
| JOURNAL | Mitcham,J.L., King,G.E., Algate,P.A. and Frudakis,T.N. | | | | | | |
| | Compositions and methods for the therapy and diagnosis of ovarian | | | | | | |
| | Patent: JP 2002532093-A 387 02-OCT-2002; | | | | | | |
| | CORIXA CORP | | | | | | |
| COMMENT | OS Homo sapiens (human) | | | | | | |
| | PN JP 2002532093-A/387 | | | | | | |
| | PD 02-OCT-2002 | | | | | | |
| | PF 17-DEC-1999 JP 2000588356 | | | | | | |
| | PR 17-DEC-1998 US 09/215681, 17-DEC-1998 US 09/216003 PR | | | | | | |
| | 23-JUN-1999 US 09/338933, 24-SEP-1999 US 09/404879 PI | | | | | | |
| | JENNIFER L MITTCHAM, GORDON B KING, PAUL A ALGATE, TONY N FRUDAKIS PC | | | | | | |
| | C12N15/09, A61K31/7115, A61K35/14, A61K35/76, A61K39/00, A61K39/395, PC | | | | | | |
| | A61K39/395, | | | | | | |
| | PC A61K48/00, A61P35/00, A61P37/04, C07K14/82, C07K19/00, C12N1/15, PC | | | | | | |
| | C12N1/19, | | | | | | |
| | PC | | | | | | |
| | C12N1/21, C12N5/06, C12N5/10, C12Q1/68, G01N33/53, G01N33/53, G01N33/ PC | | | | | | |
| | 566, | | | | | | |
| | PC G01N33/574, G01N33/577, C12N15/00, C12N5/00, C12N5/00 CC | | | | | | |
| | Compositions and methods for the therapy and diagnosis of CC | | | | | | |
| | ovarian cancer | | | | | | |
| FH | Key | Location/Qualifiers | | | | | |
| FT | source | 1.2627 | | | | | |
| | | /organism='Homo sapiens (human)' | | | | | |
| FEATURES | Location/Qualifiers | | | | | | |
| source | 1..2627 | | | | | | |

| ORIGIN | Query Match | 99.1%; | Score 2565; | DB 6; | Length 2627; |
|--------|-----------------------|---------------------------------------------------------------|--------------|------------|--------------|
| | Best Local Similarity | 100.0%; | Prod. No. 0; | | |
| | Matches 2576; | Conservative | 0; | Mismatches | 0; |
| | | | | Indels | 1; |
| | | | | Gaps | 1 |
| QY | 12 | GGCAGCTCCTCACTCAGCCAGTACCCAGATATGCTGGAACTTTCCCGACCCATGGCTTCCC | 71 | | |
| DB | 33 | GGCAGCTCCTCACTCAGCCAGTACCCAGATATGCTGGAACTTTCCCGACCCATGGCTTCCC | 92 | | |
| QY | 72 | TGGGGCAATCTCTCTTCGAGCATTAATTAGCATCATATTATTTCTGGCTGGAGCAATTG | 131 | | |
| DB | 93 | TGGGGCAATCTCTCTTCGAGCATTAATTAGCATCATATTATTTCTGGCTGGAGCAATTG | 152 | | |
| QY | 132 | CACATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGACTCTACTCTGCGCT | 191 | | |
| DB | 153 | CACATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGACTCTACTCTGCGCT | 212 | | |
| QY | 192 | CAGCTGGGAACTTGGGGAGGATGGAACTCTGAGCTGCACTTTTGAACCTGACATCAAC | 251 | | |
| DB | 213 | CAGCTGGGAACTTGGGGAGGATGGAACTCTGAGCTGCACTTTTGAACCTGACATCAAC | 272 | | |
| QY | 252 | TTTCTGATATGCTATACATAGCTGAAAGGAAGTTTATAGCTTGGTCCATGATTTCA | 311 | | |
| DB | 273 | TTTCTGATATGCTATACATAGCTGAAAGGAAGTTTATAGCTTGGTCCATGATTTCA | 332 | | |
| QY | 312 | AAGAAGCAAAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGAGCCGAGCAGAGTGT | 371 | | |
| DB | 333 | AAGAAGCAAAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGAGCCGAGCAGAGTGT | 392 | | |
| QY | 372 | TTGCTGATCAAGTATGATTTGGCAATGCTCTTTTGGCGCTGAAAAAAGCTGCACTCAAG | 431 | | |
| DB | 393 | TTGCTGATCAAGTATGATTTGGCAATGCTCTTTTGGCGCTGAAAAAAGCTGCACTCAAG | 452 | | |
| QY | 432 | ATGCTGGGACCTACAAATGTTATATCATCTTCTTAAAGGGAAGGGGAATGCTAACCTTG | 491 | | |
| DB | 453 | ATGCTGGGACCTACAAATGTTATATCATCTTCTTAAAGGGAAGGGGAATGCTAACCTTG | 512 | | |
| QY | 492 | AGTATAAAACTGAGCTTTCAGCATGCGCGAAGTGAATGTTGATTAATGCCAGCTCAG | 551 | | |
| DB | 513 | AGTATAAAACTGAGCTTTCAGCATGCGCGAAGTGAATGTTGATTAATGCCAGCTCAG | 572 | | |
| QY | 552 | AGACTTGGGCTGAGAGGCTCCCGAGTGTTCCTCCAGCCCAAGTGTCTGGGCGATCCC | 611 | | |
| DB | 573 | AGACTTGGGCTGAGAGGCTCCCGAGTGTTCCTCCAGCCCAAGTGTCTGGGCGATCCC | 632 | | |
| QY | 612 | AAGTTGACCAAGGAGCCAACTTCTCCGAAAGTCTCAATACCAAGCTTTGAGCTGAACCTTG | 671 | | |
| DB | 633 | AAGTTGACCAAGGAGCCAACTTCTCCGAAAGTCTCAATACCAAGCTTTGAGCTGAACCTTG | 692 | | |
| QY | 672 | AGAAATGTCACATGAAAGGTTGTGTCTGTGCTCTCAATATGATTCAGTCAACAACATACT | 731 | | |
| DB | 693 | AGAAATGTCACATGAAAGGTTGTGTCTGTGCTCTCAATATGATTCAGTCAACAACATACT | 752 | | |
| QY | 732 | CCTGTATGATTTGAAAATGACACTTGGCCAAAGCAAGGAGATATCAAAAGTGAACAGATGG | 791 | | |
| DB | 753 | CCTGTATGATTTGAAAATGACACTTGGCCAAAGCAAGGAGATATCAAAAGTGAACAGATGG | 812 | | |
| QY | 792 | AGATCAAAAAGGAGGATCACTCAAGCTGCTAAACTCAAAAGGCTTCTGTGTGTCTCTT | 851 | | |
| DB | 813 | AGATCAAAAAGGAGGATCACTCAAGCTGCTAAACTCAAAAGGCTTCTGTGTGTCTCTT | 872 | | |
| QY | 852 | CTTTCTTTTGCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTTAAATATAT | 911 | | |
| DB | 873 | CTTTCTTTTGCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTTAAATATAT | 932 | | |
| QY | 912 | GTCGCTTGGCCACAAAAAGCATGCAAGTATTTGTTACAAACAGGAGATCTACAGATCAT | 971 | | |
| DB | 933 | GTCGCTTGGCCACAAAAAGCATGCAAGTATTTGTTACAAACAGGAGATCTACAGATCAT | 992 | | |

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| QY | 9712 | TTCAACCAACGATATGACCTTAGTATTATTTCTGGAGGAAATGAATTCATATCTAGAA | 1031 |
| Db | 993 | TTCAACCAACGATATGACCTTAGTATTATTTCTGGAGGAAATGAATTCATATCTAGAA | 1052 |
| QY | 1032 | GTCTGGATGAGCAAAACGAGCAAGAAACAAAAGAACCCAAAGCAAGAGGCTCCAAAT | 1091 |
| Db | 1053 | GTCTGGATGAGCAAAACGAGCAAGAAACAAAAGAACCCAAAGCAAGAGGCTCCAAAT | 1112 |
| QY | 1092 | ATGAAACAAGATAAATCTATCTTCCAAAGACATATTAGAAAGTTGGGAAATAATTCATGTGA | 1151 |
| Db | 1113 | ATGAAACAAGATAAATCTATCTTCCAAAGACATATTAGAAAGTTGGGAAATAATTCATGTGA | 1172 |
| QY | 1152 | ACTAGACAAGTGTGTTAAAGATGATAGTAAATATGCCTGTGAGACAAAGTGCATCCGAG | 1211 |
| Db | 1173 | ACTAGACAAGTGTGTTAAAGATGATAGTAAATATGCCTGTGAGACAAAGTGCATCCGAG | 1232 |
| QY | 1212 | ATCTCAGGAGCTCCCCCTGCCTGCACCTGGGGAGTGAAGAGACAGGATATGTCATGTT | 1271 |
| Db | 1233 | ATCTCAGGAGCTCCCCCTGCCTGCACCTGGGGAGTGAAGAGACAGGATATGTCATGTT | 1292 |
| QY | 1272 | CTTTGTCTGTGAATTTTAAAGTAAATATGTCGTATGTTGCTCTGAGGAACCCCTGGAA | 1331 |
| Db | 1293 | CTTTGTCTGTGAATTTTAAAGTAAATATGTCGTATGTTGCTCTGAGGAACCCCTGGAA | 1352 |
| QY | 1332 | AGCTATATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATAGTATCCCTA | 1391 |
| Db | 1353 | AGCTATATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATAGTATCCCTA | 1412 |
| QY | 1392 | AGAGGCTGTATTTGACCTGGCACTTCGCACTCAGGGGGGGCTGCATTTTAGTAAAGGGT | 1451 |
| Db | 1413 | AGAGGCTGTATTTGACCTGGCACTTCGCACTCAGGGGGGGCTGCATTTTAGTAAAGGGT | 1472 |
| QY | 1452 | CAAAATGATTCCTTTTATATGATGTCCTCCAAAGTGCTGTGGCTTCTCTCCCACTGACA | 1511 |
| Db | 1473 | CAAAATGATTCCTTTTATATGATGTCCTCCAAAGTGCTGTGGCTTCTCTCCCACTGACA | 1532 |
| QY | 1512 | AATGCCAAAGTTGAGAAAAATGATCATATATTTAGCATPAAACAGACAGTGGGGACACC | 1571 |
| Db | 1533 | AATGCCAAAGTTGAGAAAAATGATCATATATTTAGCATPAAACAGACAGTGGGGACACC | 1592 |
| QY | 1572 | GATTTTATPAAATPAAACCTGACACCTTCTTTTAAACAAACAAAGCGGGTTATTTCTCA | 1631 |
| Db | 1593 | GATTTTATPAAATPAAACCTGACACCTTCTTTTAAACAAACAAAGCGGGTTATTTCTCA | 1652 |
| QY | 1632 | GATGATGTTTCATCCGTGATGGTCCAGGGAAAGACCTTTCACCTTGACTATATGGCATT | 1691 |
| Db | 1653 | GATGATGTTTCATCCGTGATGGTCCAGGGAAAGACCTTTCACCTTGACTATATGGCATT | 1712 |
| QY | 1692 | TGTTCATCAACAAGCTGTGAGGCTCTCTCTTCCATCTGCGTGAACGTTAAGACCTCAGT | 1751 |
| Db | 1713 | TGTTCATCAACAAGCTGTGAGGCTCTCTCTTCCATCTGCGTGAACGTTAAGACCTCAGT | 1772 |
| QY | 1752 | TTTTCATATAGCATCTAGAGCAGTGGGACCTCAGCTGGGGGTGATTTTGGCCCCCATCTCCGGG | 1811 |
| Db | 1773 | TTTTCATATAGCATCTAGAGCAGTGGGACCTCAGCTGGGGGTGATTTTGGCCCCCATCTCCGGG | 1832 |
| QY | 1812 | GGAAATGTCTGAAGACAATTTTGGTTAATCTCAATGAGGAGTGTGAGAGGATATACAGTGTGA | 1871 |
| Db | 1833 | GGAAATGTCTGAAGACAATTTTGGTTAATCTCAATGAGGAGTGTGAGAGGATATACAGTGTGA | 1892 |
| QY | 1872 | CTAACCAACTAGTGATPAAAGGCGAGGAGTCTGCTCAACCTTCTTCACTGTACAGACGCT | 1931 |
| Db | 1893 | CTAACCAACTAGTGATPAAAGGCGAGGAGTCTGCTCAACCTTCTTCACTGTACAGACGCT | 1952 |
| QY | 1932 | CTTCCCATTTACACTATCCCAATCCGAAAGTGTCACTGTGTGACAGACTTAAGAAACCTTGGT | 1991 |
| Db | 1953 | CTTCCCATTTACACTATCCCAATCCGAAAGTGTCACTGTGTGACAGACTTAAGAAACCTTGGT | 2012 |
| QY | 1992 | TTTGAAGTGAAGAAAGGGCGCTGGAAGAAAGGGGAGCCAAACAAATCTGTCTTGCTTCTCACATT | 2050 |
| Db | 2013 | TTTGAAGTGAAGAAAGGGCGCTGGAAGAAAGGGGAGCCAAACAAATCTGTCTTGCTTCTCACATT | 2072 |
| QY | 2051 | AGTCATTTGGCAATATAGCAATTTCTGTCTCTTTGGCTGTGCTCCTCAGACACAGAGCCAGAA | 2110 |

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| Db | 2073 | AGTCATTGGCAAAATPAAGCATTCTGTCTCTTTGGCTGCTGCTCAGCACACAGAGCCAGAA | 2132 |
| Qy | 2111 | CTCTATCGGGGACCGAGATPAACATCTCTCAGTGAACAGAGTTGCAAGGCGCTATGGGAAA | 2170 |
| Db | 2133 | CTCTATGGGGCACCGAGATPAACATCTCTCAGTGAACAGAGTTGCAAGGCGCTATGGGAAA | 2192 |
| Qy | 2171 | TGCGTGAATGGATTATCTTCAGCTTGTTAGCTTCTPAAGTTCTTTCCCTTCATTCTAAC | 2230 |
| Db | 2193 | TGCGTGAATGGATTATCTTCAGCTTGTTAGCTTCTPAAGTTCTTTCCCTTCATTCTAAC | 2252 |
| Qy | 2231 | CTGCAGCGCAAGTTCTGTGAAGAAATGCCGATTCAGCTCAGGTTTCTTACTCTGA | 2290 |
| Db | 2253 | CTGCAGCGCAAGTTCTGTGAAGAAATGCCGATTCAGCTCAGGTTTCTTACTCTGA | 2312 |
| Qy | 2291 | ATTATGATCTTCAGACCCTTCTGCGCACAAATTGAAATTAGGCAACAAATATACCTT | 2350 |
| Db | 2313 | ATTATGATCTTCAGACCCTTCTGCGCACAAATTGAAATTAGGCAACAAATATACCTT | 2372 |
| Qy | 2351 | CCATGAACGACACACAGACTTTTGAAGCAAGCAATGACTGCTGTAATTAGGCGCTTG | 2410 |
| Db | 2373 | CCATGAACGACACACAGACTTTTGAAGCAAGCAATGACTGCTGTAATTAGGCGCGTTG | 2432 |
| Qy | 2411 | AGGAATGAAGCTTTGAAGGAAAGAATACTTGTTCAGGCGCCCTTCCACACTCTTCA | 2470 |
| Db | 2433 | AGGAATGAAGCTTTGAAGGAAAGAATACTTGTTCAGGCGCCCTTCCACACTCTTCA | 2492 |
| Qy | 2471 | TGTGTTAAACAACCTGCTTCTGGAACCTTGAAGCACGGTGACTGTATTCATGTTGTAT | 2530 |
| Db | 2493 | TGTGTTAAACAACCTGCTTCTGGAACCTTGAAGCACGGTGACTGTATTCATGTTGTAT | 2552 |
| Qy | 2531 | AGAAAACGATTTAGAGTTCTGATCGTTCAAGGAATGATTAATATACATTTCTT | 2587 |
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| | | | | |
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| LOCUS | Sequence 391 from patent US 6468546. | | | PAT 20-DEC-2002 |
| DEFINITION | AR238405 | | | |
| ACCESSION | AR238405 | | | |
| VERSION | AR238405.1 | GI:27283369 | | |
| KEYWORDS | | | | |
| SOURCE | Unknown. | | | |
| ORGANISM | Unknown. | | | |
| REFERENCE | 1 (bases 1 to 2627) | | | |
| AUTHORS | Mitcham, J.L., King, G.E. and Algate, P.A. | | | |
| TITLE | Compositions and methods for therapy and diagnosis of ovarian | | | |
| JOURNAL | "Cancer | | | |
| FEATURES | Patent: US 6468546-A 391 22-OCT-2002; | | | |
| source | Location/Qualifiers | | | |
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| ORIGIN | | | | |

| Query Match | Similarity | Score | DB # | Length |
|--------------|--------------|-----------------------------------------------------------|--------------|------------------|
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| Matches 2576 | Conservative | 0 | Mismatches 0 | Indels 1, Gaps 1 |
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| DB | 33 | GGCACTTCATCTCAGCCAGTACCCAGATACCTGGGAACTTCCCGACCATGGCTTCC | 92 | |
| QY | 72 | TGGGCGAGATCCTCTTGGAGCATAAATTAGCATCATCTATTCTGGCTGGAGCAATTG | 131 | |
| DB | 93 | TGGGCGATCCTCTTGGAGCATAAATTAGCATCATCTATTCTGGCTGGAGCAATTG | 152 | |
| QY | 132 | CATCATATTGGCTTGGTATTTCAGGAGACATCATACAGTACTACTCTGGCT | 191 | |
| DB | 153 | CATCATATTGGCTTGGTATTTCAGGAGACATCATACAGTACTACTCTGGCT | 212 | |

Qy 192 CAGCTGGGAACATTTGGGAGATGGAATCCTGAGCTGACCTTTTGAACCTGACATCAAC 251
| | | | |
Db 213 CAGCTGGGAACATTTGGGAGATGGAATCCTGAGCTGACCTTTTGAACCTGACATCAAC 272
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Qy 252 TTTCTGATATCGATATCAATGCTGGAAGAGGTGTTTAAAGCTTGCTGATGAGTTCA 311
| | | | |
Db 273 TTTCTGATATCGATATCAATGCTGGAAGAGGTGTTTAAAGCTTGCTGATGAGTTCA 332
| | | | |
Qy 312 AAGAGGCAAGATGAGCTGCGGAGAGAGATGAAATGTTCAAGGCGCGGACAGAGTGT 371
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Db 333 AAGAGGCAAGATGAGCTGCGGAGAGAGATGAAATGTTCAAGGCGCGGACAGAGTGT 392
| | | | |
Qy 372 TTGCTGATCAAGTATAGTTGGCAATGCTTTTGCGGCTGAAAAAGTGCATCTCAG 431
| | | | |
Db 393 TTGCTGATCAAGTATAGTTGGCAATGCTTTTGCGGCTGAAAAAGTGCATCTCAG 452
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Qy 552 AGACCTTGCGGTGAGAGCTCCCGATGTTCCCGCAGCCACAGTGTCTGGGCAATCCC 611
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AR478744 2627 bp DNA linear PAT 14-MAY-2004
LOCUS AR478744
DEFINITION Sequence 391 from patent US 6699664.
ACCESSION AR478744
VERSION AR478744.1 GI:47237396
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W.,
Ranger,G.R., Reed,S.G., Veldrick,T.S. and Carter,D.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: US 6699664-A 391 02-MAR-2004;
FEATURES
source Location/Qualifiers
1. 2627
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ORIGIN
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Db 1413 AGACGCTGTAATTAAGCTGCACTTGCACACTCAGGAGGCGGCTGATTTAGTAATGGT 1472
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DEFINITION Sequence 207 from Patent WO0140269.
ACCESSION AX156350

VERSION AX156350.1 GI:14537350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wang, A., Day, C. H., Jiang, Y., Houghton, R. L., Mitcham, J. L. and
TITLE Compositions and methods for therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0140269-A 207 07-JUN-2001;
FEATURES CORIXA CORPORATION (US)
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| SOURCE | | | |
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| REFERENCE | | | |
| AUTHORS | | | 1 Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W., |
| | | | Fanger,G.R., Reed,S.G., Vedvick,T.S., Carter,D., Hill,P. and |
| | | | Albone,E. |
| | | | Compositions and methods for the therapy and diagnosis of ovarian |
| | | | cancer |
| | | | Patent: WO 0206317-A 391 24-JAN-2002; |
| JOURNAL | | | CORIXA CORPORATION (US) |
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LOCUS AX403048
DEFINITION Sequence 1 from Patent WO0202624.
ACCESSION AX403048
VERSION AX403048.1 GI:21388028
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. Fox, G., Sullivan, J.K. and Fang, M.
AUTHORS B7-like molecules and uses thereof
TITLE Patent: WO 0202624-A 1 10-JAN-2002;
JOURNAL Amgen, Inc. (US)
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ORIGIN

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 DEFINITION Sequence 7 from Patent WO0194641.
 ACCESSION AX375860
 VERSION AX375860.1 GI:19170332
 KEYWORDS
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 ORGANISM Homo sapiens
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 REFERENCE 1
 Ople, E., McLachlan, K. and Heard, C.
 Gene targets and ligands that bind thereto for treatment and
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 Patent: WO 0194641-A 7 13-DEC-2001;
 JOURNAL Idec Pharmaceuticals Corporation (US)
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REFERENCE 1 (bases 1 to 2671)
AUTHORS Pouscka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
Mewes, H.W., Weil, B., Amid, C., Obanger, A., Fodor, G., Han, M. and
Wiemann, S.
CONSTRM The German Human cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuberberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp79B1717) is available at the RZPD in Berlin.
Please contact the RZPD: Resourcenzentrum, Heuberweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.
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RESULT 10
HS11025A1
LOCUS
DEFINITION
Human DNA sequence from clone RPS-1025A1 on chromosome
20p11.21-11.23 Contains part of a novel gene (similar to
acetyl-coenzyme A synthetase), part of a novel gene (similar to
paired-like homobox protein), ESTs, STSs, GSSs and Cpg Islands,
complete sequence.
ACCESSION
AL080312
VERSION
AL080312.14 GI:6630798
KEYWORDS
HTG; Cpg Island.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 94664)
REFERENCE
Bates, K.
Direct Submission
Submitted (20-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Dec 22, 1999 this sequence version replaced gi:6541398.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unSURE'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
RPS-1025A1 is from the library RPS-5 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong. For further details see
http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
RPS-1025A1 it may be shorter because we only sequence overlapping
sections once, or longer because we arrange for a small overlap
between neighbouring submissions.
The true left end of clone RPS-738P15 is at 94565 in this sequence.
The right end of clone RPS-568C11 is at 104 in this sequence.
This sequence was generated from part of bacterial clone contigs of
human chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20.
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CDS 3088. .3287,20390. .20510,29609. .30431)
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/note="MIR repeat: matches 117. .189 of consensus"
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repeat_region 13308. .13604
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| Best Local Similarity | 92.9%; Pred. No. 0; | |
| Matches 2328; Conservative | 0; Mismatches 160; Indels 18; Gaps 6; | |
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LOCUS CO412191 1965 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 19262 from Patent WO0170979.
ACCESSION CO412191
VERSION CO412191.1 GI:41319972
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Lee,J. and Lillie,J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 19262 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1933; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Db 1950 TCTCCCATTAACAC 1964

RESULT 12
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LOCUS Human DNA sequence from clone RP11-229A19 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL391476
VERSION AL391476.20 GI:15131484
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 171595)
AUTHORS Wallis, J.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
Requesters: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:14970375.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Bm: EMBL; Sw:
SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human

Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP11-229A19 is from the library RPI1-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
This sequence is the entire insert of clone RP11-229A19 The true
left end of clone RP11-287H7 is at 67254 in this sequence. The true
right end of clone RP4-570D9 is at 57439 in this sequence.

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| 2392..2668 | |
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| 3758..4064 | |
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| 5330..5607 | |
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| 7287..7593 | |
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| /note="MADE1 repeat: matches 31..80 of consensus" | |
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1631; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy      2452 CCCCTTCCCACTCTTCATGTTGTTAAACACTGSCCTTCCGAGCCTTGAAGCCAGGTTGA 2511
Db      80790 CCCCTTCCCACTCTTCATGTTGTTAAACACTGSCCTTCCGAGCCTTGAAGCCAGGTTGA 80731
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VERSION
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KEYWORDS
SOURCE
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
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AUTHORS
Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakie, P.,
Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
TITLE
Compositions and methods for the diagnosis and treatment of tumor
JOURNAL
Patent: EP 1445317-A 3 11-AUG-2004;
Genentech Inc. (US)
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AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
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1 Baton,D.L., Filvaroff,E., Gerlitsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
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| 34 | 1599.8 | 61.8 | 1658 | 8 | ACD1891 | ACD1891 | Human sec |
| 35 | 1599.8 | 61.8 | 1658 | 8 | ACD13056 | ACD13056 | Human sec |
| 36 | 1599.8 | 61.8 | 1658 | 8 | ACD25159 | ACD25159 | Human sec |
| 37 | 1599.8 | 61.8 | 1658 | 8 | ACF00208 | ACF00208 | Human sec |
| 38 | 1599.8 | 61.8 | 1658 | 8 | ACA60392 | ACA60392 | Novel hum |
| 39 | 1599.8 | 61.8 | 1658 | 8 | ACA72265 | ACA72265 | Novel hum |
| 40 | 1599.8 | 61.8 | 1658 | 8 | ACD04789 | ACD04789 | Novel hum |
| 41 | 1599.8 | 61.8 | 1658 | 8 | ACD18250 | ACD18250 | Human sec |
| 42 | 1599.8 | 61.8 | 1658 | 8 | ACD08257 | ACD08257 | Human sec |
| 43 | 1599.8 | 61.8 | 1658 | 8 | ACA88691 | ACA88691 | Novel hum |
| 44 | 1599.8 | 61.8 | 1658 | 8 | ACA70133 | ACA70133 | Human sec |
| 45 | 1599.8 | 61.8 | 1658 | 8 | ACD12355 | ACD12355 | Novel hum |

ALIGNMENTS

RESULT 1
AAZ90470
ID AAZ90470 standard; cDNA; 2587 BP.
XX
XX AAZ90470;
AC
XX
DT 06-JUN-2000 (first entry)
XX
DE Cancer specific gene (CSG) sequence (clone ID 16656542).
XX
XX CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
KM endometrial; uterine; lung; cytotoxic; ss.
XX
OS Homo sapiens.
XX
XX
XX W0200012758-A1.
XX
XX 09-MAR-2000.
XX
XX 01-SEP-1999; 99WO-US019655.
XX
XX 02-SEP-1998; 98US-0098880P.
XX
XX (DIAD-) DIADEXUS LLC.
XX
XX Salceda S, Sun Y, Recipon H, Cafferkey R;
XX WPI; 2000-256657/22.
XX
PT Diagnosing, staging, monitoring, imaging and treating cancer especially
PT gynecological cancers e.g. breast, ovarian cancer and lung cancer.
PT involves measuring cancer specific gene levels in cells and body fluids.
XX
XX Claim 9; Page 44-45; 58pp; English.
XX
XX The invention relates to detecting, diagnosing metastasis and staging
XX cancer by measuring levels of cancer specific genes (CSG) in cells,
XX tissues or body fluids. Their remission and progression, decreases and
XX increases in CSG levels, is also monitored, by periodic sample analysis.
XX The methods are useful for detecting cancers, especially gynecologic
XX cancers which include ovarian, breast, endometrial and uterine cancer and
XX lung cancer. Antibodies against the CSBs labeled with paramagnetic ions
XX or a radioisotope is useful for imaging cancer and when conjugated with a

CC cytotoxic agent are useful for treating cancer. The present sequence
CC represents a CSG sequence (clone ID: 1656542 and gene ID: 234617)
XX
SQ Sequence 2587 BP; 737 A; 568 C; 580 G; 682 T; 0 U; 0 Other;


```
Db 2041 TTTCACATTAGTCAATTCATGGAATTAAGCATTTCTGTCTTTGGTGTGCTGACGACAG 2100
Qy 2101 AGAGCCGAACCTATGTGGGACCAAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGC 2160
Db 2101 AGAGCCGAACCTATGTGGGACCAAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGC 2160
Qy 2161 CTATGGGAATGCGCTGATGGGATTAATCTTCAAGCTGTGTGAGCTTCTAAGTTCTTCCCT 2220
Db 2161 CTATGGGAATGCGCTGATGGGATTAATCTTCAAGCTGTGTGAGCTTCTAAGTTCTTCCCT 2220
Qy 2221 TCATTTACCCCTGCAAGCCAAAGTTCTGTAAAGAAATGCGTGAAGTTCTAGCTCAGGTTT 2280
Db 2221 TCATTTACCCCTGCAAGCCAAAGTTCTGTAAAGAAATGCGTGAAGTTCTAGCTCAGGTTT 2280
Qy 2281 CTATCTGTGAATTTAGATCTTCAGACCCCTCTGGCCAAATTCAAATTAAGCAACAA 2340
Db 2281 CTATCTGTGAATTTAGATCTTCAGACCCCTCTGGCCAAATTCAAATTAAGCAACAA 2340
Qy 2341 CATATACCTTCATGAAGACACACAGACTTTTGAAGCAAGACATGACTGTGAAT 2400
Db 2341 CATATACCTTCATGAAGACACACAGACTTTTGAAGCAAGACATGACTGTGAAT 2400
Qy 2401 TGAAGCCTTGAGGAATGAAGCTTTGAAGAAAGAAATACTTTGTTCCAGCCCTTCCC 2460
Db 2401 TGAAGCCTTGAGGAATGAAGCTTTGAAGAAAGAAATACTTTGTTCCAGCCCTTCCC 2460
Qy 2461 ACACTCTTCATGTGTAAACAACCTGCTTCTTGAAGCCAGGTGATGATTAAC 2520
Db 2461 ACACTCTTCATGTGTAAACAACCTGCTTCTTGAAGCCAGGTGATGATTAAC 2520
Qy 2521 ATGTGTATAGAAACCTGATTTTGAAGTTCTGATGCTTGAAGAAATGATTAATTAAC 2580
Db 2521 ATGTGTATAGAAACCTGATTTTGAAGTTCTGATGCTTGAAGAAATGATTAATTAAC 2580
Qy 2581 ATTTCT 2587
Db 2581 ATTTCT 2587

RESULT 2
AAA70077
ID AAA70077 standard; cDNA; 2627 BP.
XX
AC AAA70077;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide seq ID NO:391.
XX
KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN MO200036107-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99MO-US030270.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Frudakis TN;
XX
DR MPI; 2000-431589/37.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
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PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
PS Claim 1; Page 204-205; 299pp; English.
XX
CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AA069691 to AA070077 and AB012552 to AB012557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
XX exemplification of the present invention
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
XX
Query Match 99.1%; Score 2565; DB 3; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GCGAGCTCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCAGCCATGCTTCCC 71
Db 33 GCGAGCTCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCAGCCATGCTTCCC 92
Qy 72 TGGGGAGATTCCTCTTCTGAGATTAATAGATCAATCAATTTCTGCTGGAGCAATTG 131
Db 93 TGGGGAGATTCCTCTTCTGAGATTAATAGATCAATCAATTTCTGCTGGAGCAATTG 152
Qy 132 CACTCATCATTTGGCTTTGGATTTTCAAGGAGACATCCATCAGTCACTAGTGGCT 191
Db 153 CACTCATCATTTGGCTTTGGATTTTCAAGGAGACATCCATCAGTCACTAGTGGCT 212
Qy 192 CAGCTGGGAACATTTGGGAGAGATGAATCTGAGCTGCACTTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGGAACATTTGGGAGAGATGAATCTGAGCTGCACTTTTGAACCTGACATCAAC 272
Qy 252 TTTCTGATATCGTATACATATGCTGTAAGAAAGCTTTTGAAGCTTGTGCAATGTTCA 311
Db 273 TTTCTGATATCGTATACATATGCTGTAAGAAAGCTTTTGAAGCTTGTGCAATGTTCA 332
Qy 312 AAGAAGCAAAAGTGAAGTGTGCGAGCAGAGATGAATGTTTCAAGAGCCGAGACAGATGT 371
Db 333 AAGAAGCAAAAGTGAAGTGTGCGAGCAGAGATGAATGTTTCAAGAGCCGAGACAGATGT 392
Qy 372 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTGCGGCTGAAGAAAGTGAACCTCAG 431
Db 393 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTGCGGCTGAAGAAAGTGAACCTCAG 452
Qy 432 ATGCTGGCACCTTCAAAATGTTATATGATCACTTTTAAAGCAAGGGAATGCTTAACCTTG 491
Db 453 ATGCTGGCACCTTCAAAATGTTATATGATCACTTTTAAAGCAAGGGAATGCTTAACCTTG 512
Qy 492 AGTATAAACTGGAAGCTTCAGATGCGGGAAGTGAATGGAAGTGAATGGAAGTGAAGTGA 551
Db 513 AGTATAAACTGGAAGCTTCAGATGCGGGAAGTGAATGGAAGTGAATGGAAGTGAAGTGA 572
Qy 552 AGACCTTGGGATGTGAAGCTCCCGATGTTCCCGAGGCCAAGTGTCTGGGCAATCCC 611
Db 573 AGACCTTGGGATGTGAAGCTCCCGATGTTCCCGAGGCCAAGTGTCTGGGCAATCCC 632
Qy 612 AAGTTGACCAAGGAGCACTTCTCGGAAGTCTTCAATTCAGAGTTTGAAGCTGAACCTTG 671
Db 633 AAGTTGACCAAGGAGCACTTCTCGGAAGTCTTCAATTCAGAGTTTGAAGCTGAACCTTG 692
Qy 672 AGAATGTGACATGAAGTGTGTCTGTGCTCTCAATGTTTGAAGTGAAGTGAAGTGAAGTGA 731
Db 693 AGAATGTGACATGAAGTGTGTCTGTGCTCTCAATGTTTGAAGTGAAGTGAAGTGAAGTGA 752
Qy 732 CCTGTATGATTAAGAAATGAATGATTCGAAGCAAGGGATATCAAGTGAAGCAATCGG 791
Db 753 CCTGTATGATTAAGAAATGAATGATTCGAAGCAAGGGATATCAAGTGAAGCAAGATCGG 812
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| | | | |
|----|------|----------------------------------------------------------------|------|
| OY | 792 | AGATCAAAAGCGGAGTCACTACAGCTGCTAACTCAAAGGCTTCTGTGTCTCTT | 851 |
| Db | 813 | AGATCAAAAGCGGAGTCACTACAGCTGCTAACTCAAAGGCTTCTGTGTCTCTT | 872 |
| OY | 852 | CTTTCCTTGCATCAGCTGGGCACTTCTGCCTCAGCCCTTACCTGATGTAAATAT | 911 |
| Db | 873 | CTTTCCTTGCATCAGCTGGGCACTTCTGCCTCAGCCCTTACCTGATGTAAATAT | 932 |
| OY | 912 | GTGCCTTGGCCACAAAAGCATGCAAGTGTTCACACAGGATCTACAGAACTAT | 971 |
| Db | 933 | GTGCCTTGGCCACAAAAGCATGCAAGTGTTCACACAGGATCTACAGAACTAT | 992 |
| OY | 972 | TTCAACACCAATATGACCTGATTATATTTCTGGAGGAATGAATTCATATCTGAA | 1031 |
| Db | 993 | TTCAACACCAATATGACCTGATTATATTTCTGGAGGAATGAATTCATATCTGAA | 1052 |
| OY | 1032 | GTCTGGAGTGAAGCAAAAGAGCAAGAAACAAAAGCCAAAAGCAGAGGCTCAAT | 1091 |
| Db | 1053 | GTCTGGAGTGAAGCAAAAGAGCAAGAAACAAAAGCCAAAAGCAGAGGCTCAAT | 1112 |
| OY | 1092 | ATGAACAAGATPAATCTATCTTCAAGAATATTAGAAATTGGGAAATTAATCATGTGA | 1151 |
| Db | 1113 | ATGAACAAGATPAATCTATCTTCAAGAATATTAGAAATTGGGAAATTAATCATGTGA | 1172 |
| OY | 1152 | ACTAGACAAGTGTGTTAAGTATAGTAAATATGACAGTGGAGACAAGTGCATCCCG | 1211 |
| Db | 1173 | ACTAGACAAGTGTGTTAAGTATAGTAAATATGACAGTGGAGACAAGTGCATCCCG | 1232 |
| OY | 1212 | ATCTCAGGGAAGCTCCCGCTGCCTGCCTGCACCTTGAGGAGTGAAGACAAGTATGTCATGTT | 1271 |
| Db | 1233 | ATCTCAGGGAAGCTCCCGCTGCCTGCCTGCACCTTGAGGAGTGAAGACAAGTATGTCATGTT | 1292 |
| OY | 1272 | CTTGTGTCTGTGAATTTTATGTTATATGTCTGTATATGTTGCTTGAGGAAGCCCTGAA | 1331 |
| Db | 1293 | CTTGTGTCTGTGAATTTTATGTTATATGTCTGTATATGTTGCTTGAGGAAGCCCTGAA | 1352 |
| OY | 1332 | AGTCTATCCCAATATCCACATCTTATATATTCACAATTAAGCTGTATGTATACCTA | 1391 |
| Db | 1353 | AGTCTATCCCAATATCCACATCTTATATATTCACAATTAAGCTGTATGTATACCTA | 1412 |
| OY | 1392 | AGAGCTGCTAATTGACCTGCCACTTGGCACTCAGGGCGGCTGCAATTTATGATGGGT | 1451 |
| Db | 1413 | AGAGCTGCTAATTGACCTGCCACTTGGCACTCAGGGCGGCTGCAATTTATGATGGGT | 1472 |
| OY | 1452 | CAAAATGATTCCTTTTATGATGCTTCCAAAGTGCCCTTGCTTCCCACTGACA | 1511 |
| Db | 1473 | CAAAATGATTCCTTTTATGATGCTTCCAAAGTGCCCTTGCTTCCCACTGACA | 1532 |
| OY | 1512 | AATGCCAAAAGTTGAGAAAATGATCTATATTTTATGACATTAACAGAGCAGTGGGACAC | 1571 |
| Db | 1533 | AATGCCAAAAGTTGAGAAAATGATCTATATTTTATGACATTAACAGAGCAGTGGGACAC | 1592 |
| OY | 1572 | GATTTTATTAATTAACCTGAGCACTCTTTTAAACAAAGTCGGGTTTATTTCTCA | 1631 |
| Db | 1593 | GATTTTATTAATTAACCTGAGCACTCTTTTAAACAAAGTCGGGTTTATTTCTCA | 1652 |
| OY | 1632 | GATGATGTTCACTCCGTGATGGTCCAGGGAAGACCTTTCACCTTGACTATATGACATTA | 1691 |
| Db | 1653 | GATGATGTTCACTCCGTGATGGTCCAGGGAAGACCTTTCACCTTGACTATATGACATTA | 1712 |
| OY | 1692 | TGTCTATCAACAAGCTCTGAGGCTTCTCTTTTCATCTGCGGTGGACACTAAGACTCAGT | 1751 |
| Db | 1713 | TGTCTATCAACAAGCTCTGAGGCTTCTCTTTTCATCTGCGGTGGACACTAAGACTCAGT | 1772 |
| OY | 1752 | TTTCAATATGACATTAAGAGGGAAGTCAAGTGGGGATTTTGCCCCCATCTCCGGG | 1811 |
| Db | 1773 | TTTCAATATGACATTAAGAGGGAAGTCAAGTGGGGATTTTGCCCCCATCTCCGGG | 1832 |
| OY | 1812 | GGAATGTCTGAAGACAATTTTGTGTTAAGCTCAATGAGGAGTGGAGAGATACAGTCTA | 1871 |
| Db | 1833 | GGAATGTCTGAAGACAATTTTGTGTTAAGCTCAATGAGGAGTGGAGAGATACAGTCTA | 1892 |
| OY | 1872 | CTACCACTAATGATTAAGGCAAGGATGCTGCTCAACCTTCTCACTGACAGACGT | 1931 |

| | | | |
|----------|-------------------------------|--------------------------------------------------------------------------|------|
| Db | 1893 | CTACCACTAGTGGATTAAAGGCCAGAGATGCTGCTCAACCTCTACCATGTATACAGAGAGT | 1955 |
| Qy | 1932 | CTCCCATTTACCACTACCCAAATCCGAAGTGTCAACTGTGCAGAGCTAAGAAACCTGGT | 1994 |
| Db | 1953 | CTCCCATTTACCACTACCCAAATCCGAAGTGTCAACTGTGTGACAGACTAAGAAACCTGGT | 2012 |
| Qy | 1992 | TTTGAAGTGAAGAAAGGGCCTGGAAAGAGGGAGCCAAAGAAATCTGTCTCTT-CTCAAGTT | 2050 |
| Db | 2013 | TTTGAAGTGAAGAAAGGGCCTGGAAAGAGGGAGCCAAAGAAATCTGTCTCTTCTTCAAT | 2072 |
| Qy | 2051 | AGTCATTGGCAAAATTAAGCATTCTGTCTTTGGCTGTGCTCTCAGCAAGAGAGCCAGAA | 2110 |
| Db | 2073 | AGTCATTGGCAAAATTAAGCATTCTGTCTTTGGCTGTGCTCTCAGCAAGAGAGCCAGAA | 2130 |
| Qy | 2111 | CTCTATCGGGGACACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTTAGGAAA | 2170 |
| Db | 2133 | CTCTATCGGGGACACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTTAGGAAA | 2192 |
| Qy | 2171 | TGCTGTATGGAGTTATCTTCAAGCTTTGTAGACTTTAAGTTTCTTCCCTCATTTAC | 2230 |
| Db | 2193 | TGCTGTATGGAGTTATCTTCAAGCTTTGTAGACTTTAAGTTTCTTCCCTCATTTAC | 2250 |
| Qy | 2231 | CTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA | 2290 |
| Db | 2253 | CTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA | 2312 |
| Qy | 2291 | ATTTAGATCTCCAGACCTTCTGCGCACAATTCAAATTAAGCAACAAATATACCTT | 2350 |
| Db | 2313 | ATTTAGATCTCCAGACCTTCTGCGCCACAAATTCAAATTAAGCAACAAATATACCTT | 2372 |
| Qy | 2351 | CCATGAAGCAACACAGACTTTTGAAGCAAGACAAATGACCTGTGAATTGAGGCCCTTG | 2411 |
| Db | 2373 | CCATGAAGCAACACAGACTTTTGAAGCAAGACAAATGACCTGTGAATTGAGGCCCTTG | 2433 |
| Qy | 2411 | AGGAATGAAGCTTTGAAGAAAGAAATTACTTTGTTTCAGGCCCTTCCACACTCTTCA | 2470 |
| Db | 2433 | AGGAATGAAGCTTTGAAGAAAGAAATTACTTTGTTTCAGGCCCTTCCACACTCTTCA | 2492 |
| Qy | 2471 | TGTGTTAACCACTGCTTCTTGAGACTTGAAGCCACGGTGACTGTATTACATGTTGTTAT | 2530 |
| Db | 2493 | TGTGTTAACCACTGCTTCTTGAGACTTGAAGCCACGGTGACTGTATTACATGTTGTTAT | 2552 |
| Qy | 2531 | AGAAACCTGATTTTGAAGTTCTGATCGTTCAAGAGATGATTTAAATATACATTTCTT | 2587 |
| Db | 2553 | AGAAACCTGATTTTGAAGTTCTGATCGTTCAAGAGATGATTTAAATATACATTTCTT | 2609 |
| RESULT 3 | | | |
| AAH55681 | | | |
| ID | AAH55681 | standard; DNA; 2627 BP. | |
| AC | AAH55681; | | |
| DT | 04-SEP-2001 | (first entry) | |
| DE | | Human ovarian tumour-derived antigen O8E DNA sequence. | |
| XX | | | |
| KW | | Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour; | |
| XX | | antigen; O8E; ds. | |
| OS | | Homosapiens. | |
| PN | WO200140269-A2. | | |
| PD | 07-JUN-2001. | | |
| PF | 29-NOV-2000; 2000WO-US032520. | | |
| XX | | | |
| PR | 30-NOV-1999; 99US-00451651. | | |
| PR | 22-FEB-2000; 2000US-00510662. | | |
| PR | 10-MAR-2000; 2000US-00523586. | | |
| PR | 07-APR-2000; 2000US-00545068. | | |

PR 15-MAY-2000; 2000US-00571025.
 XX (CORI-) CORIXA CORP.
 XX Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
 XX WPI; 2001-356154/37.
 XX DR N-PSDB; AAB99204, AAB99205.
 XX
 XX Breat tumor polypeptides and the nucleic acids that encode them, useful
 PT for the prevention, diagnosis and treatment of breast cancer.
 XX
 XX Claim 24; Page 189; 221pp; English.
 XX
 XX The present invention relates to human breast tumour protein coding
 CC sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-
 CC AAH55762). The breast tumour protein DNA sequences may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the breast tumour protein e.g. breast cancer.
 CC The present sequence is a human ovarian tumour-derived antigen coding
 CC sequence, which was used in an example from the present invention
 SQ
 SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
 Query Match 99.1%; Score 2565; DB 4; Length 2627;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 12 GGGAGCTCCACAGCAGCAGTACCCAGATACGCTGGAACTTCCCGCCAGCCATGGCTTCCC 71
 DB 33 GGGAGCTCCACAGCAGCAGTACCCAGATACGCTGGAACTTCCCGCCAGCCATGGCTTCCC 92
 QY 72 TGGGCGAGATCTCTTCTTGGAGCAATTAATGATCATCATATTATTCTGGCTGGAGCAATTG 131
 DB 93 TGGGCGAGATCTCTTCTTGGAGCAATTAATGATCATCATATTATTCTGGCTGGAGCAATTG 152
 QY 132 CACTCATCATTTGGCTTTGGATTTTCAGGGAGACATCTCAGTACAGTACTAGTGGCTT 191
 DB 153 CACTCATCATTTGGCTTTGGATTTTCAGGGAGACATCTCAGTACAGTACTAGTGGCTT 212
 QY 192 CAGCTGGGAACATTTGGGAGATGGAATCTTGAGCTGCACTTTTGAACCTGATCAATCAAC 251
 DB 213 CAGCTGGGAACATTTGGGAGATGGAATCTTGAGCTGCACTTTTGAACCTGATCAATCAAC 272
 QY 252 TTTTCTGATTCGTGATTCATATGCTGGAAGGAGGTGTTTAAAGCTTGCTCATGAGTTCA 311
 DB 273 TTTTCTGATTCGTGATTCATATGCTGGAAGGAGGTGTTTAAAGCTTGCTCATGAGTTCA 332
 QY 312 AAGAAGGCAAGATGAGCTCTCGGAGAGATGAAAATGTTCAAGGCGCGGACAGCAGTGT 371
 DB 333 AAGAAGGCAAGATGAGCTCTCGGAGAGATGAAAATGTTCAAGGCGCGGACAGCAGTGT 392
 QY 372 TTGCTGATCAAGTATGATGGAATGCTCTTTGCGGCTGAAAAAGTCAATCTCAG 431
 DB 393 TTGCTGATCAAGTATGATGGAATGCTCTTTGCGGCTGAAAAAGTCAATCTCAG 452
 QY 432 ATGCTGGACCTTCAAAATGTTATATCATCTTTAAAGGCAAGGGAATGCTTAACTTGG 491
 DB 453 ATGCTGGACCTTCAAAATGTTATATCATCTTTAAAGGCAAGGGAATGCTTAACTTGG 512
 QY 492 AGATTAATAAATGAGACCTTTCAGCATGCGGGAAGGAAATGGAATTAATGCAAGCTCAG 551
 DB 513 AGATTAATAAATGAGACCTTTCAGCATGCGGGAAGGAAATGGAATTAATGCAAGCTCAG 572
 QY 552 AGACCTTTCGAGTGAAGGCTCCCGGATGTTCCCGGACCAAGTGGTCTGGGCAATCCC 611
 DB 573 AGACCTTTCGAGTGAAGGCTCCCGGATGTTCCCGGACCAAGTGGTCTGGGCAATCCC 632
 QY 612 AAGTTGACCAAGGAGCACTTTCGGAAGTCTTCAATACCAAGTTTGAAGTGAATCTG 671
 DB 633 AAGTTGACCAAGGAGCACTTTCGGAAGTCTTCAATACCAAGTTTGAAGTGAATCTG 692
 QY 672 AGATGTGACCAATGAAGGTTGTGTGTGCTTCAATGTTAAGATGAACAACATCACT 731

DB 693 AGAATGTGACCAATGAAGGTTGTGTGTGCTCTGATGTTACATGTTACCAACAACATCACT 752
 QY 732 CCTGTATGATTTGAAAAATGACATTTGCCAAGCAACAGGGGATATCAAAAGTGAAGAATCCG 791
 DB 753 CCTGTATGATTTGAAAAATGACATTTGCCAAGCAACAGGGGATATCAAAAGTGAAGAATCCG 812
 QY 792 AGATCAAAAGGGGAGCTCCTACAGCTGCTAAACCTCAAAAGGCTTCTGTGTGCTCTT 851
 DB 813 AGATCAAAAGGGGAGCTCCTACAGCTGCTAAACCTCAAAAGGCTTCTGTGTGCTCTT 872
 QY 852 CTTTCTTTGCCATCACTGAGGCACTTCTGCTCTCAGCCCTTACCTGATGCTTAAATTAAT 911
 DB 873 CTTTCTTTGCCATCACTGAGGCACTTCTGCTCTCAGCCCTTACCTGATGCTTAAATTAAT 932
 QY 912 GTGCTTTGGCCACAAAAAAGCATGCAAGATCATTTTACACAGGATCTACGAACATAT 971
 DB 933 GTGCTTTGGCCACAAAAAAGCATGCAAGATCATTTTACACAGGATCTACGAACATAT 992
 QY 972 TTCACACAGATATGACCTAGTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAA 1031
 DB 993 TTCACACAGATATGACCTAGTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAA 1052
 QY 1032 GTCTGAGTGAAGCAACAAAGCAAGAAACAAAAAGCCAAAGCCAGAGGCTCCAAT 1091
 DB 1053 GTCTGAGTGAAGCAACAAAGCAAGAAACAAAAAGCCAAAGCCAGAGGCTCCAAT 1112
 QY 1092 ATGAACAAGATTAATCTATCTTCAAGACATATTAGAGTTGGGAAATATATCATGTGA 1151
 DB 1113 ATGAACAAGATTAATCTATCTTCAAGACATATTAGAGTTGGGAAATATATCATGTGA 1172
 QY 1152 ACTAGCAAGTGTGTTAAGATGATAAGTAAATGACGTGAGACAAAGTGCATCTCCGAG 1211
 DB 1173 ACTAGCAAGTGTGTTAAGATGATAAGTAAATGACGTGAGACAAAGTGCATCTCCGAG 1232
 QY 1212 ATCTCAGGAGACCTCCCTGCTGCTCACTGGGAGTGAAGGACAGATAGTGCATGTT 1271
 DB 1233 ATCTCAGGAGACCTCCCTGCTGCTCACTGGGAGTGAAGGACAGATAGTGCATGTT 1292
 QY 1272 CTTTGTCTCTGAATTTTATGATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAA 1331
 DB 1293 CTTTGTCTCTGAATTTTATGATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAA 1352
 QY 1332 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTAGATCTACCTTA 1391
 DB 1353 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTAGATCTACCTTA 1412
 QY 1392 AGACGCTGCTAATTTGACTGCTCACTTGCACAACTCAGGGGCGGCTGCAATTTTAAATGGGT 1451
 DB 1413 AGACGCTGCTAATTTGACTGCTCACTTGCACAACTCAGGGGCGGCTGCAATTTTAAATGGGT 1472
 QY 1452 CAATGATTTCACTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1511
 DB 1473 CAATGATTTCACTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1532
 QY 1512 AATGCCAAAGTTGAGAAAAATGATCATTAATTTTGAATAAACAAGACAGTGGCGGACACC 1571
 DB 1533 AATGCCAAAGTTGAGAAAAATGATCATTAATTTTGAATAAACAAGACAGTGGCGGACACC 1592
 QY 1572 GATTTTATATAATTAACCTGAGACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1631
 DB 1593 GATTTTATATAATTAACCTGAGACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1652
 QY 1632 GATGATGTTTCATCTGGAATGCTGACAGGAAAGACCTTTTCACTTATATATGCAATTA 1691
 DB 1653 GATGATGTTTCATCTGGAATGCTGACAGGAAAGACCTTTTCACTTATATATGCAATTA 1712
 QY 1692 TGTGATCAAAAGCTCTGAAGCTTCTTCCATCTGCTGAGGAGAGCTTAAGACTCAGT 1751
 DB 1713 TGTGATCAAAAGCTCTGAAGCTTCTTCCATCTGCTGAGGAGAGCTTAAGACTCAGT 1772
 QY 1752 TTTCAATAGCATTTAAGCAGTGGACTCAGCTGGGATATTTCCGCCCACTTCGCGG 1811

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Db 1773 TTTCAATGATCATAGAGCAATGGGAGCTGAGCTGGGGTATTTTCGCCCCCATCTCCGGG 1832
Qy 1812 GGAATGTCTGAAGACAATTTTGGTTAATCTCAATGAGGAGTGGAGAGATCAATGCTGA 1871
Db 1833 GGAATGTCTGAAGACAATTTTGGTTAATCTCAATGAGGAGTGGAGAGATCAATGCTGA 1892
Qy 1872 CTACCAACTAGTGGATTAAGAGCCAGGGATGTCTCAACCTCTCAACATGTATGAGAGAGT 1931
Db 1893 CTACCAACTAGTGGATTAAGAGCCAGGGATGTCTCAACCTCTCAACATGTATGAGAGAGT 1952
Qy 1932 CTCCCATTTACAATCAATCCCAATCCGAAGTGTCAACTGTGTGAGAGCTTAAGAAACCTGTGT 1991
Db 1953 CTCCCATTTACAATCAATCCCAATCCGAAGTGTCAACTGTGTGAGAGCTTAAGAAACCTGTGT 2012
Qy 1992 TTTGAGTAAAAAGGGCTTGGAAAGGGGGAGCCCAAAATCTGTCTGTCTTCTCAAT 2050
Db 2013 TTTGAGTAAAAAGGGCTTGGAAAGGGGGAGCCCAAAATCTGTCTGTCTTCTCAAT 2072
Qy 2051 AGTCATTTGGCAAAATAGCAATCTGTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAA 2110
Db 2073 AGTCATTTGGCAAAATAGCAATCTGTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAA 2132
Qy 2111 CTCTATCGGGACACAGAGATTAATCTCTCAATGAGAGAGAGCTTGAAGAGCTTATGGGAA 2170
Db 2133 CTCTATCGGGACACAGAGATTAATCTCTCAATGAGAGAGAGCTTGAAGAGCTTATGGGAA 2192
Qy 2171 TGGCTGATGGGATTAATCTCTCAATGAGAGAGAGCTTGAAGAGCTTATGGGAA 2230
Db 2193 TGGCTGATGGGATTAATCTCTCAATGAGAGAGAGCTTGAAGAGCTTATGGGAA 2252
Qy 2231 CTGCAAGCCAAAGTTGTGAAGAGAAATGCTGAGTTCTAGCTCAGAGTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAAAGTTGTGAAGAGAAATGCTGAGTTCTAGCTCAGAGTTTCTTACTCTGA 2312
Qy 2291 ATTTAGATCTCCAGACCTTCTCTGAGCCACAAATTAAGGCAACAAATATACCTT 2350
Db 2313 ATTTAGATCTCCAGACCTTCTCTGAGCCACAAATTAAGGCAACAAATATACCTT 2372
Qy 2351 CCATGAGACACACAGAGCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2410
Db 2373 CCATGAGACACACAGAGCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2432
Qy 2411 AGGAATGAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2470
Db 2433 AGGAATGAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2492
Qy 2471 TGTGTTAACCACTGCTTCTGAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2530
Db 2493 TGTGTTAACCACTGCTTCTGAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2552
Qy 2531 AGAAACTGATTTTGAAGTTCTGATGCTCAAGAGAGATTAATAATCAATTTCT 2587
Db 2553 AGAAACTGATTTTGAAGTTCTGATGCTCAAGAGAGATTAATAATCAATTTCT 2609

RESULT 4
ABN72971
ID ABN72971 standard; DNA; 2627 BP.
XX
AC ABN72971;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ovarian carcinoma polynucleotide O8B.
XX
KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; de.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX
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PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00678857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Piling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill F, Albone E;
XX
DR WPI; 2002-164781/21.
XX
P-PsDB; ABP30900, ABP30901.
XX
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
PS Example 2; Page 319-320; 408pp; English.
XX
CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents DNA related
CC to the invention
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
XX
Query Match 99.1%; Score 2565; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 12 GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAACTTCCAGCCATGCTTCCC 71
Db 33 GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAACTTCCAGCCATGCTTCCC 92
Qy 72 TGGGCGAGATCTCTTCTGAGAGATTAATGATCAATATTTCTGGCTGGAGCAATTG 131
Db 93 TGGGCGAGATCTCTTCTGAGAGATTAATGATCAATATTTCTGGCTGGAGCAATTG 152
Qy 122 CACTCATATGAGCTTGGTATTTTCAAGGAGACATCCATCAGTCACTATGCTGCT 191
Db 153 CACTCATATGAGCTTGGTATTTTCAAGGAGACATCCATCAGTCACTATGCTGCT 212
Qy 192 CAGCTGGGAACATTTGGGAGAGATGGAATCTGAGCTGACCTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGGAACATTTGGGAGAGATGGAATCTGAGCTGACCTTTGAACCTGACATCAAC 272
Qy 252 TTTCTGATATCGTATTAATGAGCTGAAAGAGTGTGTTAGCTTGGCTTCCATGAGTCA 311
Db 273 TTTCTGATATCGTATTAATGAGCTGAAAGAGTGTGTTAGCTTGGCTTGGCTGCA 332
Qy 312 AAGAGGCAAGAGATGAGCTGCGAGAGAGATGAATGTTCAAGAGCCGAGACAGAGTGT 371
Db 333 AAGAGGCAAGAGATGAGCTGCGAGAGAGATGAATGTTCAAGAGCCGAGACAGAGTGT 392
Qy 372 TTTGATATCAATGATGATTTGGCAATGCTCTTTGGCTGAGAAACCTGCAATCAAG 431
Db 393 TTTGATATCAATGATGATTTGGCAATGCTCTTTGGCTGAGAAACCTGCAATCAAG 452
Qy 432 ATGCTGGACCTTAAGATGTTATATCATCTTTCAAGGCAAGGGGAAATGTTAATCTTG 491
Db 453 ATGCTGGACCTTAAGATGTTATATCATCTTTCAAGGCAAGGGGAAATGTTAATCTTG 512
Qy 492 AGTATTAACCTGAGAGCTTCAAGCATGCGGAGAGATGATGAGATTAATGAGCTGAG 551
Db 513 AGTATTAACCTGAGAGCTTCAAGCATGCGGAGAGATGATGAGATTAATGAGCTGAG 572
Qy 552 AGACCTTGGGATGATGAGCTCCCGATGATTTCCCGACCCAGTGTGTTGGGATGCC 611
```

Db 573 AGACCTTGCGGTGAGGCTCCCGATGGTTCCTCCCGACCGCAGTGTGTGGGCATCTCC 632
Qy 612 AAGTTGACGAGGAGCCCACTTCTCGGAAGTCTCCATACCAAGTTTGAAGTCACTCTG 671
Db 633 AAGTTGACGAGGAGCCCACTTCTCGGAAGTCTCCATACCAAGTTTGAAGTCACTCTG 692
Qy 672 AGAATGACCATGAAGGTTGTGTCTGTGCTCTCAATGTGTAAGTCAAGACATACCT 731
Db 693 AGAATGACCATGAAGGTTGTGTCTGTGCTCTCAATGTGTAAGTCAAGACATACCT 752
Qy 732 CCTGTATGATGAAATAGACATTCGCAAGCAACAGGGATATCAAGATGACAGATCG 791
Db 753 CCGTATGATTTGAAATAGACATTCGCAAGCAACAGGGATATCAAGATGACAGATCG 812
Qy 792 AGATCAAAAGCGGAGTCACTACAGTGTCTAACTCAAGGCTTCTGTGTGTCTCT 851
Db 813 AGATCAAAAGCGGAGTCACTACAGTGTCTAACTCAAGGCTTCTGTGTGTCTCT 872
Qy 852 CTTTCTTTGGCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATAT 911
Db 873 CTTTCTTTGGCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATAT 932
Qy 912 GTGCTTTGGCACAAGAAAGCATGCAAGTCAATGTTTACAAAGGATCTACAGAACTAT 971
Db 933 GTGCTTTGGCACAAGAAAGCATGCAAGTCAATGTTTACAAAGGATCTACAGAACTAT 992
Qy 972 TTTACCAACGAGATATGACCTAGTTTATATTTCTGGAGAGAAATGAAATCTATCT 1031
Db 993 TTTACCAACGAGATATGACCTAGTTTATATTTCTGGAGAGAAATGAAATCTATCT 1052
Qy 1032 GTCTGGAGTAGGCAACCAAGCAGAAAGCAAAAGGCAAAAGGCAAGAGGCTCAAT 1091
Db 1053 GTCTGGAGTAGGCAACCAAGCAGAAAGCAAAAGGCAAAAGGCTCAAT 1112
Qy 1092 ATGACCAAGATTAATCTATCTTCAAGACATATTAGAAATGGGAAATATTCATGTGA 1151
Db 1113 ATGACCAAGATTAATCTATCTTCAAGACATATTAGAAATGGGAAATATTCATGTGA 1172
Qy 1152 ACTAGACAGTGTGTTAAGAGTATAGTAAATGCACTGTGAGACAAAGTCAATCCCG 1211
Db 1173 ACTAGACAGTGTGTTAAGAGTATAGTAAATGCACTGTGAGACAAAGTCAATCCCG 1232
Qy 1212 ATCTCAGGAGCTCCCCCTGCTGTGCTGAGGAGGAGAGAGACAGGATAGTCAAT 1271
Db 1233 ATCTCAGGAGCTCCCCCTGCTGTGCTGAGGAGGAGAGAGACAGGATAGTCAAT 1292
Qy 1272 CTTTGTCTCTGAATTTTGTATGTATGTGCTGTATGTGCTCTGAGGAAAGCCCTGGAA 1331
Db 1293 CTTTGTCTCTGAATTTTGTATGTATGTGCTGTATGTGCTCTGAGGAAAGCCCTGGAA 1352
Qy 1332 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATGTATACCTTA 1391
Db 1353 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATGTATACCTTA 1412
Qy 1392 AGAGCGTCTAATTTGATGCTGCACTGTGCACTGAGGGGCGGCTGCAATTTAGTAAGGCT 1451
Db 1413 AGAGCGTCTAATTTGATGCTGCACTGTGCACTGAGGGGCGGCTGCAATTTAGTAAGGCT 1472
Qy 1452 CAATGATTTCACTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGAC 1511
Db 1473 CAATGATTTCACTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGAC 1532
Qy 1512 AATGCCAAAGTTGAGAAAAATGATCATATTTTGAAGTAAACAGAGAGTGGCGACAC 1571
Db 1533 AATGCCAAAGTTGAGAAAAATGATCATATTTTGAAGTAAACAGAGAGTGGCGACAC 1592
Qy 1572 GATTTATATAATTAACCTGAGCACTTCTTTTAAACAAATGCGGGTTATTTCTCA 1631
Db 1593 GATTTATATAATTAACCTGAGCACTTCTTTTAAACAAATGCGGGTTATTTCTCA 1652
Qy 1632 GATGATGTTTCATCGTGAATGTCTCAGGGAAGACCTTTACCTGATATATGCAATTA 1691

Db 1653 GATGATGTTTCATCGTGAATGTCTCAGGGAAGACCTTTACCTGATATATGCAATTA 1712
Qy 1692 TGTTCATCAACAAGCTCTGAGGCTTCTCTTTCATCTCTGGGTGAGACGTAAAGCTCACT 1751
Db 1713 TGTTCATCAACAAGCTCTGAGGCTTCTCTTTCATCTCTGGGTGAGACGTAAAGCTCACT 1772
Qy 1752 TTTCAATAGCATATGAGAGCTGAGGAGTCAAGCTGAGGAGTATTTGGCCCCCATCTCGGG 1811
Db 1773 TTTCAATAGCATATGAGAGCTGAGGAGTCAAGCTGAGGAGTATTTGGCCCCCATCTCGGG 1832
Qy 1812 GGAATGTCTGAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGTCTTA 1871
Db 1833 GGAATGTCTGAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGTCTTA 1892
Qy 1872 CTACCAACTAGTGAATTAAGGAGGAGAGTGTCTCAACCTCTACCATGTATACAGACGT 1931
Db 1893 CTACCAACTAGTGAATTAAGGAGGAGAGTGTCTCAACCTCTACCATGTATACAGACGT 1952
Qy 1932 CTCCTCATTAACAACCTCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAAGAAACCTGT 1991
Db 1953 CTCCTCATTAACAACCTCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAAGAAACCTGT 2012
Qy 1992 TTTGAGTAGAAGAGGCTGGAAGAGGAGGAGCAAAATCTGTCTGTT-CTCACTT 2050
Db 2013 TTTGAGTAGAAGAGGCTGGAAGAGGAGGAGCAAAATCTGTCTGTTCTCTCACTT 2072
Qy 2051 AGTCAATTTGGCAATTAAGCAATCTGTCTCTTTTGGCTGTCTGTCTGTCTGTCTGTCT 2110
Db 2073 AGTCAATTTGGCAATTAAGCAATCTGTCTCTTTTGGCTGTCTGTCTGTCTGTCTGT 2132
Qy 2111 CTCTATCGGAGCACAGAGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTATGAGAA 2170
Db 2133 CTCTATCGGAGCACAGAGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTATGAGAA 2192
Qy 2171 TGCCTATGAGGATTAATCTTCAAGTGTGTGAGCTTCTAAGTTCTTCCCTCACTTAC 2230
Db 2193 TGCCTATGAGGATTAATCTTCAAGTGTGTGAGCTTCTAAGTTCTTCCCTCACTTAC 2252
Qy 2231 CTGCAAGCCCAAGTCTGTGAAGAAATGCTGTGAGTCTGTGAGTCTGTGAGTCTGTG 2290
Db 2253 CTGCAAGCCCAAGTCTGTGAAGAAATGCTGTGAGTCTGTGAGTCTGTGAGTCTGTG 2312
Qy 2291 ATTATGATCTCCAGACCTTCTCTGAGCAATTTCAATTAAGCAACAATATACCTT 2350
Db 2313 ATTATGATCTCCAGACCTTCTCTGAGCAATTTCAATTAAGCAACAATATATACCTT 2372
Qy 2351 CCATGAAGCACAACAGACTTTTGAAGCAAGACATGACTGTGAATTGAGGCTTG 2410
Db 2373 CCATGAAGCACAACAGACTTTTGAAGCAAGACATGACTGTGAATTGAGGCTTG 2432
Qy 2411 AGGAATGAAGCTTTGAAGAAAAAATATCTTTGTTCCAGCCCTTCCCACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAAAAAATATCTTTGTTCCAGCCCTTCCCACTCTTCA 2492
Qy 2471 TGTGTTAACCACTGCTTCTGAGACCTTGTGAGGAGCAAGGAGTGTATCATGTTTAT 2530
Db 2493 TGTGTTAACCACTGCTTCTGAGACCTTGTGAGGAGCAAGGAGTGTATCATGTTTAT 2552
Qy 2531 AGAAAACTGATTTTGAAGTTCTGATGTTCAAGAGATGATTAATATATCATTTCT 2587
Db 2553 AGAAAACTGATTTTGAAGTTCTGATGTTCAAGAGATGATTAATATATCATTTCT 2609

RESULT 5
ADA08544
ID ADA08544 standard; cDNA; 2627 BP.
XX
XX ADA08544;
AC
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Human ovarian carcinoma polynucleotide OBE.
XX

ss; human; gene therapy; ovarian cancer; cancer.
XX Homo sapiens.
OS
XX US2003091580-A1.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-JUL-2001; 2001US-00907969.
PF
XX
XX 18-JUN-2001; 2001US-00884441.
PR
XX
XX (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
XX (MITCHAM J L, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX MPI; 2003-532352/50.
DR
XX
XX New isolated 0772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
XX Example 2; SEQ ID NO 391; 371pp; English.
PS
XX The invention relates to an isolated 0772P polypeptide, which has the
XX structure fully defined in the specification. The composition containing
XX the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
XX or antigen presenting cells are useful for stimulating an immune response
XX and treating ovarian cancer. Detecting the presence of the
XX polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
XX carcinoma cDNAs and protein cDNAs were identified using microarray
XX technology. The present sequence represents a human ovarian carcinoma
XX antigen polynucleotide.
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 99.1%; Score 2565; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 12 GGCAGCTCAGCTCAGCAGCAGTACCCAGTACGCTGGGAGCCTCCAGCAGTGGCTGCC 71
DB 33 GGGAGCTCCAGCTCAGCAGCAGTACCCAGTACGCTGGGAGCCTCCAGCAGTGGCTGCC 92
QY 72 TGGGAGAGATCCCTCTCTGAGCATATTAAGCATCATTAATTCTGCTGGAGCAATTG 131
DB 93 TGGGAGAGATCCCTCTCTGAGCATATTAAGCATCATTAATTCTGCTGGAGCAATTG 152
QY 132 CACTCATCTATTGGCTTTGGTATTTTCAGGAGACATCTCATCAGTCACTAAGTTCGCT 191
DB 153 CACTCATCTATTGGCTTTGGTATTTTCAGGAGACATCTCATCAGTCACTAAGTTCGCT 212
QY 192 CAGCTGGGAGAACTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC 251
DB 213 CAGCTGGGAGAACTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC 272
QY 252 TTTTGTATATCGTATACATAGGCTGTAAGAGAGAGTGTATTAAGCTTGTCTCAAGTTCA 311
DB 273 TTTTGTATATCGTATACATAGGCTGTAAGAGAGTGTATTAAGCTTGTCTCAAGTTCA 332
QY 312 AAGAGGCAAGATGAGCTGTGAGAGCAGAGTGAATTTTCAAGGCGCGAGACAGCTGT 371

DB 333 AAGAGGCAAGATGAGCTGTGAGAGCAGAGTGAATTTTCAAGGCGCGAGACAGCTGT 392
QY 372 TTTGCTATCAAGTATAGTGGCAATGCTCTTTGCGGCTGAAAAACGTGCACATCAGAG 431
DB 393 TTTGCTATCAAGTATAGTGGCAATGCTCTTTGCGGCTGAAAAACGTGCACATCAGAG 452
QY 432 ATGCTGGACCTTACAAATGTTATATCATCACTTCTTAAAGGCAAGGGAAATGCTTAA 491
DB 453 ATGCTGGACCTTACAAATGTTATATCATCACTTCTTAAAGGCAAGGGAAATGCTTAA 512
QY 492 AGTATTAATTAAGTGGACCTTTCAGCATGCGGAGAGTGAATGTGAGATCTAATATCCAG 551
DB 513 AGTATTAATTAAGTGGACCTTTCAGCATGCGGAGAGTGAATGTGAGATCTAATATCCAG 572
QY 552 AGACCTTGGGAGTGGAGCTCCCGATGTTCCCGACCCCAAGTGGTCTGGGATCCC 611
DB 573 AGACCTTGGGAGTGGAGCTCCCGATGTTCCCGACCCCAAGTGGTCTGGGATCCC 632
QY 612 AAGTTGACCAAGGAGCCAACTTCTGGAAGTCTCCAAATACCAAGCTTTGAGCTGAATCTG 671
DB 633 AAGTTGACCAAGGAGCCAACTTCTGGAAGTCTCCAAATACCAAGCTTTGAGCTGAATCTG 692
QY 672 AGAATGTGACCATGAAGTGTGTGTGTCTGTCAATGTTACGATCAACAACATCACT 731
DB 693 AGAATGTGACCATGAAGTGTGTGTGTCTGTCAATGTTACGATCAACAACATCACT 752
QY 732 CCTGTATGATTTGAATAATGACATTTGCCAAGCAAGGGATATCAAGTGA CAGAAATCG 791
DB 753 CCTGTATGATTTGAATAATGACATTTGCCAAGCAAGGGATATCAAGTGA CAGAAATCG 812
QY 792 AGATCAAAAAGGCGAGTCACTCAAGCTGTCAAACTCAAAAGGCTTCTGTGTGTCTT 851
DB 813 AGATCAAAAAGGCGAGTCACTCAAGCTGTCAAACTCAAAAGGCTTCTGTGTGTCTT 872
QY 852 CTTTCTTTGCCATCAGCTGGGAGCTTGCCTCTCAGCCCTTACCTGATGCTAAATAT 911
DB 873 CTTTCTTTGCCATCAGCTGGGAGCTTGCCTCTCAGCCCTTACCTGATGCTAAATAT 932
QY 912 GTGCTTGGCCCAAAAAAGCATGCAAGTCAATGTTTCAACAGGATCTACAGAACTAT 971
DB 933 GTGCTTGGCCCAAAAAAGCATGCAAGTCAATGTTTCAACAGGATCTACAGAACTAT 992
QY 972 TTCACCAACAGATATGACCTTATGTTTATATTTCTGGAGAGAAATGATTCATATCA 1031
DB 993 TTCACCAACAGATATGACCTTATGTTTATATTTCTGGAGAGAAATGATTCATATCA 1052
QY 1032 GTCTGAGTGGAGCAAAAGAGCAAGAAACAAAAGAGCAAGAGGCTCCAT 1091
DB 1053 GTCTGAGTGGAGCAAAAGAGCAAGAAACAAAAGAGCAAGAGGCTCCAT 1112
QY 1092 ATGAACAAGATTAATCTATCTTCAAAAGCATATTAAGTGGAAATTAATTCATGTA 1151
DB 1113 ATGAACAAGATTAATCTATCTTCAAAAGCATATTAAGTGGAAATTAATTCATGTA 1172
QY 1152 ACTAGCAAGTGTGTTAAGAGTATTAAGTAAATGCAAGTGAAGCAAGTGCATCCAG 1211
DB 1173 ACTAGCAAGTGTGTTAAGAGTATTAAGTAAATGCAAGTGAAGCAAGTGCATCCAG 1232
QY 1212 ATCTCAGGAGACCTCCCGGCTGTCACTGGGAGTGAAGAGCAGGATAGTGCATGT 1271
DB 1233 ATCTCAGGAGACCTCCCGGCTGTCACTGGGAGTGAAGAGCAGGATAGTGCATGT 1292
QY 1272 CTTTGTCTCTGAATTTTGAATTAATGCTGTGAATGTTGCTCTGAGGAAGCCCTGGA 1331
DB 1293 CTTTGTCTCTGAATTTTGAATTAATGCTGTGAATGTTGCTCTGAGGAAGCCCTGGA 1352
QY 1332 AGTCTATCCCAACATATCAACTTTATATTCACAAATTAAGCTGTATGTAACCTTA 1391
DB 1353 AGTCTATCCCAACATATCAACTTTATATTCACAAATTAAGCTGTATGTAACCTTA 1412
QY 1392 AGAGCTGTCTAATTAAGTGCACCTTGGCAACTCAGAGGCGGCTGATTTTGTATGGGT 1451
DB 1413 AGAGCTGTCTAATTAAGTGCACCTTGGCAACTCAGAGGCGGCTGATTTTGTATGGGT 1472

QY 1452 CAATGATTCATTTTATGATGCTTCCAAAGGCTTGCGCTTCTTCCCAACTGACA 1511
| | | | |
Db 1473 CAATGATTCATTTTATGATGCTTCCAAAGGCTTGCGCTTCTTCCCAACTGACA 1532
| | | | |
QY 1512 AATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAAGAGAGAGTGGCGACACC 1571
| | | | |
Db 1533 AATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAAGAGAGAGTGGCGACACC 1592
| | | | |
QY 1572 GATTTTATTAATTAACAGAGACCTTCTTTTAAACAAACAAATGGGGTTTATTTCTCA 1631
| | | | |
Db 1593 GATTTTATTAATTAACAGAGACCTTCTTTTAAACAAACAAATGGGGTTTATTTCTCA 1652
| | | | |
QY 1632 GATGATGTTGATCGGTAATGTCAGAGGAAAGACCTTTCACCTGATATATGAGCATTA 1691
| | | | |
Db 1653 GATGATGTTGATCGGTAATGTCAGAGGAAAGACCTTTCACCTGATATATGAGCATTA 1712
| | | | |
QY 1692 TGTGATCACAAGCTCTGAGGCTTCTCTTTCATCCCTGAGCAGCTAAGACCTCAGT 1751
| | | | |
Db 1713 TGTGATCACAAGCTCTGAGGCTTCTCTTTCATCCCTGAGCAGCTAAGACCTCAGT 1772
| | | | |
QY 1752 TTTCAATAGCATTTAAGCAGTGGGACTCAGCTGGGGTGATTTTGGCCCCCATCTCGGG 1811
| | | | |
Db 1773 TTTCAATAGCATTTAAGCAGTGGGACTCAGCTGGGGTGATTTTGGCCCCCATCTCGGG 1832
| | | | |
QY 1812 GGAATGTCGAAACAATTTTGGTTACCTCAATGAGGAGATGAGAGATAGAGTGTCTA 1871
| | | | |
Db 1833 GGAATGTCGAAACAATTTTGGTTACCTCAATGAGGAGATGAGAGATAGAGTGTCTA 1892
| | | | |
QY 1872 CTACCAACTAGTGTGATTAAGGCGAGGAGTCTGCTCACTCCTCAATGATAGAGACGT 1931
| | | | |
Db 1893 CTACCAACTAGTGTGATTAAGGCGAGGAGTCTGCTCACTCCTCAATGATAGAGACGT 1952
| | | | |
QY 1932 CTGCCCATTTGCACTACCTCAATCCGAAAGTGTCACTGTGTGAGAGCTAAGAAACCTTGGT 1991
| | | | |
Db 1953 CTGCCCATTTGCACTACCTCAATCCGAAAGTGTGTGAGAGCTAAGAAACCTTGGT 2012
| | | | |
QY 1992 TTTGAGTGAAGAAAGGCGTGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCAATT 2050
| | | | |
Db 2013 TTTGAGTGAAGAAAGGCGTGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCAATT 2072
| | | | |
QY 2051 AGTCATTTGGCAATTAAGCAATCTGTCTTTTGGCTGCTGCTGAGCAGAGAGCCAGAA 2110
| | | | |
Db 2073 AGTCATTTGGCAATTAAGCAATCTGTCTTTTGGCTGCTGCTGAGCAGAGAGCCAGAA 2132
| | | | |
QY 2111 CTCTATCGGGCAGCAGGATTAATCTCTCAGTGAAGAGAGTGAACAAGGCTTATGGGAAA 2170
| | | | |
Db 2133 CTCTATCGGGCAGCAGGATTAATCTCTCAGTGAAGAGAGTGAACAAGGCTTATGGGAAA 2192
| | | | |
QY 2171 TGGCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTTCTTCCCTCAATTCTAC 2230
| | | | |
Db 2193 TGGCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTTCTTCCCTCAATTCTAC 2252
| | | | |
QY 2231 CTGCAAGCCAAAGTTCTGTAGAGAAATGCTGAGTCTAGAGCTTTTCTTACTCTGA 2290
| | | | |
Db 2253 CTGCAAGCCAAAGTTCTGTAGAGAAATGCTGAGTCTAGAGTCTTCTTACTCTGA 2312
| | | | |
QY 2291 ATTAGATCTCCAGACCTTCTGCGCACAATTCAAATTAAGCAACAACATATACCTT 2350
| | | | |
Db 2313 ATTAGATCTCCAGACCTTCTGCGCACAATTCAAATTAAGCAACAACATATACCTT 2372
| | | | |
QY 2351 CCATGAGAGCAGACAGACTTTTGAAGAGAGCAATGCTGCTGAATGAGGCTTG 2410
| | | | |
Db 2373 CCATGAGAGCAGACAGACTTTTGAAGAGAGCAATGCTGCTGAATGAGGCTTG 2432
| | | | |
QY 2411 AGGAATGAAGCTTTGAAGAGAAATACCTTTTTCAGACCCCTTCCACACTCTTCA 2470
| | | | |
Db 2433 AGGAATGAAGCTTTGAAGAGAAATACCTTTTTCAGACCCCTTCCACACTCTTCA 2492
| | | | |
QY 2471 TGTGTTAACCACTGCTTCTGAGCCTTGGAGCAGCGTGAAGCTGTATTAATGTTGTAT 2530
| | | | |
Db 2493 TGTGTTAACCACTGCTTCTGAGCCTTGGAGCAGCGTGAAGCTGTATTAATGTTGTAT 2552
| | | | |

QY 2531 AGAAACTGATTTTATGATGCTTCAAGAGATGATTAATATATACATTTCT 2587
| | | | |
Db 2553 AGAAACTGATTTTATGATGCTTCAAGAGATGATTAATATATACATTTCT 2609
| | | | |
RESULT 6
ADF08887
ID ADF08887 standard; cDNA; 2627 BP.
XX
AC ADF08887;
XX
DT 12-FEB-2004 (first entry)
XX
DE cDNA encoding secreted ovarian carcinoma antigen seqid 391.
XX
KW gene therapy; protein therapy; vaccine; antibody inhibition;
KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
KW secreted ovarian carcinoma antigen; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003124140-A1.
XX
PD 03-JUL-2003.
XX
PF 17-JUL-2002; 2002US-00198053.
XX
PR 17-DEC-1998; 98US-00215681.
XX
PR 17-DEC-1998; 98US-00216003.
XX
PR 23-JUN-1999; 99US-00338933.
XX
PR 24-SEP-1999; 99US-00404879.
XX
PR 17-JUL-2000; 2000US-00617747.
XX
PR 10-AUG-2000; 2000US-00636801.
XX
PR 20-SEP-2000; 2000US-00667857.
XX
PR 04-APR-2001; 2001US-00827271.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PR 17-JUL-2001; 2001US-00907969.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Retter MW, Fanger GR, Hill P;
XX
DR WPI; 2003-897152/82.
XX
PT P-PSDB; ADF08888, ADF08889.
XX
PT Oncogenic nucleic acids useful for the prevention, diagnosis and
XX treatment of breast cancer.
PS Example 2; SEQ ID NO 391; 399pp; English.
XX
CC The invention describes nucleic acids (I) and the polypeptides (II) they
CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
CC treating diseases related to their aberrant expression i.e. breast
CC cancers. For example, (I) and (II) may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of (II) by expressing
CC inactive proteins or to supplement the patient's own production of (II).
CC Additionally, (I) may be used to produce (II), by inserting (I) into a
CC host cell and culturing the cell to express the protein (II). (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids in
CC samples, and therefore which patients may be in need of restorative
CC therapy. The host cell may also be used as antigen in the production of
CC antibodies against (II) and in assays to identify modulators of (II)'s
CC expression and activity. The anti-(II) antibodies, agonists and
CC antagonists may be used to regulate expression and activity and as
CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
CC immunoassay). This sequence represents a polynucleotide encoding a
CC secreted ovarian carcinoma antigen.
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
XX
XX
Query Match 99.1%; Score 2565; DB 10; Length 2627;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 12 GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCAGCATGGCTTCCC 71
Db 33 GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCAGCATGGCTTCCC 92
QY 72 TGGGGCAGATCCTCTTCTGAGCATATATAGCATCATATATCTGGCTGGAGCAATTG 131
Db 93 TGGGGCAGATCCTCTTCTGAGCATATATAGCATCATATATCTGGCTGGAGCAATTG 152
QY 132 CACTCATCTTGGCTTGGTATTTGAGGAGACATCTCATCAAGTCACTACTGTGGCT 191
Db 153 CACTCATCTTGGCTTGGTATTTGAGGAGACATCTCATCAAGTCACTACTGTGGCT 212
QY 132 CAGCTGGGAACTTGGGAGAGATGGAAATCTTGAAGCTGCACTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGGAACTTGGGAGAGATGGAAATCTTGAAGCTGCACTTTGAACCTGACATCAAC 272
QY 252 TTTCTGATATCGATACAAATGGCTGAAGAGAGTGTATAGGCTTGGTCCATGAGTTCA 311
Db 273 TTTCTGATATCGATACAAATGGCTGAAGAGAGTGTATAGGCTTGGTCCATGAGTTCA 332
QY 312 AAGAAAGCAAGATGAGCTGTGAGCAGAGATGAAATGTTCAAGGCGGAGCAGAGTGT 371
Db 333 AAGAAAGCAAGATGAGCTGTGAGCAGAGATGAAATGTTCAAGGCGGAGCAGAGTGT 392
QY 372 TTGCTGATCAATGATAGTTGGCAATGCTCTTTGGGCTGAAAAACCTGACATCAAG 431
Db 393 TTGCTGATCAATGATAGTTGGCAATGCTCTTTGGGCTGAAAAACCTGACATCAAG 452
QY 432 ATGCTGGCACTACAAATGTTATCATCACTCTTAAAGCAAGGGAATGCTAACTTG 491
Db 453 ATGCTGGCACTACAAATGTTATCATCACTCTTAAAGCAAGGGAATGCTAACTTG 512
QY 492 AGTATPAAACTGAGGCTTCAAGATGCGGAAGTGAATGTGAATTAATGTCAGCTCAG 551
Db 513 AGTATPAAACTGAGGCTTCAAGATGCGGAAGTGAATGTGAATTAATGTCAGCTCAG 572
QY 552 AATCCTTGGGCTGAGAGGCTCCCGCATGGTTCCCGAGCCACAGTGTCTGGGATCCC 611
Db 573 AATCCTTGGGCTGAGAGGCTCCCGCATGGTTCCCGAGCCACAGTGTCTGGGATCCC 632
QY 612 AAGTTGACAGGAGGCACTTCTGGAAGTCTCCAATACAGACTTGGAGTGAACCTG 671
Db 633 AAGTTGACAGGAGGCACTTCTGGAAGTCTCCAATACAGACTTGGAGTGAACCTG 692
QY 672 AGAATGTGACATGAAGGTTGTGTCTGCTCTCAATGTTACGATCAACACACTACT 731
Db 693 AGAATGTGACATGAAGGTTGTGTCTGCTCTCAATGTTACGATCAACACACTACT 752
QY 732 CCTGATGATTTGAAAATGCAATTGCCAAGCAACAGGGAATATCAAAAGTGAACGAATCG 791
Db 753 CCTGATGATTTGAAAATGCAATTGCCAAGCAACAGGGAATATCAAAAGTGAACGAATCG 812
QY 792 AGATCAAAAGGCGAGTCACTACAGCTGCTAAACTCAAAAGGCTTCTGTGTCTCTT 851
Db 813 AGATCAAAAGGCGAGTCACTACAGCTGCTAAACTCAAAAGGCTTCTGTGTCTCTT 872
QY 852 CTTTCTTTGGCATCAGCTGGGACATTTCTGCTCTCAGCCCTTAACCTGATGCTAAATAAT 911
Db 873 CTTTCTTTGGCATCAGCTGGGACATTTCTGCTCTCAGCCCTTAACCTGATGCTAAATAAT 932
QY 912 GTGCTTGGCCCAAAAAAAGCATGCAAAAGTCAATTGTTACACAGGATCTACAGAACTAT 971
Db 933 GTGCTTGGCCCAAAAAAAGCATGCAAAAGTCAATTGTTACACAGGATCTACAGAACTAT 992
QY 972 TTCAACACAGATPAGATCTAGTTTATATTTCTGGGAGAAATGAATCATATCTAGAA 1031
Db 993 TTCAACACAGATPAGATCTAGTTTATATTTCTGGGAGAAATGAATCATATCTAGAA 1052
QY 1032 GTCTGAGTGAACAAACAGAGCAAGAAACAAAAGAACCAAAAGCAGAGGCTTCAAT 1091
Db 1053 GTCTGAGTGAACAAACAGAGCAAGAAACAAAAGAACCAAAAGCAGAGGCTTCAAT 1091
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Db 1053 GTCTGAGTGAACAAACAGAGCAAGAAACAAAAGAACCAAAAGCAGAGGCTTCAAT 1112
QY 1092 ATGAACAGATPAAATCTATCTTCAAGAAGCATATTAAGAGTTGGGAAATTAATTCATGTA 1151
Db 1113 ATGAACAGATPAAATCTATCTTCAAGAAGCATATTAAGAGTTGGGAAATTAATTCATGTA 1172
QY 1152 ACTAGCAAGTGTGTTAAGATGATTAAGTAAATGCAAGTGAAGCAAGTCAATCCAG 1211
Db 1173 ACTAGCAAGTGTGTTAAGATGATTAAGTAAATGCAAGTGAAGCAAGTCAATCCAG 1232
QY 1212 ATCTAGAGGACCTCCCGCTGCTGCTCACTGGGAGTGAAGGACAGATAGTGATCTT 1271
Db 1233 ATCTAGAGGACCTCCCGCTGCTGCTCACTGGGAGTGAAGGACAGATAGTGATCTT 1292
QY 1272 CTTTGTCTGTGAATTTTATAGTTATATGCTGTATAGTTGCTCTGAGGAAACCCCTGAA 1331
Db 1293 CTTTGTCTGTGAATTTTATAGTTATATGCTGTATAGTTGCTCTGAGGAAACCCCTGAA 1352
QY 1332 AGTCTATCCCAACATATCCAGATCTTATATTCACAAATTAAGCTGATATGATCCCTA 1391
Db 1353 AGTCTATCCCAACATATCCAGATCTTATATTCACAAATTAAGCTGATATGATCCCTA 1412
QY 1392 AGACGCTGCTAATTAAGCTGCCACTTGGCACTCAGAGGCGGCTGCATTTAGTATGGGT 1451
Db 1413 AGACGCTGCTAATTAAGCTGCCACTTGGCACTCAGAGGCGGCTGCATTTAGTATGGGT 1472
QY 1452 CAATATGATTCATTTTATAGTGTCTTCCAAAGTGTCTTCCAACTGAC 1511
Db 1473 CAATATGATTCATTTTATAGTGTCTTCCAAAGTGTCTTCCAACTGAC 1532
QY 1512 AATGCAAAAGTTGAGAAAATGATCATATTTATAGCATPAAACAGAGCTGGGACACC 1571
Db 1533 AATGCAAAAGTTGAGAAAATGATCATATTTATAGCATPAAACAGAGCTGGGACACC 1592
QY 1572 GATTTTATPAAATPAACTGAGACCTTCTTTTAAACAAACAAAGCGGTTATTTTCCA 1631
Db 1593 GATTTTATPAAATPAACTGAGACCTTCTTTTAAACAAACAAAGCGGTTATTTTCCA 1652
QY 1632 GATGATGTTCAATCGGTGAATGGTCCAGGGAAGAGACCTTCACTGATATATGAGATTA 1691
Db 1653 GATGATGTTCAATCGGTGAATGGTCCAGGGAAGAGACCTTCACTGATATATGAGATTA 1712
QY 1692 TGTCAATCAAAAGCTGTAGGCTTCTCTTCCATCTGCTGAGACAGCTAAGACCTCACT 1751
Db 1713 TGTCAATCAAAAGCTGTAGGCTTCTCTTCCATCTGCTGAGACAGCTAAGACCTCACT 1772
QY 1752 TTTCAATAGCATCTAGACAGTGGGACCTCACTGGGGTGAATTTGCCCCCATCTCGGG 1811
Db 1773 TTTCAATAGCATCTAGACAGTGGGACCTCACTGGGGTGAATTTGCCCCCATCTCGGG 1832
QY 1812 GGAATGTCTGAAGACAAATTTTGTGTTAAGTCAATGAGGAGTGAAGAGATACAGTCTA 1871
Db 1833 GGAATGTCTGAAGACAAATTTTGTGTTAAGTCAATGAGGAGTGAAGAGATACAGTCTA 1892
QY 1872 CTACCACTAGTGAATPAAAGGCGAGGATGTCTGCAACTTCTTACATGATACAGAGCT 1931
Db 1893 CTACCACTAGTGAATPAAAGGCGAGGATGTCTGCAACTTCTTACATGATACAGAGCT 1952
QY 1932 CTCCCATTTACAACTCAACCAATCCGAAGTGTCACTGTGTCAAGGCTPAAAGAAACCTGT 1991
Db 1953 CTCCCATTTACAACTCAACCAATCCGAAGTGTCACTGTGTCAAGGCTPAAAGAAACCTGT 2012
QY 1992 TTTGATGAAGAAAGGCGCTGGAAGAGAGGAGCCAAACAAATCTGTCTGCTT-CTCACATT 2050
Db 2013 TTTGATGAAGAAAGGCGCTGGAAGAGAGGAGCCAAACAAATCTGTCTGCTTCTCACATT 2072
QY 2051 AGTCATTTGGCAAAATTAAGCATTTCTGTCTTTTGGCTGTCTGCTCAGACAGAGAGCAGAA 2110
Db 2073 AGTCATTTGGCAAAATTAAGCATTTCTGTCTTTTGGCTGTCTGCTCAGACAGAGAGCAGAA 2132
QY 2111 CTCTATGGGACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTATGGGAAA 2170
Db 2133 CTCTATGGGACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTATGGGAAA 2192
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QY 2171 TGGCTGATGGGATTATCTTACGCTTGTAGCTTCTTAAGTTCTTCCCTTCAATTCACC 2230
DB 2193 TGCCGTATGGGATTATCTTACGCTTGTAGCTTCTTAAGTTCTTCCCTTCAATTCACC 2252
QY 2231 CTGCAAGCCAAAGTTCTGTAGAGAAAAGCTGAGTTCTAGCTGAGTTTCTTACTCTGA 2290
DB 2253 CTGCAAGCCAAAGTTCTGTAGAGAAAAGCTGAGTTCTAGCTGAGTTTCTTACTCTGA 2312
QY 2291 ATTGAGTCTCGACCCCTTCTGGCCCAATTCAATTAAAGCAACAAATATACCTT 2350
DB 2313 ATTGAGTCTCGACCCCTTCTGGCCCAATTCAATTAAAGCAACAAATATACCTT 2372
QY 2351 CCAATGAGCAACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTGAGGCTTGG 2410
DB 2373 CCAATGAGCAACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTGAGGCTTGG 2432
QY 2411 AGGAATGAGCTTTGAGAAAAGAAATATCTTGTTCACAGCCCTTCCACACTCTTCA 2470
DB 2433 AGGAATGAGCTTTGAGAAAAGAAATATCTTGTTCACAGCCCTTCCACACTCTTCA 2492
QY 2471 TGTGTAAACCACTGCTTCTCTGGAACCTTGGAGCCAGGTGACTGTATTAATGTTTAT 2530
DB 2493 TGTGTAAACCACTGCTTCTCTGGAACCTTGGAGCCAGGTGACTGTATTAATGTTTAT 2552
QY 2531 AGAAAATGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATTAATTAATTCCT 2587
DB 2553 AGAAAATGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATTAATTAATTCCT 2609

RESULT 7
ADG46174
ID ADG46174 standard; cDNA; 2627 BP.
XX
AC ADG46174;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human ovarian carcinoma polynucleotide #387.
XX
KM Human; ovarian carcinoma; gene; ss; OBE; ovarian cancer;
XX secreted tumour antigen; cytosolic; 0772P.
OS Homo sapiens.
XX
PN US2003165504-A1.
XX
PD 04-SEP-2003.
XX
PF 04-APR-2001; 2001US-00827271.
XX
PR 17-DEC-1998; 980US-00215681.
XX
PR 17-DEC-1998; 980US-00216003.
XX
PR 23-JUN-1999; 99US-00338933.
XX
PR 24-SEP-1999; 99US-00404879.
XX
PR 17-JUL-2000; 2000US-00617747.
XX
PR 10-AUG-2000; 2000US-00636801.
XX
PR 20-SEP-2000; 2000US-0067857.
XX
PA (RETT/) RETTER M W.
XX
PA (FANG/) FANGER G R.
XX
PI Retter MW, Fanger GR;
XX
DR MPI; 2003-898035/82.
XX
PT New isolated OBE or 0772P polypeptides, useful for diagnosing,
XX
PT stimulating, treating and monitoring cancer, e.g. ovarian cancer,
XX
PS Example 2; SEQ ID NO 391; 290bp; English.
XX
XX The invention relates to human ovarian carcinoma polypeptides, designated

CC OBE or 0772P, and the polynucleotides encoding them. The invention also
CC relates to methods for inhibiting the development of cancer, e.g. ovarian
CC cancer in a patient, methods for stimulating and/or expanding T cells and
CC methods for identifying secreted tumour antigens. The polypeptides,
CC compositions, antibodies to the polypeptides and methods are useful for
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC cancer. The composition is particularly useful for stimulating an immune
CC response in patient. This sequence represents a human ovarian carcinoma
CC polynucleotide of the invention.
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
XX
Query Match 99.1%; Score 2565; DB 10; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 12 GGCAGCTCCACTAGCCAGTACCAGATACGCTGGGAACCTTCCAGCCATGGCTTCCC 71
DB 33 GGCAGCTCCACTAGCCAGTACCAGATACGCTGGGAACCTTCCAGCCATGGCTTCCC 92
QY 72 TGGGGCAAGTCTCTTCTGAGCATTAATTAACATCATTAATTTCTGGTGGAGCAATTG 131
DB 93 TGGGGCAAGTCTCTTCTGAGCATTAATTAACATCATTAATTTCTGGTGGAGCAATTG 152
QY 132 CACTCATCAATTGGCTTGGATTTGAGGAGACATCCATCAAGTCACTACTGTGCGCT 191
DB 153 CACTCATCAATTGGCTTGGATTTGAGGAGACATCCATCAAGTCACTACTGTGCGCT 212
QY 192 CAGCTGGGAACATTTGGGGAGATGAGATCTTGAAGTCACTTTTGAACCTGATCAAAAC 251
DB 213 CAGCTGGGAACATTTGGGGAGATGAGATCTTGAAGTCACTTTTGAACCTGATCAAAAC 272
QY 252 TTTCTGATATCGTATGATCAATGCTGAGAGAGGTGTTTGAAGTCTGCTGATGATTC 311
DB 273 TTTCTGATATCGTATGATCAATGCTGAGAGAGGTGTTTGAAGTCTGCTGATGATTC 332
QY 312 AAGAAGCAAAAGATGAGCTGTGGAGCAGAGATGAATGTTCAAGGCCGGAAGCAGAGTGT 371
DB 333 AAGAAGCAAAAGATGAGCTGTGGAGCAGAGATGAATGTTCAAGGCCGGAAGCAGAGTGT 392
QY 372 TTGCTGATCAAGTATGATGATGCGATGCTCTTTGGCGGTGAAGAAAGTGCACATCAG 431
DB 393 TTGCTGATCAAGTATGATGATGCGATGCTCTTTGGCGGTGAAGAAAGTGCACATCAG 452
QY 432 ATGCTGGCACCTTAAGATGTTATATCATCACTTCTAAAGCAAGGGAATGCTAACCTTG 491
DB 453 ATGCTGGCACCTTAAGATGTTATATCATCACTTCTAAAGCAAGGGAATGCTAACCTTG 512
QY 492 AGTATAAACTGGAGCTTCAGCATGCCGAAGTGAATGAGCTAATTAATGCCAGCTCAG 551
DB 513 AGTATAAACTGGAGCTTCAGCATGCCGAAGTGAATGAGCTAATTAATGCCAGCTCAG 572
QY 552 AGACCTTGGGCTGTGAGGCTCCCGATGGTTCCCGCAGCCACAGTGGTCTGGGCAATCCC 611
DB 573 AGACCTTGGGCTGTGAGGCTCCCGATGGTTCCCGCAGCCACAGTGGTCTGGGCAATCCC 632
QY 612 AAGTTGACCAAGGAGCCAACTTCTCGGAAGTCTTCAATACACAGCTTTGAGCTGAATCTG 671
DB 633 AAGTTGACCAAGGAGCCAACTTCTCGGAAGTCTTCAATACACAGCTTTGAGCTGAATCTG 692
QY 672 AGAATGAGCAATGAAGGTTGTCTGTGCTCAAGATGTTAGATCAACCAACATCACTACT 731
DB 693 AGAATGAGCAATGAAGGTTGTGTGTGTCTTCAATATTTAGATCAACCAACATCACTACT 752
QY 732 CCGTATGATTTGAAAATGACATTTGCCAAAGCAACAGGGATATCAAAAGTACAGAAATCGG 791
DB 753 CCGTATGATTTGAAAATGACATTTGCCAAAGCAACAGGGATATCAAAAGTACAGAAATCGG 812
QY 792 AGATCAAAAAGCGGAGTCACTTAAGCTGTAATCAAAAGGCTTCTGTGTGTCTCTT 851
DB 813 AGATCAAAAAGCGGAGTCACTTAAGCTGTAATCAAAAGGCTTCTGTGTGTCTCTT 872
QY 852 CTTTCTTGGCATACAGCTGGGACCTTCTGCTCTCAGCCCTTAAGTATCAATTAAT 911

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Db      873 CTTTCCTTGCATCAGCTGGGCACTTCTGCTCTGAGCCCTTACCTGATGTAATAT 932
Qy      912 GTGCGCTTGGCCACAAAAAGCATGCAAGTCACTGTTAACAAGGATCTACAGAACTAT 971
Db      933 GTGCGCTTGGCCACAAAAAGCATGCAAGTCACTGTTAACAAGGATCTACAGAACTAT 992
Qy      972 TTCACACAGATATGATGACTAGTTTATATTTCTGGAGGAATGTAATCATATCTAGA 1031
Db      993 TTCCACACAGATATGATGACTAGTTTATATTTCTGGAGGAATGTAATCATATCTAGA 1052
Qy      1032 GTCTGAGTGAACAACAAGCAAGAAAACAAAAAGACCAAAAGCAGAGGCTTCCAA 1091
Db      1053 GTCTGAGTGAACAACAAGCAAGAAAACAAAAAGACCAAAAGCAGAGGCTTCCAA 1112
Qy      1092 ATGAACAAGATTAATCTATCTTCAAGAATATAGAACTTGGGAAAAATATTCATGTA 1151
Db      1113 ATGAACAAGATTAATCTATCTTCAAGAATATAGAACTTGGGAAAAATATTCATGTA 1172
Qy      1152 ACTAGCAAGTGTATGATGATTAAGATTAAGTAAATGCACTGGAGACAAGTATGCAAT 1211
Db      1173 ACTAGCAAGTGTATGATGATTAAGATTAAGTAAATGCACTGGAGACAAGTATGCAAT 1232
Qy      1212 ATCTCAGGAGCTCCCTGCTGCTGCACTGGAGAGTGAAGAGACAGATAGTCAAT 1271
Db      1233 ATCTCAGGAGCTCCCTGCTGCTGCACTGGAGAGTGAAGAGACAGATAGTCAAT 1292
Qy      1272 CTTTGTCTCTGAATTTTGTATATATGTCGTAAATGTTGCTCTGAGGAAGCCCTGGA 1331
Db      1293 CTTTGTCTCTGAATTTTGTATATATGTCGTAAATGTTGCTCTGAGGAAGCCCTGGA 1352
Qy      1332 AGTCTATCCCAACATATCAATCTATATTCACAATTAAGCTGTATATGATCCCTA 1391
Db      1353 AGTCTATCCCAACATATCAATCTATATTCACAATTAAGCTGTATATGATCCCTA 1412
Qy      1392 AGACGCTGTAAATGATGATGCACTGCACTGAGGAGCGGCTGCATTTTAAATGAGT 1451
Db      1413 AGACGCTGTAAATGATGATGCACTGCACTGAGGAGCGGCTGCATTTTAAATGAGT 1472
Qy      1452 CAAGAATTCACCTTTTATGATGCTTCCAAAGTGCCTGGCTCTCCCAACGAGA 1511
Db      1473 CAAGAATTCACCTTTTATGATGCTTCCAAAGTGCCTGGCTCTCCCAACGAGA 1532
Qy      1512 AATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAACAAGACATCGGCGACAC 1571
Db      1533 AATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAACAAGACATCGGCGACAC 1592
Qy      1572 GATTTTATAAATACTGAGCACTTTCTTTTAAACAACAAATGCGGCTTATTTCTCA 1631
Db      1593 GATTTTATAAATACTGAGCACTTTCTTTTAAACAACAAATGCGGCTTATTTCTCA 1652
Qy      1632 GATGATGTTCAATCCCGGATGTCGAGGAGGAGGACCTTTCACCTTGACATATGAGATTA 1691
Db      1653 GATGATGTTCAATCCCGGATGTCGAGGAGGAGGACCTTTCACCTTGACATATGAGATTA 1712
Qy      1692 TGTATCACAAGCTCTGAGGCTTCTCTTTCATCTGCGGAGACAGTAAAGCTCACT 1751
Db      1713 TGTATCACAAGCTCTGAGGCTTCTCTTTCATCTGCGGAGACAGTAAAGCTCACT 1772
Qy      1752 TTTCAATAGCATCTAGAGCATGAGGATCTGATGAGGAGGATGAGGAGATCAGTGCTA 1811
Db      1773 TTTCAATAGCATCTAGAGCATGAGGATCTGATGAGGAGGATGAGGAGATCAGTGCTA 1832
Qy      1812 GGAATGTCTGAGAGCAATTTTGGTTACCTCAATGAGGAGGATGAGGAGATCAGTGCTA 1871
Db      1833 GGAATGTCTGAGAGCAATTTTGGTTACCTCAATGAGGAGGATGAGGAGATCAGTGCTA 1892
Qy      1872 CTACCAACTAGTGAATAAGGCGAGGAGATGCTGCTCAACTCTCAATGATCAGGACCT 1931
Db      1893 CTACCAACTAGTGAATAAGGCGAGGAGATGCTGCTCAACTCTCAATGATCAGGACCT 1952
Qy      1932 CTCCTCATTTACAACTACCAATTCGAAAGTGTCACTGTCTCAGGACTAAAGAACTCTGCT 1991

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Db      1953 CTCCTCATTTACAACTACCAATTCGAAAGTGTCACTGTGTGAGACTAAGAAACCTGCT 2012
Qy      1992 TTTGATGAAAGAGGCGCTGGAAAGAGGAGCCCAACAATCTGTCTCTT-CTGACATTT 2050
Db      2013 TTTGATGAAAGAGGCGCTGGAAAGAGGAGCCCAACAATCTGTGTCTCTCTCTCACTTT 2072
Qy      2051 AGTCATTTGGCAAAATTAAGCATTTCTGTCTTTTGGCTGTGCTCAGACACAGAGCCAGAA 2110
Db      2073 AGTCATTTGGCAAAATTAAGCATTTCTGTCTTTTGGCTGTGCTCAGACACAGAGCCAGAA 2132
Qy      2111 CTCTATCGGCGACACAGATTAATCTCTCAGTGAACAAAGTTGACAAAGGCTATGAGGAAA 2170
Db      2133 CTCTATCGGCGACACAGATTAATCTCTCAGTGAACAAAGTTGACAAAGGCTATGAGGAAA 2192
Qy      2171 TGCCGTATGAGGATTAATCTCTCAGTGTGAGCTTCTAAGTTTCTTCCCTCATTTCACT 2230
Db      2193 TGCCGTATGAGGATTAATCTCTCAGTGTGAGCTTCTAAGTTTCTTCCCTCATTTCACT 2252
Qy      2231 CTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
Db      2253 CTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
Qy      2291 ATTTAGATCTCGAGCCCTTCTGCGCCCAATTTCAATTAAGGCAACAATATATACCTT 2350
Db      2313 ATTTAGATCTCGAGCCCTTCTGCGCCCAATTTCAATTAAGGCAACAATATATACCTT 2372
Qy      2351 CCATGAGCACAACAGACTTTTGAAGCAAGAACATGATGCTTGAATTAAGGCGCTTG 2410
Db      2373 CCATGAGCACAACAGACTTTTGAAGCAAGAACATGATGCTTGAATTAAGGCGCTTG 2432
Qy      2411 AGGAATGAAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCCACACTCTTCA 2470
Db      2433 AGGAATGAAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCCACACTCTTCA 2492
Qy      2471 TGTGTTAACCACTGCTTCTCTGAGCTTGGAGCCAGGCTGACTGATTAACATGTTGTTAT 2530
Db      2493 TGTGTTAACCACTGCTTCTCTGAGCTTGGAGCCAGGCTGACTGATTAACATGTTGTTAT 2552
Qy      2531 AGAAACTGATTTTGAAGTTCGATCGTTCAAGAGATGATTAATATACATTTTCT 2587
Db      2553 AGAAACTGATTTTGAAGTTCGATCGTTCAAGAGATGATTAATATACATTTTCT 2609

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RESULT 8
 ADN40452
 ID ADN40452 strand: cdna; 2627 BP.
 XX
 AC ADN40452;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human breast cancer associated cdna sequence #203.
 XX
 KW Human; breast cancer; T cell; tumour protein; antigen presenting cell;
 KW Immune response; CD4+; CD8+; cytostatic; gene therapy; gene; ss.
 OS Homo sapiens.
 PN US2004101899-A1.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003US-00714389.
 XX
 PR 30-NOV-1999; 99US-00451651.
 PR 22-FEB-2000; 2000US-00510662.
 PR 10-MAR-2000; 2000US-00523586.
 PR 07-APR-2000; 2000US-00545068.
 PR 15-MAY-2000; 2000US-00571025.
 PR 06-FEB-2001; 2001US-00778320.
 XX
 PA (CORI-) CORIXA CORP.
 XX

PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;
PI McNeill PD;
XX
DR WPI; 2004-399689/37.
XX P-PSDB; ADN40453, ADN40454.
XX
PT New polynucleotides, useful for treating and diagnosing cancer,
PT particularly breast cancer by stimulating immune response in a patient
PT and inhibiting the development of cancer.
XX
PS Claim 1; SEQ ID NO 207; 151bp; English.
XX
XX The present invention relates to polynucleotide and polypeptide sequences
XX associated with breast cancer. Also disclosed are expression vectors
XX comprising the polynucleotide sequences of the invention operably linked
XX to an expression control sequence, host cells comprising the vector,
XX antibodies (or antigen binding fragments of antibodies) specifically
XX binding the polypeptides of the invention, fusion proteins comprising at
XX least one of the polypeptides, stimulating and/or expanding T cells
XX specific for a tumour protein. The polynucleotide sequences, polypeptide
XX sequences, and antigen presenting cells can be administered
XX therapeutically/prophylactically to induce an immune response. They can
XX be included with a physiological carrier/immunostimulant in compositions
XX such as vaccines, particularly to treat or prevent cancers such as breast
XX cancer. They can also be used to inhibit the development of cancer by
XX incubating one or more of them with CD4+ and/or CD8+ T cells isolated
XX from a patient, such that the T cells proliferate, and administering the
XX proliferated T cells to the patient. The polynucleotide sequences are
XX useful for detecting cancer in a patient, producing fusion proteins,
XX producing T cell populations and antigen presenting cells. The present
XX sequence represents a polynucleotide sequence of the invention.
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 99.1%; Score 2565; DB 12; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 12 GGGAGCTCCCTAGCCAGTACCCAGATACGCTGGGAACCTTCCCGACATGGCTTCCC 71
DB 33 GGGAGCTCCCTAGCCAGTACCCAGATACGCTGGGAACCTTCCCGACATGGCTTCCC 92
QY 72 TGGGGAGATCTCTTCTGGAGCATATTTAGCATTCATTTATTTGGCTGGAGCAATTG 131
DB 93 TGGGGAGATCTCTTCTGGAGCATATTTAGCATTCATTTATTTGGCTGGAGCAATTG 152
QY 132 CACTCATTCATTTGGCTTGTATTTTCAGGAGACACTCCATCAGATCATACTGTGCGCT 191
DB 153 CACTCATTCATTTGGCTTGTATTTTCAGGAGACACTCCATCAGATCATACTGTGCGCT 212
QY 192 CAGCTGGGAACATTTGGGAGATGGAATCTGAGCTGACATTTTGAACCTGACATCAAC 251
DB 213 CAGCTGGGAACATTTGGGAGATGGAATCTGAGCTGACATTTTGAACCTGACATCAAC 272
QY 252 TTTCTGATTCGATGATCAATGGCTGAAGGAAGTGTATTTAGCTTGTCTCAGATGTC 311
DB 273 TTTCTGATTCGATGATCAATGGCTGAAGGAAGTGTATTTAGCTTGTCTCAGATGTC 332
QY 312 AAGAGGCAAAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGGCGGAGCAGAGTGT 371
DB 333 AAGAGGCAAAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGGCGGAGCAGAGTGT 392
QY 372 TTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGGTGAAGAAACGTGCAATCAG 431
DB 393 TTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGGTGAAGAAACGTGCAATCAG 452
QY 432 ATGCTGGACCTTCAATATGTTATATCACTCTTAAGGCAAGGGAATGCTAACTG 491
DB 453 ATGCTGGACCTTCAATATGTTATATCACTCTTAAGGCAAGGGAATGCTAACTG 512
QY 492 AGTATAAACTGAGGCTTCAGATGCGGAGATGATGATGATGATGATGATGATGATG 551
DB 513 AGTATAAACTGAGGCTTCAGATGCGGAGATGATGATGATGATGATGATGATGATG 572

QY 552 AGACCTTGGGGTGTGAGGCTCCCGATGTGTCGCCAGGCCAAGTGTGTGGGATGCC 611
DB 573 AGACCTTGGGGTGTGAGGCTCCCGATGTGTCGCCAGGCCAAGTGTGTGGGATGCC 632
QY 612 AAGTTGACAGGAGGCAACTTCTCGAAGTCTCAATACAGACTTTGAGCTGAACCTG 671
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QY 732 CCTGTATGATGAAATGACATTTGCCAAAGCAACAGGGATATCAAGGACAGATTCG 791
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DB 1593 GATTTTATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGCTTATTTCTCA 1652

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OY 1632 GATGATGTCATCCGGAATGTCACAGGAAAGACCTTTCACCTTGACTATATGACATTA 1691
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Db 1653 GATGATGTCATCCGGAATGTCACAGGAAAGACCTTTCACCTTGACTATATGACATTA 1712
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Db 1713 TGTGATCACAAGCTTGAGGCTTCTCTTTCATCTCTGCTGAGACAGTAAAGACTTCAGT 1772
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OY 1752 TTTGCAATGATCTTGAGAGAGTGGAGCTAGCTGGGGTGAATTTCCGCCCTCCCGG 1811
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Db 1773 TTTGCAATGATCTTGAGAGAGTGGAGCTAGCTGGGGTGAATTTCCGCCCTCCCGG 1832
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Db 2253 CTGCAAGCCCAAGTCTGTGAAGAAATGCTGATCTGAGCTTCTTCTTACTCTGA 2312
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OY 2531 AGAAAACTGATTTAGAGTTCTGATCGTTCAAGAGATGTTAAATATACATTTCT 2587
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Db 2553 AGAAAACTGATTTAGAGTTCTGATCGTTCAAGAGATGTTAAATATACATTTCT 2609
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DE Human B7-H8 gene.
KW Human; B7-like protein; inflammation; tissue damage; immune disorder;
KW Addison's disease; autoimmune haemolytic anaemia; autoimmune thyroiditis;
KW diabetes mellitus; Crohn's disease; multiple sclerosis; allergy; cancer;
KW rheumatoid arthritis; cardiovascular disorder; nervous system disorder;
KW myocardial ischaemia; ulcerative colitis; reproductive system disorder;
KW Alzheimer's disease; Parkinson's disease; endocrine disorder; hepatitis;
KW diabetes mellitus; Grave's disease; Paget's disease; liver disorder;
KW gastrointestinal disorder; irritable bowel syndrome; cerebral anoxia;
KW dysphagia; hepatomegaly; neurological disease; infectious disease;
KW epilepsy; gene therapy; B7-H8 protein; chromosome 1; gene; ds.
OS Homo sapiens.
PH Key Location/Qualifiers
FT CDS 419..1267
FT /tag= a
FT /product= "Human B7-H8 protein"
FT sig_peptide 419..490
FT /tag= b
FT mat_peptide 491..1264
FT /tag= c
FT /product= "Human mature B7-H8 protein"
PD WO200202587-A1.
PD 10-JUN-2002.
PF 29-JUN-2001; 2001WO-US020917.
PR 30-JUN-2000; 2000US-0251335P.
PR 14-AUG-2000; 2000US-0225266P.
PA (HUMA-) HUMAN GENOME SCT INC.
PI Fiselcia M, Ni J, Ruben SM;
PI MPI: 2002-257198/30.
DR P-PSDB; MAE20311.
DR
PT Isolated nucleic acids encoding human B7-like polypeptides, useful for
PT diagnosis and treatment of e.g. inflammation, cancer, immune disorders
PT such as Addison's disease, and cardiovascular disorders such as
PT myocardial ischaemia.
PS Example 1; Fig 1; 493bp; English.
XX
XX The present invention relates to novel human B7-like polypeptides and
XX polynucleotides encoding such proteins. Sequences of the invention are
XX used for preventing, treating or ameliorating a medical condition in a
XX mammalian subject. The polynucleotides and polypeptides are administered
XX to subjects having a disorder related to B-7 Like polypeptides, such as
XX inappropriate or excessive inflammation which can lead to tissue damage
XX or even death, where the inflammation is brought about by the activation
XX of certain cells in the body e.g. T cells and may involve disorders
XX related to immune system. The nucleic acids, proteins, antibodies,
XX agonists and antagonists of the invention are useful in the diagnosis,
XX treatment and prevention of cancer (e.g. cancers of the adrenal gland,
XX bone, bone marrow, breast, gastrointestinal tract, liver, urogenital or
XX lung), immune disorders (e.g., Addison's disease, allergies, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX disease, multiple sclerosis, rheumatoid arthritis, ulcerative colitis),
XX cardiovascular disorders (e.g., myocardial ischaemia), nervous system
XX disorders (Alzheimer's disease, Parkinson's disease), endocrine disorders
XX (e.g., diabetes mellitus, Grave's disease), reproductive system disorders
XX (e.g., cryptorchism, Paget's disease), gastrointestinal disorders (e.g.,
XX dysphagia, irritable bowel syndrome), liver disorders (e.g., hepatitis,
XX hepatomegaly), neurological diseases (e.g., cerebral anoxia and epilepsy)
XX and infectious diseases such as viral, bacterial, fungal and parasitic
XX infections. Sequences of the invention are also used in gene therapy. The
XX present sequence is a DNA encoding human B7-H8 protein. B7-H8 gene is
XX located on chromosome 1

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QY 2111 CTCTATCGGGACACAGATATACATCTCTGAGTGAAGAGAGTTCAGAGGCTATGGGAAA 2170
 DB 2469 CTCTATCGGGACACAGATATACATCTCTGAGTGAAGAGAGTTCAGAGGCTATGGGAAA 2528
 QY 2171 TCCCTGATGGGATTTATCTTCACTGTTGAGCTTCTTAAGTTTCTTCCCTCAATCTAC 2230
 DB 2529 TCCCTGATGGGATTTATCTTCACTGTTGAGCTTCTTAAGTTTCTTCCCTCAATCTAC 2588
 QY 2231 CTGCAAGCCAAAGTCTGTGAAGAAATGCTGAGTCTGAGGTTTCTTACCTGTA 2290
 DB 2589 CTGCAAGCCAAAGTCTGTGAAGAAATGCTGAGTCTGAGGTTTCTTACCTGTA 2648
 QY 2291 ATTATGATCTCCAGACCTTCCCTGCGCAATTTCAATTAAGCAAAACATATACCTT 2350
 DB 2649 ATTATGATCTCCAGACCTTCCCTGCGCAATTTCAATTAAGCAAAACATATACCTT 2708
 QY 2351 CCATGAAGACACACAGACTTTTGAAGAAGACACATGACTGTTGAATGAGGCTTG 2410
 DB 2709 CCATGAAGACACACAGACTTTTGAAGAAGACACATGACTGTTGAATGAGGCTTG 2768
 QY 2411 AGGAATGAAGCTTTGAAGAAAGAAATGCTTGTTCAGCCCTTCCCAACTCTTA 2470
 DB 2769 AGGAATGAAGCTTTGAAGAAAGAAATGCTTGTTCAGCCCTTCCCAACTCTTA 2828
 QY 2471 TGTGTTAACCACTGCTTCTGAGACCTTGAAGCAAGTACTGTTATCATGTTGTTAT 2530
 DB 2829 TGTGTTAACCACTGCTTCTGAGACCTTGAAGCAAGTACTGTTATCATGTTGTTAT 2888
 QY 2531 AGAAACTGATTTTGAAGTCTGATGTTCAAGAAATGATTAATATCATTTGCT 2587
 DB 2889 AGAAACTGATTTTGAAGTCTGATGTTCAAGAAATGATTAATATCATTTGCT 2945

RESULT 10

AAD29253
 ID AAD29253 standard; DNA; 2603 BP.

AAD29253;

07-MAY-2002 (first entry)

Human B7-like protein (B7-L) DNA.

Human; B7-like protein; B7-L; reproductive disorder; autoimmune disease; proliferative disorder; infertility; hyperplasia; cancer; lung; breast; brain; seminal vesicle; haematopoietic system; tumour; diabetes mellitus; rheumatoid arthritis; systemic lupus erythematosus; toxic shock syndrome; inflammatory bowel disease; psoriasis; allergy; Crohn's disease; vaccine; Grave's disease; arteriosclerosis; multiple sclerosis; hypersensitivity; nephropathy; skin disorder; endocrinopathy; vasculopathy; gynaecological; myasthenia gravis; anaemia; lymphoproliferative disorder; neuroprotective; cytostatic; multiple myeloma; tissue-degenerating disease; nephrotropic; immunosuppressive; asthma; virucide; gene therapy; ds.

Homo sapiens.

Location/Qualifiers

Key CDS 53..901

sig_peptide 53..124

mat_peptide 125..898

/product= "Human mature B7-L protein"

WO200202624-A2.

10-JAN-2002.

29-JUN-2001; 2001WO-US021297.

PR 30-JUN-2000; 2000US-0215645P.
 PA (AMGE-) AMGEN INC.
 PI Fox M, Sullivan JK, Pang M;
 DR WPI, 2002-171639/22.
 P-PSDB; AME18336.
 PT Novel B7-like polypeptides, polynucleotides and their modulators useful for prevention and treatment of reproductive, immune and proliferative disorders, e.g. cancer, arteriosclerosis.

Claim 1; Fig 1A-1C; 133pp; English.

The present invention relates to an isolated B7-like (B7-L) polypeptide and its polynucleotide. B7-1 and its modulators are useful for treating reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L are useful for enhancing the immune response to tumours. B7-1 plays a role in growth and maintenance of cancer cells based on the observation of seminal vesicle hyperplasia in transgenic mice overexpressing B7-1. Modulators of B7-1 are useful for the treatment of cancer e.g. seminal vesicle, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-1 and their modulators are useful to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. Modulators of B7-L are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, arteriosclerosis and vascular stenosis. Soluble B7-L serves as vaccine adjuvants. Antagonists of B7-L are useful for alleviation of toxic shock syndrome or allo sensitisation due to blood transfusions, and for treatment of multiple sclerosis, allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies, various pneumopathies, vasculopathies, coeliac disease, anaemia, thrombocytopenia, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. B7-L gene is useful in gene therapy and to map the locations of B7-L gene and related genes on chromosomes, as hybridisation probes in diagnostic assays, for isolating corresponding chromosomal B7-L genes, and to identify heritable tissue-degenerating diseases. The present sequence is human B7-L protein DNA

Sequence 2603 BP; 758 A; 589 C; 573 G; 682 T; 0 U; 1 Other;

Query Match 99.1%; Score 2563; DB 6; Length 2603;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2574; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 12 GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCAGCATGCTTCCC 71
 DB 3 GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCAGCATGCTTCCC 62
 QY 72 TGGGGCAATCCTCTTTCGAGCATATTTAGCATATATTTGCTGGAGCAATTG 131
 DB 63 TGGGGCAATCCTCTTTCGAGCATATTTAGCATATATTTGCTGGAGCAATTG 122
 QY 132 CACTCATATGCGCTTGTGATATTTTCAGGAGACACTCCATCACTACTACTGCGCT 191
 DB 123 CACTCATATGCGCTTGTGATATTTTCAGGAGACACTCCATCACTACTACTGCGCT 182
 QY 192 CAGCTGGAAACATTGGGAGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAC 251
 DB 183 CAGCTGGAAACATTGGGAGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAC 242
 QY 252 TTTCTGATATCGTATTAATGAGTGAAGAAAGTGTGCTTGGCTTGCATGATGTTCA 311
 DB 243 TTTCTGATATCGTATTAATGAGTGAAGAAAGTGTGCTTGGCTTGCATGATGTTCA 302

QY 312 AAGAGGCAAAAGATGAGCTGTCGGAGCAGGATGGAATGTTCAAGAGCCGGACAGAGTGT 371
DB 303 AAGAGGCAAAAGATGAGCTGTCGGAGCAGGATGGAATGTTCAAGAGCCGGACAGAGTGT 362
QY 372 TTGCTGATCAAGATGATGTTGGCAATGCTTTTGCGGCTGAAAAAGTGCACATCAGAC 431
DB 363 TTGCTGATCAAGATGATGTTGGCAATGCTTTTGCGGCTGAAAAAGTGCACATCAGAC 422
QY 432 ATGCTGGCACCTACAAATGTTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTG 491
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QY 492 AGATATAAAGCTGAGCCTTGAGCATGCGGAGGAAATGAGACTATATAGCCAGCTCAG 551
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QY 552 AGACCTTGGCGGTGAGAGCTCCCGATGTTCCCGCAGCCAGAGTGGTCTGGGCAATCCC 611
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QY 612 AAGTTGACAGGAGGACCACTTCTCGGAAGTCTTCCAAATACCAAGCTTTGAGCTGAATCTTG 671
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QY 672 AGAATGACCATGAGAGGTTGTCGTGCTGCTCAATGTTTACATGATCAAGCAACATCACT 731
DB 663 AGAATGACCATGAGAGGTTGTCGTGCTGCTCAATGTTTACATGATCAAGCAACATCACT 722
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DB 783 AGATCAAAAGGCGAGTCACTTCAAGCTGCTTAACTCAAAAGCTTCTGTGTGTCTT 842
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QY 912 GTGCTTGGCCACAAAAAAGCATGCAAGTCAATGTTTACAAAGGAGTCTACAGAACTAT 971
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QY 972 TTGACCAACAGATATGACCTAGTTTATATTTCTGGAGGAAATGAAATTCATATCTAGAA 1031
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QY 1572 GATTTATATAATTAATTAATGAGACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
DB 1563 GATTTATATAATTAATTAATGAGACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1622
QY 1632 GATGATGTTATATCCGTAATGCTGCAAGGAAAGACCTTTACCTTGATATATAGCATTA 1691
DB 1623 GATGATGTTATATCCGTAATGCTGCAAGGAAAGACCTTTACCTTGATATATAGCATTA 1682
QY 1692 TGTATATCAAGATCTGAGGCTTCTCTTCCATCTGCTGAGACAGCTAAGCTCACT 1751
DB 1683 TGTATATCAAGATCTGAGGCTTCTCTTCCATCTGCTGAGACAGCTAAGCTCACT 1742
QY 1752 TTTCAATAGATCTAGAGGAGTGGACCTGAGCTGGGGTGAATTTGGCCCCCATCTCCGGG 1811
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QY 1812 GGAATGCTGAAGACAAATTTTGTGTTACTCAATGAGGAGTGGAGAGATACAGTCTTA 1871
DB 1803 GGAATGCTGAAGACAAATTTTGTGTTACTCAATGAGGAGTGGAGAGATACAGTCTTA 1862
QY 1872 CTACCACTAGTGGATTAAGAGGCGCAGGAGTGTCTCAACTCTTCAATGATACAGACT 1931
DB 1863 CTACCACTAGTGGATTAAGAGGCGCAGGAGTGTCTCAACTCTTCAATGATACAGACT 1922
QY 1932 CTCGCCATTACAACTTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTGT 1991
DB 1923 CTCGCCATTACAACTTACCCCAATCCGAAGTGTCAACTGTGTGTCAAGACTAAGAAACCTGTGT 1982
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QY 2351 CCATGAAGCACACACAGCTTTTGAAGAGAGACAAATGACCTTGAATTAAGGCTTGG 2410
DB 2343 CCATGAAGCACACACAGCTTTTGAAGAGAGACAAATGACCTTGAATTAAGGCTTGG 2402
QY 2411 AGGAATGAAGCTTTGAAGAGAAAGATATCTTTGTTTCCAGCCCTTCCCAACTCTTCA 2470
DB 2403 AGGAATGAAGCTTTGAAGAGAAAGATATCTTTGTTTCCAGCCCTTCCCAACTCTTCA 2462
QY 2471 TGTGTTAACCACTGCTTCTGTGAACCTTGAAGCCACAGGAGCTGTATATCATGTTGTAT 2530

|||||
Db 2463 TGTGTTAAACCACTGCTTCCTGGAACCTTGAGACCAAGGAGCTGATTTACATGTTGTAT 2522
QY 2531 AAAAAACGATTTTGAAGTTCGATCGTTCAGAGAAATGATTAATATCATTTCT 2587
Db 2523 AAAAACTGATTTTAAAGTTTGATGTTCAAGAGATATTAATATCATTTCT 2579
RESULT 11
ABU57354
ID ABU57354 standard; cDNA; 2591 BP.
XX
AC ABU57354;
XX
DT 12-AUG-2002 (first entry)
XX
DE Breast BS265 gene EST clone 3038129.
XX
BS265; human; breast; cancer; tumour; metastasis; diagnosis;
KM gene therapy; expressed sequence tag; EST; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61..909
FT /tag= a
FT /product= "BS265"
XX
PN US2002034749-A1.
XX
PD 21-MAR-2002.
XX
PF 07-MAY-2001; 2001US-00850178.
XX
PR 18-NOV-1997; 97US-00972376.
PR 18-NOV-1998; 98US-00193944.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLE/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L A.
PA (RUSSE/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI Grandos EN, Hodges SC, Kلاس MR, Kratochvil JD, Roberts-Rapp LA,
PI Russell JC, Stroupe SD;
XX
DR WPI; 2002-403712/43.
XX P-PSDB; ABB76274.
XX
PT New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
PT staging, monitoring, prognosticating, in vivo imaging, preventing,
PT treating, or determining the predisposition of an individual to breast
PT cancer.
XX
PS Claim 52; Page 41-42; 52pp; English.
XX
CC The present sequence is of human breast BS265 gene expressed sequence tag
CC (EST) clone 3038129. ESTs were derived from cDNA libraries made from
CC breast tumour tissues, breast non-tumour tissues and numerous other
CC tissues, and entered into a database as gene transcript images. They were
CC then evaluated to identify EST sequences that were representative
CC primarily of the breast tissue libraries, and were ranked according to
CC their abundance in the target libraries and absence from background
CC libraries. 4 Partial clones (see ABU57345-48) represented the minimum
CC number of clones that, together with the full-length sequence of clone

CC 3090752H1 (see ABU57349), were needed to form a contig and from which a
CC consensus sequence (see ABU57350) for BS265 was derived. Other clones
CC appeared at positions in the assembly upstream of the above sequences.
CC Clone 3038129 spanned the entire assembly, and encoded the protein given
CC in ABB76274. The set of contiguous and partially overlapping cDNA
CC sequences, designated as BS265 and transcribed from breast tissue, and
CC the polypeptides encoded by them, are useful for detecting, diagnosing,
CC staging, monitoring, prognosticating, in vivo imaging, preventing,
CC treating, or determining the predisposition of an individual to diseases
CC and conditions of the breast, especially tumours and metastases

XX Sequence 2591 BP; 739 A; 591 C; 579 G; 682 T; 0 U; 0 Other;

Query Match 98.7%; Score 2554; DB 6; Length 2591;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2576; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 12 GGCAGCTCACTCAGCCGATGCCAGATACCGTGGAAACCTTCCCAAGCATGGCTTCCC 71
Db 11 GGCAGCTCACTCAGCCGATGCCAGATACCGTGGAAACCTTCCCAAGCATGGCTTCCC 70
QY 72 TGGGGCAGATCCCTCTTCGAGCATTAATTAGCATCATTTATTTGCTGGAGCAATTG 131
Db 71 TGGGGCAGATCCCTCTTCGAGCATTAATTAGCATCATTTATTTGCTGGAGCAATTG 130
QY 132 CACTCATATTGGCTTTGGTATTTTCAGGAGACATCTCCATCAAGTCACTAATGCGCT 191
Db 131 CACTCATATTGGCTTTGGTATTTTCAGGAGACATCTCCATCAAGTCACTAATGCGCT 190
QY 192 CAGCTGGGAAATCTGGGAGATGGAATCCAGTGCATCTTTGAACCTTGAACCTGAAC 251
Db 191 CAGCTGGGAAATCTGGGAGATGGAATCCAGTGCATCTTTGAACCTTGAACCTGAAC 250
QY 252 TTTCTGATATGATGATTAATATGATGCTGAAGAGAGGTGTTTGGCTTGTCCATGAGTTCA 311
Db 251 TTTCTGATATGATGATTAATATGATGCTGAAGAGAGGTGTTTGGCTTGTCCATGAGTTCA 310
QY 312 AAGAAAGCAAGATGAGCTGTGAGCAGATGAATGTTCAAGAGCCGGAACAGAGTGT 371
Db 311 AAGAAAGCAAGATGAGCTGTGAGCAGATGAATGTTCAAGAGCCGGAACAGAGTGT 370
QY 372 TTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTGAAAAACGTGACATCAAG 431
Db 371 TTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTGAAAAACGTGACATCAAG 430
QY 432 ATGCTGGACCTCAAAATGTTATATCATCACTTCAAGGCAAGGGAGATGTAACCTTG 491
Db 431 ATGCTGGACCTCAAAATGTTATATCATCACTTCAAGGCAAGGGAGATGTAACCTTG 490
QY 492 AGTATMAAATGGAACCTTCAGCATGCCGGAAGTGAATGTGATTAATGCAAGCTCAG 551
Db 491 AGTATMAAATGGAACCTTCAGCATGCCGGAAGTGAATGTGATTAATGCAAGCTCAG 550
QY 552 AGACCTTGGGCTGTGAGGCTCCCGATGTTCCCAAGCCCAAGTGTCTGGGATCCC 611
Db 551 AGACCTTGGGCTGTGAGGCTCCCGATGTTCCCAAGCCCAAGTGTCTGGGATCCC 610
QY 612 AAGTTGACAGGAGCAACCTTCTGGAAGTCCCAATACAGAGCTTGAAGCTGAACTCG 671
Db 611 AAGTTGACAGGAGCAACCTTCTGGAAGTCCCAATACAGAGCTTGAAGCTGAACTCG 670
QY 672 AGAATGTGACATGAAGGTTGTCTGTGCTTCAATAGTTAAGTCAACAACATCACT 731
Db 671 AGAATGTGACATGAAGGTTGTGTGTCTGTCTCAATAGTTAAGTCAACAACATCACT 730
QY 732 CCGTATGATTTAAATGACATTTGCAAGCAAGGAGATATCAAAAGTGAAGATGG 791
Db 731 CCGTATGATTTAAATGACATTTGCAAGCAAGGAGATATCAAAAGTGAAGATGG 790
QY 792 AGATCAAAAGGGAGTCACTCAAGCTGCTTAACTCAAGGCTTCTGTGTCTCT 851
Db 791 AGATCAAAAGGGAGTCACTCAAGCTGCTTAACTCAAGGCTTCTGTGTCTCT 850

| | | | |
|----|-----|----------------------------------------------------------------|-----|
| OY | 12 | GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCGAGCAATGGCTCCC | 71 |
| Db | 11 | GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCGAGCAATGGCTCCC | 70 |
| OY | 72 | TGGGGCAGATCTCTTCTTGAGCATTAATTAGCATCATCTATTATTCGGCTGGAGCAATTG | 131 |
| Db | 71 | TGGGGCAGATCTCTTCTTGAGCATTAATTAGCATCATCTATTATTCGGCTGGAGCAATTG | 130 |
| OY | 132 | CACATCATATTGGCTTTGGTATTTCAGGGAGACATCCATCAACATCACTCATCTGCGCT | 191 |
| Db | 131 | CACATCATATTGGCTTTGGTATTTCAGGGAGACATCCATCAACATCACTCATCTGCGCT | 190 |
| OY | 192 | CAGCTGGGAACATTTGGGGAGATGGAATTCCTGACGTGCACTTTGAAACCTGACATCAAAAC | 251 |
| Db | 191 | CAGCTGGGAACATTTGGGGAGATGGAATTCCTGACGTGCACTTTGAAACCTGACATCAAAAC | 250 |
| OY | 252 | TTTCTGATATCGTATACATAGGCTGAAGAGTCTTTTAGGCTTGCTCCATGATTTCA | 311 |
| Db | 251 | TTTCTGATATCGTATACATAGGCTGAAGAGTCTTTTAGGCTTGCTCCATGATTTCA | 310 |
| OY | 312 | AAGAAAGCAAGAATGAGCTGTCGGAGCAGAGTGAATGTTCAGAGGCCGAGACGACGTGT | 371 |
| Db | 311 | AAGAAAGCAAGAATGAGCTGTCGGAGCAGAGTGAATGTTCAGAGGCCGAGACGACGTGT | 370 |
| OY | 372 | TTGCTGATTAATGATAGTTGGCAATGGCTCTTTGGGGCTGAAAAACGTGGAACTCACAG | 431 |
| Db | 371 | TTGCTGATTAATGATAGTTGGCAATGGCTCTTTGGGGCTGAAAAACGTGGAACTCACAG | 430 |
| OY | 432 | ATGCTGGCACCTACAAATGTTATATCATCACTTCTAAAGCAGAGGGAATGCTAACCTTG | 491 |
| Db | 431 | ATGCTGGCACCTACAAATGTTATATCATCACTTCTAAAGCAGAGGGAATGCTAACCTTG | 490 |
| OY | 492 | AGTATAAAACTGAGCTTCAAGCATCCGGAATGATGTGACCTATTAATGCCAGCTCAG | 551 |
| Db | 491 | AGTATAAAACTGAGCTTCAAGCATCCGGAATGATGTGACCTATTAATGCCAGCTCAG | 550 |
| OY | 552 | AGACCTTGGGGTGTAGAGCTCCGCCATTGTTCCCCCAGCCCAAGAGTGTCTGGGCAATCCC | 611 |
| Db | 551 | AGACCTTGGGGTGTAGAGCTCCGCCATTGTTCCCCCAGCCCAAGAGTGTCTGGGCAATCCC | 610 |
| OY | 612 | AAGTTGACACGGAGGCACTTCTCGGAAGTCCAAATACCAAGCTTTGAGCTGAACCTG | 671 |
| Db | 611 | AAGTTGACACGGAGGCACTTCTCGGAAGTCCAAATACCAAGCTTTGAGCTGAACCTG | 670 |
| OY | 672 | AGAAATGTGACCAATGAAGTTGTGTCTGTGCTTACATGTTATGACATCAACCAACATACT | 731 |
| Db | 671 | AGAAATGTGACCAATGAAGTTGTGTCTGTGCTTACATGTTATGACATCAACCAACATACT | 730 |

| | | | |
|----|------|-----------------------------------------------------------------|------|
| QY | 732 | CTGTGATGATTGAAAATGACATTGCCAAAGCACAGGGGATATCTAAAGTGCACGAATCCG | 791 |
| Db | 731 | CCCTGATGATTTGAAAATGACATTGCCAAAGCACAGGGGATATCTAAAGTGCACGAATCCG | 790 |
| QY | 792 | AGATCAAAAGGCGGAGTCACTTACAGGGCTTAACTCAAAAGGCTTCTGTGTCTCTT | 851 |
| Db | 791 | AGATCAAAAGGCGGAGTCACTTACAGGGCTTAACTCAAAAGGCTTCTGTGTCTCTT | 850 |
| QY | 852 | CTTTCTTTGCCATCAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATPAT | 911 |
| Db | 851 | CTTTCTTTGCCATCAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATPAT | 910 |
| QY | 912 | GTGCTTGGCCAC-AAAAAGCATGCAAAGTCATTTGTTACACAGGGATCTACGAAGCTA | 970 |
| Db | 911 | GTGCTTGGCCACAAAAAAGCATGCAAAGTCATTTGTTACACAGGGATCTACGAAGCTA | 970 |
| QY | 971 | TTTACCAACCAAGATATGACCTAGTTTATATTTCTGGGAGGAATGAAATCATATCTAGA | 1030 |
| Db | 971 | TTTACCAACCAAGATATGACCTAGTTTATATTTCTGGGAGGAATGAAATCATATCTAGA | 1030 |
| QY | 1031 | AGCTGAGTGAAGCAAAACAAGACAGAAAACAAAAGAGCCAAAGCAGAGGCTCCAA | 1090 |
| Db | 1031 | AGCTGAGTGAAGCAAAACAAGACAGAAAACAAAAGAGCCAAAGCAGAGGCTCCAA | 1090 |
| QY | 1091 | TATGAAACAGATTAATCTATCTTCAAGAATATTGAAGTTGGGAAAATATTCATATGTG | 1150 |
| Db | 1091 | TATGAAACAGATTAATCTATCTTCAAGAATATTGAAGTTGGGAAAATATTCATATGTG | 1150 |
| QY | 1151 | AACCTAGAACAATGTGTTAAGATGATATGATAAGTAAATGACGTTGAGAGCAAGTGCATCCCA | 1210 |
| Db | 1151 | AACCTAGAACAATGTGTTAAGATGATATGATAAGTAAATGACGTTGAGAGCAAGTGCATCCCA | 1209 |
| QY | 1211 | GATCTCAAGGACCTCCCTGCTGTCACCTGGGAGTGAAGGACAGATATGTCATGT | 1270 |
| Db | 1210 | GATCTCAAGGACCTCCCTGCTGTCACCTGGGAGTGAAGGACAGATATGTCATGT | 1269 |
| QY | 1271 | TCTTTGCTCTGGAATTTTAACTTATATGATGCTGTAATGTTGCTCTGAGAAAGCCCTTGA | 1330 |
| Db | 1270 | TCTTTGCTCTGGAATTTTAACTTATATGATGCTGTAATGTTGCTCTGAGAAAGCCCTTGA | 1329 |
| QY | 1331 | AAGCTAATCCCAACATATCCACATCTTAATTCACAAATTAAGCTGATGATGACCT | 1390 |
| Db | 1330 | AAGCTAATCCCAACATATCCACATCTTAATTCACAAATTAAGCTGATGATGACCT | 1389 |
| QY | 1391 | AAGACGCTGCTAATTTGACTGCTGCTGCACTCAGGGGCGGCTGCAATTTAGTATGAG | 1450 |
| Db | 1390 | AAGACGCTGCTAATTTGACTGCTGCTGCACTCAGGGGCGGCTGCAATTTAGTATGAG | 1449 |
| QY | 1451 | TCAATGATTCACCTTTTATATGATGCTTCCAAAGGCTCTTGCGCTTCTTCCCAATGAC | 1510 |
| Db | 1450 | TCAATGATTCACCTTTTATATGATGCTTCCAAAGGCTCTTGCGCTTCTTCCCAATGAC | 1509 |
| QY | 1511 | AAATGCCAAAGTGAAGAAAATGATCAATTTTAACTAAACAGAGCAGTCCGCGACAC | 1570 |
| Db | 1510 | AAATGCCAAAGTGAAGAAAATGATCAATTTTAACTAAACAGAGCAGTCCGCGACAC | 1569 |
| QY | 1571 | CGATTTTAAATAACTGAGCACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTC | 1630 |
| Db | 1570 | CGATTTTAAATAACTGAGCACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTC | 1629 |
| QY | 1631 | AGATGATGTCATCCGTGAATGTCACAGGAGGACCTTCACTTGAATATGAGCATTT | 1690 |
| Db | 1630 | AGATGATGTCATCCGTGAATGTCACAGGAGGACCTTCACTTGAATATGAGCATTT | 1689 |
| QY | 1691 | ATGTCATCAACAAGCTCTGAGGCTTCTCTTCCATCTCGGCTGACAGCTAAGACCTAG | 1750 |
| Db | 1690 | ATGTCATCAACAAGCTCTGAGGCTTCTCTTCCATCTCGGCTGACAGCTAAGACCTAG | 1749 |
| QY | 1751 | TTTTCAATAGATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTTCGCCCCCATCTCCG | 1810 |
| Db | 1750 | TTTTCAATAGATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTTCGCCCCCATCTCCG | 1809 |
| QY | 1811 | GGAATGTCAGAGCAATTTTGTATCCTCAATGAGGAGTGAAGAGATACATGCT | 1870 |


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Db      1810 GGGATATCTGAGAGACATTTTGGTTACCTCAATGAGGAGTGGAGGATACAGTCT 1869
Qy      1871 ACTACCACTAGTGTGATTAAGGCCAGGATGTCTCAACCTCTACATGTACAGAGC 1930
Db      1870 ACTACCACTAGTGTGATTAAGGCCAGGATGTCTCAACCTCTACATGTACAGAGC 1929
Qy      1931 TCTCCCATTAACACTGACCAATCCGAAGTGTCACTGTGTGAGGACTAAGAAACCTCG 1990
Db      1930 TCTCCCATTAACACTGACCAATCCGAAGTGTCACTGTGTGAGGACTAAGAAACCTCG 1989
Qy      1991 TTTTGTAGTAAAAAGGCGCTGAAAAAGAGGGAGCCAAATCTGTCTGCTT-CTCACAT 2049
Db      1990 TTTTGTAGTAAAAAGGCGCTGAAAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAT 2049
Qy      2050 TAGCTATGGCAATTAAGCAATCTGTCTCTTTGGCTCTGCTCTGACAGACAGAGCCAGA 2109
Db      2050 TAGCTATGGCAATTAAGCAATCTGTCTCTTTGGCTCTGCTCTGACAGAGAGCCAGA 2109
Qy      2110 ACTCTATCGGGGACCAAGATTAACATCTCTGAGTAAGAGAGTTGACAAAGGCTTATGGAA 2169
Db      2110 ACTCTATCGGGGACCAAGATTAACATCTCTGAGTAAGAGAGTTGACAAAGGCTTATGGAA 2169
Qy      2170 ATGCTGTAGTGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTAC 2229
Db      2170 ATGCTGTAGTGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTAC 2229
Qy      2230 CTTGCAAGCCAAAGTCTGTAAAGAAATGCTGAGTTCTAGCTCAAGGTTTCTTACTCTG 2289
Db      2230 CTTGCAAGCCAAAGTCTGTAAAGAAATGCTGAGTTCTAGCTCAAGGTTTCTTACTCTG 2289
Qy      2290 AATTTGATGTCAGACCCCTTCCGAGCAATTCAAATTAAGCAACAAACATATACCT 2349
Db      2290 AATTTGATGTCAGACCCCTTCCGAGCAATTCAAATTAAGCAACAAACATATATACCT 2349
Qy      2350 TCCATGAGACACACAGACTTTTGAAGAGACATAGCTTGAATTTGAGGCTT 2409
Db      2350 TCCATGAGACACACAGACTTTTGAAGAGACATAGCTTGAATTTGAGGCTT 2409
Qy      2410 GAGGAATGAAGCTTTGAAGAAAGAAATCTTTTCCAGCCCCCTTCCACACTCTTC 2469
Db      2410 GAGGAATGAAGCTTTGAAGAAAGAAATCTTTTCCAGCCCCCTTCCACACTCTTC 2469
Qy      2470 ATGTGTTAAACACCTGCTTCTGAGACCTTGGAGCAAGGTGATTAATCATTTGTTA 2529
Db      2470 ATGTGTTAAACACCTGCTTCTGAGACCTTGGAGCAAGGTGATTAATCATTTGTTA 2529
Qy      2530 TAGAAAACTGATTTTGAAGTTCTGATGTTCAAGAGATGATTAATATACATTTCT 2587
Db      2530 TAGAAAACTGATTTTGAAGTTCTGATGTTCAAGAGATGATTAATATACATTTCT 2587

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RESULT 13

ADP81075 standard; DNA; 2690 BP.

ADP81075;

09-SEP-2004 (first entry)

Human ovarian specific gene, SEQ ID No 109.

normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;

metastatic; cancer; vaccine; cytosolic; human; gene; ds.

Homo sapiens.

WO2004053079-A2.

24-JUN-2004.

08-DEC-2003; 2003WO-US038855.

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PR      06-DEC-2002; 2002US-0431301P.
PR      06-DEC-2002; 2002US-0431321P.
PR      30-JUN-2003; 2003US-0484584P.
PR      07-NOV-2003; 2003US-0518607P.
PA      (DIAD-) DIADEXUS INC.
PI      Medina RA, Turner LR, Sun Y, Liu S, Chen H;
XX      WPI; 2004-468850/44.
DR      P-PSDB; ADP81235, ADP81236.
XX      New ovarian specific nucleic acid molecules and polypeptides useful for
PT      diagnosing, preventing or treating ovarian cancer, for producing
PT      transgenic animals or cells, or for research purposes.
XX      Claim 1; SEQ ID NO 109; 754pp; English.
XX      The invention relates to novel isolated nucleic acid molecules and
CC      polypeptides present in normal and neoplastic ovarian cells. These
CC      comprise a nucleic acid sequence encoding any of the 167 amino acid
CC      sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
CC      specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
CC      the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
CC      in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
CC      further comprises: a method for determining the presence of a ovarian
CC      specific nucleic acid (OSNA) in a sample; a vector comprising the above
CC      nucleic acid molecule; a host cell comprising the vector; a method for
CC      producing a polypeptide encoded by the above nucleic acid molecule; a
CC      polypeptide encoded by the nucleic acid molecule cited above; an antibody
CC      or its fragment that specifically binds to the above polypeptide; a
CC      method for determining the presence of an ovarian specific protein in a
CC      sample; a method for diagnosing or monitoring the presence and metastases
CC      of ovarian cancer in a patient; a kit for detecting a risk of cancer or
CC      presence of cancer in a patient; a kit for detecting a means for
CC      determining the presence of the above nucleic acid molecule or
CC      polypeptide; a method of treating a patient with ovarian cancer; and a
CC      vaccine comprising the above polypeptide or nucleic acid encoding the
CC      polypeptide. The isolated nucleic acid molecules and polypeptides have
CC      cytotoxic activity. The isolated polypeptides may be used to create a
CC      vaccine. The isolated nucleic acid molecules and polypeptides can be used
CC      for diagnosing or monitoring the presence and metastases of ovarian
CC      cancer and treating ovarian cancer. This polynucleotide sequence
CC      represents an ovarian specific gene of the invention.
XX      Sequence 2690 BP; 760 A; 611 C; 603 G; 716 T; 0 U; 0 Other;
SQ
Query Match      95.1%; Score 2460; DB 12; Length 2690;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 2571; Conservative 0; Mismatches 0; Indels 91; Gaps 2;
Qy      17 CTCCTAGCCAGTACCCAGATACGCTGGAACTTCCCAAGCCTGCTTCCCTGGGG 76
Db      28 CTCCTAGCCAGTACCCAGATACGCTGGAACTTCCCAAGCCTGCTTCCCTGGGG 87
Qy      77 CAGATCCTCTTGGAGCATTAATTAACATCATTAATTTGCTGCTGAGCAATTTGCACTC 136
Db      88 CAGATCCTCTTGGAGCATTAATTAACATCATTAATTTGCTGCTGAGCAATTTGCACTC 147
Qy      137 ATCATTTGGCTTTGGTATTT----- 155
Db      148 ATCATTTGGCTTTGGTATTTTTCAGAAAGTCTGCTGCTTTCAGCAATGAAGGTTTGTT 207
Qy      156 -----CAGGAGACAC 166
Db      208 GTAGAAGTTCAGAGCTTCCCTTAGCATTAATTTGCTTCCGAAGTGCAGGAGACAC 267
Qy      167 TCCATACAGTCACTAGTGTGCTGCTGAGTGGAAATTTGGGAGAGATGAATTCCTGAGC 226
Db      268 TCCATACAGTCACTAGTGTGCTGCTGAGTGGAAATTTGGGAGAGATGAATTCCTGAGC 327
Qy      227 TGCACTTTGAACCTACATCAAACTTTGATATGATGATCAATGAGTGAAGAGGT 286

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Db 328 TGCACCTTTGAACTGACATCAAACTTTCTGATATGATGATCAAAATGCGTGAAGAAAGGT 387
OY 287 GTTTTAAGCTTGTCATGATGATTCAAAGAGCAAAAGATGAGCTGCGAGAGAGATGAA 346
Db 388 GTTTTAAGCTTGTCATGATGATTCAAAGAGCAAAAGATGAGCTGCGAGAGAGATGAA 447
OY 347 ATGTTCAAGAGCGCGACAGACAGTGTGTTGCTGATCAAGATGATGTTGGCAATGCTCTTTG 406
Db 448 ATGTTCAAGAGCGCGACAGACAGTGTGTTGCTGATCAAGATGATGTTGGCAATGCTCTTTG 507
OY 407 CGGCTGAAAAACGTGCACTCAACAGATGCTGACACTTACAAATGTTATATCATCTTCT 466
Db 508 CGGCTGAAAAACGTGCACTCAACAGATGCTGACACTTACAAATGTTATATCATCTTCT 567
OY 467 AAAGCAAGGGGAAATGCTAAGCTGATGATTAACCTGAGCCCTTACAGATGCGGAAAGT 526
Db 568 AAAGCAAGGGGAAATGCTAAGCTGATGATTAACCTGAGCCCTTACAGATGCGGAAAGT 627
OY 527 AATGTGACTATATATGCACTCAGACCTTGAGACCTTGCGGTGTGAGGCTCCCGATGTTCC 586
Db 628 AATGTGACTATATATGCACTCAGACCTTGAGACCTTGCGGTGTGAGGCTCCCGATGTTCC 687
OY 587 CAGCCCAAGTGTGCTGCGCATCCCAAGTTGACAGGAGCCCACTTCTCGAAGTCTCC 646
Db 688 CAGCCCAAGTGTGCTGCGCATCCCAAGTTGACAGGAGCCCACTTCTCGAAGTCTCC 747
OY 647 AATACAGCTTTGAGCTGAACTCTGAGATGAGACCATGAGGTTGTGTCGTGCTTAC 706
Db 748 AATACAGCTTTGAGCTGAACTCTGAGATGAGACCATGAGGTTGTGTCGTGCTTAC 807
OY 707 AATGTTACGATCAACACACATATCTCTGATGATTTGAAATGACATTTGCCAAGCAACA 766
Db 808 AATGTTACGATCAACACACATATCTCTGATGATTTGAAATGACATTTGCCAAGCAACA 867
OY 767 GGGGATATCAAAAGTGCACAAATCGAGATCAAAAGCGGAGTCACTTACAGTCTTAAAC 826
Db 868 GGGGATATCAAAAGTGCACAAATCGAGATCAAAAGCGGAGTCACTTACAGTCTTAAAC 927
OY 827 TCAAAAGGCTTCTGTGTGCTCTTCTTCTTGGCCATGAGCTGGGCACTTCTGCTCTC 886
Db 928 TCAAAAGGCTTCTGTGTGCTCTTCTTCTTGGCCATGAGCTGGGCACTTCTGCTCTC 987
OY 887 AGCCCTTACCTGATGCTAAATATATGTCCTTGGCCACAAAAGCATGCAAAATG 946
Db 988 AGCCCTTACCTGATGCTAAATATATGTCCTTGGCCACAAAAGCATGCAAAATG 1047
OY 947 TTAACAAGAGGATCTACAGAACTATTTTCAACACAGATATGACTTATATTTCTG 1006
Db 1048 TTAACAAGAGGATCTACAGAACTATTTTCAACACAGATATGACTTATATTTCTG 1107
OY 1007 GGAGGAAATGAATTCATATCTGAAGTCTGAGTGAACAAAGCAAGGAAACAAA 1066
Db 1108 GGAGGAAATGAATTCATATCTGAAGTCTGAGTGAACAAAGCAAGGAAACAAA 1167
OY 1067 GAAGCCAAAGAGAGAGGCTCCAAATATGAAACAAGATTAATCTTCAAGACATATTA 1126
Db 1168 GAAGCCAAAGAGAGAGGCTCCAAATATGAAACAAGATTAATCTTCAAGACATATTA 1227
OY 1127 GAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGATGTAAGTAAATG 1186
Db 1228 GAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGATGTAAGTAAATG 1287
OY 1187 CAGGTGAGACAAAGTGCATCCAGATCTCAGGGAACCTCCCTGCTGACCTGAGGA 1246
Db 1288 CAGGTGAGACAAAGTGCATCCAGATCTCAGGGAACCTCCCTGCTGACCTGAGGA 1347
OY 1247 GTGAGAGACAGAGATAGTCAATGTTCTTGTCTGTAATTTTAAATATATGCTGTA 1306
Db 1348 GTGAGAGACAGAGATAGTCAATGTTCTTGTCTGTAATTTTAAATATATGCTGTA 1407
OY 1307 TGTGCTCTGAGAGAGCCCTGGAAGTCTATCCCAACATATCCATCTTATATTCAC 1366
Db 1408 TGTGCTCTGAGAGAGCCCTGGAAGTCTATCCCAACATATCCATCTTATATTCAC 1467

OY 1367 AAATTAAGCTGATGATGATACCTTAAGACGCTGCTAATTTGACTGCCACTTGGCAACTGAG 1426
Db 1468 AAATTAAGCTGATGATGATGATACCTTAAGACGCTGCTAATTTGACTGCCACTTGGCAACTGAG 1527
OY 1427 GGGCGGCTGCATTTTATGATGAGGTCAAAATGATTCATCTTTTATGATGCTTCCAAAGTG 1486
Db 1528 GGGCGGCTGCATTTTATGATGAGGTCAAAATGATTCATCTTTTATGATGCTTCCAAAGTG 1587
OY 1487 CCTTGGCTTCTCTTCCCACTGACAAATGCGCAAGTTGAGAAAAATGATCAATTTTATG 1546
Db 1588 CCTTGGCTTCTCTTCCCACTGACAAATGCGCAAGTTGAGAAAAATGATCAATTTTATG 1647
OY 1547 CATAAACAAGACAGTGGCGCACACCGATTTTATTAATTAACCTGACACTTCTTTTAAA 1606
Db 1648 CATAAACAAGACAGTGGCGCACACCGATTTTATTAATTAACCTGACACTTCTTTTAAA 1707
OY 1607 CAACAAATGCGGGTTTATTTTCTAGATGATGATTCCTGTAATGTCAGGAGAGAC 1666
Db 1708 CAACAAATGCGGGTTTATTTCTAGATGATGATTCCTGTAATGTCAGGAGAGAC 1767
OY 1667 CTTTACCTGATCTATATGAGATTAATGATCAACAGCTGAGAGCTTCTGCTTCCATC 1726
Db 1768 CTTTACCTGATCTATATGAGATTAATGATCAACAGCTGAGAGCTTCTGCTTCCATC 1827
OY 1727 CTGCGTGAACAGCTTAAGACCTCAGTTTCAATAGCATTAAGAGAGTGGGACTCAGCTG 1786
Db 1828 CTGCGTGAACAGCTTAAGACCTCAGTTTCAATAGCATTAAGAGAGTGGGACTCAGCTG 1887
OY 1787 GGTGATTTGCCCCCATCTCCGGGGGAATGTCGAGACAAATTTGGTTACCTCAATGA 1846
Db 1888 GGTGATTTGCCCCCATCTCCGGGGGAATGTCGAGACAAATTTGGTTACCTCAATGA 1947
OY 1847 GGGAGTGAAGAGGATACAGTCTACTTACCAACTAGTGAATTAAGGCCAGGAGATGCTGCT 1906
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Db 2068 TGTGTGAGGACTTAAGAAACCTGTTTGAATGAGAAAAGGCTCGAAGAGGAGGACCA 2127
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Db 2128 ACAATCTGCTGCTTCTTCACTTATGATTTGCAATTAAGCAATCTGCTCTTGTGCT 2187
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OY 2146 CAGAGTGAACAAGCTTATGAGAAATGCTGTAAGGATTAATCTTCACTTGTGAGCTTC 2205
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Qy      2495 CCTTGAGCCACGAGTATTTATCATGTTGTTATATAAAACGATTTTGAAGTTCTGA 2554
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RESULT 15
AAD32526
ID      AAD32526 standard; DNA; 2626 BP.
XX
XX      AAD32526;
AC
XX
XX      18-JUN-2002 (first entry)
DT
XX
XX      Human B7-H8 gene #2.
DE
XX
XX      Human; B7-like protein; inflammation; tissue damage; immune disorder;
KW      Addison's disease; autoimmune haemolytic anaemia; autoimmune thyroiditis;
KW      diabetes mellitus; Crohn's disease; multiple sclerosis; allergy; cancer;
KW      rheumatoid arthritis; cardiovascular disorder; nervous system disorder;
KW      myocardial ischaemia; ulcerative colitis; reproductive system disorder;
KW      Alzheimer's disease; Parkinson's disease; endocrine disorder; hepatitis;
KW      diabetes mellitus; Grave's disease; Paget's disease; liver disorder;
KW      gastrointestinal disorder; irritable bowel syndrome; cerebral anoxia;
KW      dysphagia; hepatomegaly; neurological disease; infectious disease;
KW      epilepsy; gene therapy; B7-H8 protein; chromosome 1; gene; ds.
XX
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OS
XX
XX      Key
FH      Location/Qualifiers
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XX
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XX
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XX
XX      29-JUN-2001; 2001WO-US020917.
XX
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XX      PR 14-AUG-2000; 2000US-0225266P.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
XX
XX      PISCCELLIA M, Ni J, Ruben SM;
XX
XX      WPI; 2002-257198/30.
XX      DR P-PSDB; AAE20318.
XX
XX      Isolated nucleic acids encoding human B7-like polypeptides, useful for
XX      diagnosis and treatment of e.g. inflammation, cancer, immune disorders
XX      such as Addison's disease, and cardiovascular disorders such as
XX      myocardial ischaemia.
XX
XX      Example 1; Page 457-458; 493bp; English.
XX
XX      The present invention relates to novel human B7-like polypeptides and
XX      polynucleotides encoding such proteins. Sequences of the invention are
XX      used for preventing, treating or ameliorating a medical condition in a

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Db 1796 CTGAGCTGGGGTGAATTTCCGCCCCCATCTCCGGGGGAATGTCTGAAGACAATTTTGTGA 1855
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Job time : 1597.66 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 17:54:16 ; Search time 1774.97 Seconds
(without alignments)
8948.327 Million cell updates/sec

Title: US-09-763-978B-1

Perfect score: 2587
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 306979757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|----------------------------------------|
| 1 | 2565 | 99.1 | 2627 | 9 | US-09-778-320-207 Sequence 207, App |
| 2 | 2565 | 99.1 | 2627 | 9 | US-09-910-689-207 Sequence 207, App |
| 3 | 2565 | 99.1 | 2627 | 9 | US-09-884-441-391 Sequence 391, App |
| 4 | 2565 | 99.1 | 2627 | 10 | US-09-807-969-391 Sequence 391, App |
| 5 | 2565 | 99.1 | 2627 | 10 | US-09-827-271-391 Sequence 391, App |
| 6 | 2565 | 99.1 | 2627 | 13 | US-10-010-742-207 Sequence 207, App |
| 7 | 2565 | 99.1 | 2627 | 15 | US-10-198-053-391 Sequence 391, App |
| 8 | 2565 | 99.1 | 2627 | 18 | US-10-714-389-207 Sequence 207, App |
| 9 | 2565 | 99.1 | 2627 | 18 | US-10-717-296-207 Sequence 207, App |
| 10 | 2565 | 99.1 | 2627 | 19 | US-10-860-790-391 Sequence 391, App |
| 11 | 2563.4 | 99.1 | 3357 | 17 | US-10-023-339-2 Sequence 2, Appl |

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| 12 | 2563 | 99.1 | 2603 | 9 | US-09-896-738-1 Sequence 1, Appl |
| 13 | 2554 | 98.7 | 2591 | 9 | US-09-850-178-23 Sequence 23, Appl |
| 14 | 2527.2 | 97.7 | 2626 | 9 | US-09-877-065-7 Sequence 7, Appl |
| 15 | 2421.8 | 93.6 | 2626 | 17 | US-10-023-339-9 Sequence 9, Appl |
| 16 | 1921.4 | 74.3 | 1965 | 10 | US-09-814-353-19262 Sequence 19262, A |
| 17 | 1599.8 | 61.8 | 1658 | 9 | US-09-889-722-290 Sequence 290, App |
| 18 | 1599.8 | 61.8 | 1658 | 9 | US-09-889-723-290 Sequence 290, App |
| 19 | 1599.8 | 61.8 | 1658 | 9 | US-09-889-723-290 Sequence 290, App |
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ALIGNMENTS

RESULT 1

US-09-778-320-207
Sequence 207, Application US/09778320

Patent No. US20010034052A1

GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.

APPLICANT: Day, Craig H.

APPLICANT: Jiang, Yugu

APPLICANT: Houghton, Raymond L.

APPLICANT: Mitcham, Jennifer

APPLICANT: Wang, Tongtong

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.491C5

CURRENT APPLICATION NUMBER: US/09/778,320

CURRENT FILING DATE: 2001-02-06

NUMBER OF SEQ ID NOS: 301

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 207

LENGTH: 2627

TYPE: DNA

ORGANISM: Homo sapiens

US-09-778-320-207

Query Match 99.1%; Score 2565; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2565; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 33 GCGAGCTCACTCAGCAGCAGTACCGATACGCTGGAGAACCTTCCCGACGATGGCTTCCC 92

QY 72 TGGGAGATCCCTCTTCTGAGAGATATAGATATATATATTTCTGGCTGAGCAATG 131

Db 93 TGGGGAGATCCCTTCCTGAGCATTAATTAGCATCATTAATTCGTGGCTGGAGCAATTG 152
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Db 1353 AGCTATCCCAACATATCCACATCTTAATATTCACAAATTAAGGCTGATATGATACCTTA 1412
Qy 1392 AGAGCTGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1451
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Qy 1452 CAATGATTCACCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1511
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Qy 1512 AATGCAAGATGAGAAATGATCAATATTTTGAAGATTAACAGAGCATGAGGAGAGCAGC 1571
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Db 1593 GATTTTATTAATTAACCTGAGCCTTCTTTTAAACAAACAAATGCGGATTTATTTCTCA 1652
Qy 1632 GATGATGTTCAATCGTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1691
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Qy 1752 TTTCAATGACATCTAGACAGATGAGGATCAGCTGGGATGATTTGCGCCCATCTCCGGG 1811
Db 1773 TTTCAATGACATCTAGACAGATGAGGATCAGCTGGGATGATTTGCGCCCATCTCCGGG 1832
Qy 1812 GGAATGCTGAAAGCAATTTTGTGTTAATCTCAATGAGGAGTGTGAGAGATACATGCTTA 1871
Db 1833 GGAATGCTGAAAGCAATTTTGTGTTAATCTCAATGAGGAGTGTGAGAGATACATGCTTA 1892
Qy 1872 CTACCAACTAGTGATTAAGGCGAAGGATGCTGATCAACTCTCAACATGATACAGAGAGT 1931
Db 1893 CTACCAACTAGTGATTAAGGCGAAGGATGCTGATCAACTCTCAACATGATACAGAGAGT 1952
Qy 1932 CTCCCATTTAACAATACCAATCCGAAGTGTCAACTGTGTGAGGATTAAGAAACCTTGGT 1991
Db 1953 CTCCCATTTAACAATACCAATCCGAAGTGTCAACTGTGTGAGGATTAAGAAACCTTGGT 2012
Qy 1992 TTTGATGAAAGGGCTGTGAAAGAGGGAGGCCAAATCTGTCTCTT-CTCACATT 2050
Db 2013 TTTGATGAAAGGGCTGTGAAAGAGGGAGGCCAAATCTGTCTCTTCTTCTCACTT 2072
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Db 2073 AGTCAATGCAAAATTAAGGATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2132
Qy 2111 CTCTATCGGGGACAGATTAACATCTCACTGATGAAACAGAGTTGACAAAGGCTATGGGAA 2170
Db 2133 CTCTATCGGGGACAGATTAACATCTCACTGATGAAACAGAGTTGACAAAGGCTATGGGAA 2192
Qy 2171 TGCCTGATGGGATTAATCTTCAAGCTTTGAGCTTCAAGTTTCTTTCCCTTCAATTTACC 2230
Db 2193 TGCCTGATGGGATTAATCTTCAAGCTTTGAGCTTCAAGTTTCTTTCCCTTCAATTTACC 2252
Qy 2231 CTGCAAGCAAGTCTGTGAAGAAATGCCGAGTCTTCAAGCTGCTTCTTCACTGCA 2290
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Qy 2291 ATTGATCTCCAGACCCCTTCCTGGCCCAATTGCAATTAAGCAAGAAACATFACCTT 2350
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Db 2553 AGAAACCTGATTTAGAGTTCTGATCGTCAAGAGATGATTAATATACCTTCT 2609
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RESULT 2

US-09-910-689-207
; Sequence 207, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yujin
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910.689
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-689-207

Query Match 99.1%; Score 2565; DB 9; Length 2627;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTCACTAGCAGCATACCCAGATAGCTGGGAACCTTCCCGACATGGCTTCCC 71
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Db 33 GGCAGCTCACTAGCAGCATACCCAGATAGCTGGGAACCTTCCCGACATGGCTTCCC 92
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Db 93 TGGGGCAGATCTCTTCTGAGCATTAATAGCATCATCATTTATCTGGCTGAGCAATTG 152
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Qy 132 CACTCATCATTTGGCTTGTGATTTTCAAGGAGACCTCATCAAGTACATAGTGGCT 191
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Db 213 CAGCTGGGAACATTTGGGAGATGGAATCTGAGCTCACTTTGAACTGACATCAAC 272
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Qy 312 AAGAAGCAAAAGATGAGCTGCGAGAGAGATGAAATGTTCAAGAGGCGGACAGCACTGT 371
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Db 513 AGATTAATACTGAGGCTTCAAGATGCAATGATGACTATTAATGCCAGCTCAG 572
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Db 693 AGATGAGACCATGAAGGTTGTCTGTCTACATGATGTTACATCAACACACTACT 752
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Db 1113 ATGAACAAGTAATATCTATCTTCAAGACATATTAAGAGTTGGGAAATTAATTCATGTGA 1172
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Db 1353 AGTCTATCCCAATATATCCATCTTATATTCACAAATTAAGCTGTAGATATACCTTA 1412
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Db 1413 AGACCTGCTAATGACCTGCACTTGCACACTCAGGGGCGGCTGCATTTTAAATGAGGT 1472
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Qy 1572 GATTTTATTAATTAATCTGACACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
Db 1593 GATTTTATTAATTAATCTGACACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1652
Qy 1632 GATGATGTTCACTCGGAAATGCTCCAGGAGAGACCTTTCACTTGACTATATGACATTA 1691
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Qy 1692 TGTCAATCACAAGCTTGAAGGCTTCTCTTTCATCCTGCGTGAACAGCTAAGCTCACT 1751
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Qy 1812 GGAAATGCTGAAGACAAATTTGGTTACCTCAATGAGGAGTGAAGAGGATCAGTGTCTA 1871
Db 1833 GGAAATGCTGAAGACAAATTTGGTTACCTCAATGAGGAGTGAAGAGGATCAGTGTCTA 1892
Qy 1872 CTACCAACTAGTGGATTAAGAGCCAGGAGTGTCTTCAACCTCTCAATGATGACAGACGT 1931
Db 1893 CTACCAACTAGTGGATTAAGAGCCAGGAGTGTCTTCAACCTCTCAATGATGACAGACGT 1952
Qy 1932 CTCCCATTTAACAATCCCAATCCCAAGTGTCACTGTGTGAGACTAAGAAACCTGGT 1991
Db 1953 CTCCCATTTAACAATCCCAATCCCAAGTGTCACTGTGTGAGACTAAGAAACCTGGT 2012
Qy 1992 TTTGATAGAAAAGGCGCTGAAAAGGAGGAGCAACAAATGCTGTGCTT-CTCACAT 2050
Db 2013 TTTGATAGAAAAGGCGCTGAAAAGGAGGAGCAACAAATGCTGTGCTTCTCACAT 2072
Qy 2051 AGTCAATTTGCAAAATTAAGCAATTTCTGCTCTTTGGCTGTCTCAGACAGAGGCGAGAA 2110
Db 2073 AGTCAATTTGCAAAATTAAGCAATTTCTGCTCTTTGGCTGTCTCAGACAGAGGCGAGAA 2132
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Db 2193 TGCCTGATGGATTAATCTTCAAGTTGTGAGCTTCAAGTTCTTTCCCTTCACTTAC 2252
Qy 2231 CTGCAAGCCAGTTCTGTAAGAGAAATGCTGAGTTCTAAGCTCAAGTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAGTTCTGTAAGAGAAATGCTGAGTTCTAAGCTCAAGTTTCTTACTCTGA 2312
Qy 2291 ATTTAGATTTCCAGACCTTCTCTGCGCAAAATTTAAGGCAACAAATATATACCTT 2350
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Db 2373 CCATGAGGACACACAGACTTTTGAAGAGAGACAAATGACTGCTTGAATTAAGGCTTG 2432
Qy 2411 AGGAATGAAGCTTTGAAGAGAGAAATATCTTTGTTTCCAGCCCTTCCCAACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAGAGAAATATCTTTGTTTCCAGCCCTTCCCAACTCTTCA 2492
Qy 2471 TGTGTTAACTGCTCTTCTGAGACTTGGAGCAGGCTGATTAATCATGTTGTTAT 2530
Db 2493 TGTGTTAACTGCTCTTCTGAGACTTGGAGCAGGCTGATTAATCATGTTGTTAT 2552

Qy 2531 AGAAACTGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAATATATATCT 2587
Db 2553 AGAAACTGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAATATATATCT 2609

RESULT 3
US-09-884-441-391
; Sequence 391, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884.441
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-441-391

Query Match 99.1%; Score 2565; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTTCACCTCAGCCAGTACCCAGATACCTGTGGAAACCTTCCAGCCATGCTTCCC 71
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Db 93 TGGGCGAATCTCTTCTGAGCAATTAATTAATATATATATATATATATATATATATAT 152
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Db 153 CACTCATATTTGGCTTGTGATTTTCAAGGAGACACTCCATCAGTCACTACTGTGCT 212
Qy 192 CAGCTGGAGACATTTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGAGACATTTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC 272
Qy 252 TTTCTGATATGATATTAATATGCTGAGAGAAAGGTTTGAAGGCTTGTGATGATTTCA 311
Db 273 TTTCTGATATGATATTAATATGCTGAGAGAAAGGTTTGAAGGCTTGTGATGATTTCA 332
Qy 312 AAGAAGCAAGATGAGCTGTGAGAGAGATGGAATGTTCAAGGCGGAGCAGCAGTGT 371
Db 333 AAGAAGCAAGATGAGCTGTGAGAGAGATGGAATGTTCAAGGCGGAGCAGCAGTGT 392
Qy 372 TTTCTGATATGATATTAATATGCTGAGAGAAAGGTTTGAAGGCTTGTGATGATTTCA 431
Db 393 TTTCTGATATGATATTAATATGCTGAGAGAAAGGTTTGAAGGCTTGTGATGATTTCA 452
Qy 432 ATGCTGGAGACCTTCAAAATGTTATATCATCATCTTCAAAAGGAGGAGAAATGTAACCTTG 491
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Db 633 AAGTTGACCAAGGAGCCACTTCTCGGAAGTCTCAATACAGCTTTGAGCTGAACCTG 692

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 DB 753 CCTGTATGATTTGAATAATGACATTGCGCAAGCAACAGGGGATATCAAAATGACAGAACTCG 812
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 DB 813 AGATCAAAAGCGGAGTCACTTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTCT 872
 QY 852 CTTTCTTTGCGCATGAGCTGGGCACTTGTGCTCTGAGCCCTTACCTGATGCTAAATAT 911
 DB 873 CTTTCTTTGCGCATGAGCTGGGCACTTGTGCTCTGAGCCCTTACCTGATGCTAAATAT 932
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 QY 1032 GTCTGGAGTGAAGCAACAAAGCAAGAAACAAAAGGCAAAAGGAGGCTCCAT 1091
 DB 1053 GTCTGGAGTGAAGCAACAAAGCAAGAAACAAAAGGAGGAGGCTCCAT 1112
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 DB 1713 TGTGATCAACAAGCTCTGAGGCTTCTCTTTCATCTGCTGAGACAGCTAAGACCTCAGT 1772

QY 1752 TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTCCGCCCATCTCCCGG 1811
 DB 1773 TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTCCGCCCATCTCCCGG 1832
 QY 1812 GGAATGCTGGAACAATTTTGGTTACTTCAATGAAGGAGTGAAGAGATTAAGTGTCTA 1871
 DB 1833 GGAATGCTGGAACAATTTTGGTTACTTCAATGAAGGAGTGAAGAGATTAAGTGTCTA 1892
 QY 1872 CTACCAACTGTGTGAATTAAGGCGCAGGAGATGCTCTCAACTCTTACATGTAAGAGCT 1931
 DB 1893 CTACCAACTGTGTGAATTAAGGCGCAGGAGATGCTCTCAACTCTTACATGTAAGAGCT 1952
 QY 1932 CTCGCCATTTCACTACCTCCCAATCCGAAGTGTCAACTGTGTGACAGACTTAAGAAACCTGCT 1991
 DB 1953 CTCGCCATTTCACTACCTCCCAATCCGAAGTGTCAACTGTGTGACAGACTTAAGAAACCTGCT 2012
 QY 1992 TTTGAGTGAAGAAAGGCGCTGGAAGAGGGAGCCAACTGTCTGCTT-CTCACTT 2050
 DB 2013 TTTGAGTGAAGAAAGGCGCTGGAAGAGGGAGCCAACTGTCTGCTTCTTCACTT 2072
 QY 2051 AGTCAATTTGCAATTAAGCATTTCTGTCTCTTGGCTGTGCTGACACAGAGGCCAGAA 2110
 DB 2073 AGTCAATTTGCAATTAAGCATTTCTGTCTCTTGGCTGTGCTGACACAGAGGCCAGAA 2132
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 DB 2493 TGTGTTAACCACTGCTTCTGAGCCTTGAAGCCTTGAAGCCTGATGATTAATGTTAT 2552
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 DB 2553 AGAAAACGATTTTGAAGTTCGATGCTTCAAGAGATGATTAATATATCATTTCC 2609

RESULT 4
 US-09-763-978b-1
 ; Sequence 391, Application US/09907969
 ; Publication No. US20030091580A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Fling, Steven P.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Ranger, Gary Richard
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Hill, Paul
 ; APPLICANT: Albane, Earl

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C8
CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 391
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-907-969-391

Query Match 99.1%; Score 2565; DB 10; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 25/6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

12 GGCAGCTCAGTCCAGGACAGATACGCTGGAACTTCCAGCCATGCTCC
33 GGCAGCTCAGTCCAGGACAGATACGCTGGAACTTCCAGCCATGCTCC
72 TGGGCGAGATCCTCTTCTGAGCATTAATGATCATCTTATTCGCTGGAGCAATTG
93 TGGGCGAGATCCTCTTCTGAGCATTAATGATCATCTTATTCGCTGGAGCAATTG
132 CACTCATCTTGGCTTTGGTATTTTCAGGAGACATCCATCAAGTCACTGCTGCT
153 CACTCATCTTGGCTTTGGTATTTTCAGGAGACATCCATCAAGTCACTGCTGCT
192 CAGCTGGAGAACATTGGGAGAGATGGAATCTGAGCTGCACTTTGAACTGATCAAC
213 CAGCTGGAGAACATTGGGAGAGATGGAATCTGAGCTGCACTTTGAACTGATCAAC
252 TTTTGTGATTCGTGATACATAGCTGGAAGAGTGTCTTAACTGCTGCTGATGCTCA
273 TTTTGTGATTCGTGATACATAGCTGGAAGAGTGTCTTAACTGCTGCTGATGCTCA
312 AAGAAAGCAAGATGAGCTGTCGAGCAGATGAATGTTTCAGAGCCGAGACAGAGTGT
333 AAGAAAGCAAGATGAGCTGTCGAGCAGATGAATGTTTCAGAGCCGAGACAGAGTGT
372 TTTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGGCTGAAAAAGTGCATCTCAG
393 TTTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGGCTGAAAAAGTGCATCTCAG
432 ATGCTGGCACTTAACTGATTAATGATCACTTCTTAAAGCAAGGAGATGCTAACCTTG
453 ATGCTGGCACTTAACTGATTAATGATCACTTCTTAAAGCAAGGAGATGCTAACCTTG
492 AGTATTAAGTGAAGCTTCAAGATCCGGAAGTGAATGATCTTAAATGCTCAAGTCTCAG
513 AGTATTAAGTGAAGCTTCAAGATCCGGAAGTGAATGATCTTAAATGCTCAAGTCTCAG
552 AGAAGCTTGGGCTGAGGCTCCCGATGTTCCCGAGCCCAAGTGTCTGGGCAATCCC
573 AGAAGCTTGGGCTGAGGCTCCCGATGTTCCCGAGCCCAAGTGTCTGGGCAATCCC
612 AAGTTGACCAAGGAGCACTTCTGGAAGTCTCCAAATCAAGCTTTGAGCTGAAGTCTG
633 AAGTTGACCAAGGAGCACTTCTGGAAGTCTCCAAATCAAGCTTTGAGCTGAAGTCTG
672 AGAATGTGACCAAGGAGCTTCTGAGATCCGGAAGTGAATGATCTTAAATGCTCAAGTCTCAG
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852 CTTTCTTTCCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATAT
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912 GTGCTTGGCCCAAAAAAGATGCAAGTATTTTTCATCAAGGATCTCAGAACTAT
933 GTGCTTGGCCCAAAAAAGATGCAAGTATTTTTCATCAAGGATCTCAGAACTAT
972 TTACCAACCAATATGACCTAGTTTATTTCTGGAGGAAATGAAATTCATATCTAGAA
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1053 GTCTGAGTGAAGCAAAAGAGCAAGAAACAAAGAACCAAGGAGCTCCAT
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1272 CTTTGTCTCTGAATTTTATGATTAATGCTGATATGTTGCTGAGGAAAGCTCCGAA
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1332 AGTCTATCCCAACATATCAGATCTTATATTTCAAAATTAAGCTGATGATGATCCTTA
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1812 GGAATGTCTGAAGACAAATTTTGTGTTACTCAATGAGGAGTGAAGGAGATACGTTGCTA
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1932 CTCCCATTTACAACTACCAATCCGAGATGTTCACTGTGTCAAGATCAAGAAACCTGAGT

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Db 1953 CTCCCATTCACATACCCATCCGAAGTGTCACTGTGACAGACTTAAGAACCTTGTT 2012
Qy 1992 TTGAGTGAAGAAAGGGCTGGAAAGAGGGAGCCAAATCTGTCTGCTT-CTCAATTT 2050
Db 2013 TTGAGTGAAGAAAGGGCTGGAAAGAGGGAGCCAAATCTGTGCTTCTTCTCAATTT 2072
Qy 2051 AGTCATTTGGCAATAATACATTTCTCTTTGGCTGCTGCTCAGCAAGAGAGCCAGAA 2110
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Qy 2111 CTCTATGGGCAACAGAGATTAATCTCTCACTGTAACAGAGTTGACAAAGCCCTATGGAAA 2170
Db 2133 CTCTATGGGCAACAGAGATTAATCTCTCACTGTAACAGAGTTGACAAAGCCCTATGGAAA 2192
Qy 2171 TGCTGTATGGGATTTATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCTACC 2230
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Db 2313 ATTTAGATGTCAGACCTTCTCTGGCCAAATTTAAAGCCAAACATATACCTT 2372
Qy 2351 CCATGAAGCACACACACTTTTGAAGCAAGACATGACTGTTGAATTTAGAGCTTG 2410
Db 2373 CCATGAAGCACACACACTTTTGAAGCAAGACATGACTGTTGAATTTAGAGCTTG 2432
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Db 2493 TGTGTTAACCACTGCTTCTCTGGAAGCTTGGAGCCAGCAGTGTATATGATGTTTAT 2552
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Db 2553 AGAAACTGATTTTGAAGTTCTGATGCTTCAAGAAATGATTAATATACATTTCTT 2609

RESULT 5
US-09-827-271-391
; Sequence 391, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; NUMBER OF SEQ. ID NOS: 461
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-271-391

Query Match 99.1%; Score 2565; DB 10; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGGAGCTCCACTAGCCAGTACCAAGATACGCTGGGAACCTTCCCGACCATGGCTTCCC 71
Db 33 GGGAGCTCCACTAGCCAGTACCAAGATACGCTGGGAACCTTCCCGACCATGGCTTCCC 92
Qy 72 TGGGAGAGATCTCTTCTGAGCATATATGATCATCATTTATTTGGGCTGAGCAATTG 131

|||||
Db 93 TGGGAGAGATCTCTTCTGAGCATATATGATCATCATTTATTTGGGCTGAGCAATTG 152
Qy 132 CACTCATCATTTGGCTTTGGTATTTTCAGAGAGAACATCTCATCAAGTCACTACTGTGGCTT 191
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Qy 192 CAGCTGGGAACATTTGGGAGAGATGGAATCCTGAGCTGACATTTTGAACCTGATCAAC 251
Db 213 CAGCTGGGAACATTTGGGAGAGATGGAATCCTGAGCTGACATTTTGAACCTGATCAAC 272
Qy 252 TTTCTGATATCGTATACAAATGAGCTGAAGAGAGTGTATTTAGGCTTGGTTCATGAGTTCA 311
Db 273 TTTCTGATATCGTATACAAATGAGCTGAAGAGAGTGTATTTAGGCTTGGTTCATGAGTTCA 332
Qy 312 AAGAGGCAAAAGATGAGCTGTCCGAGCAGATGAATATTTTCAGAGCCGAGCAGCAGTGT 371
Db 333 AAGAGGCAAAAGATGAGCTGTCCGAGCAGATGAATATTTTCAGAGCCGAGCAGCAGTGT 392
Qy 372 TTGCTGATCAAGATAGTTGGAATGCTTCTTGGGCTGAAATAAGTCACTGACAG 431
Db 393 TTGCTGATCAAGATAGTTGGAATGCTTCTTGGGCTGAAATAAGTCACTGACAG 452
Qy 432 ATGCTGGACCTTCAAAATGTTATATCATCACTTCTAAAGCAAGGGAATGCTAACCTTG 491
Db 453 ATGCTGGACCTTCAAAATGTTATATCATCACTTCTAAAGCAAGGGAATGCTAACCTTG 512
Qy 492 AGTATTAAGTGAAGCTTCTGAGATGCCGGAAGTGAATGTGACTATATATGCACTGAG 551
Db 513 AGTATTAAGTGAAGCTTCTGAGATGCCGGAAGTGAATGTGACTATATATGCACTGAG 572
Qy 552 AGACCTTGGGAGTGAAGGCTCCCGATGTTCCCGAGCCCAAGAGTCTGGGCAATCCC 611
Db 573 AGACCTTGGGAGTGAAGGCTCCCGATGTTCCCGAGCCCAAGAGTCTGGGCAATCCC 632
Qy 612 AAGTTGACAGGAGGACCACTTCTCGGAAGTCTCAATACAGACTTTGAGCTGAAGCTTG 671
Db 633 AAGTTGACAGGAGGACCACTTCTCGGAAGTCTCAATACAGACTTTGAGCTGAAGCTTG 692
Qy 672 AGAATGTGACATGAAAGTGTGTCTGTGCTCTACATGTTACATGATCAACACATACT 731
Db 693 AGAATGTGACATGAAAGTGTGTGTGTCTCTCAATGATTTACATCAACACATACT 752
Qy 732 CCTGTATGATTTGAATAATGACATTTGCCAAGCAACAGGGATATCAAGTGAAGATCCG 791
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Db 813 AGATCAAAAGGCGAGTCACTACAGCTGCTAACTCAAAAGCTTCTGTGTGTCTCTT 872
Qy 852 CTTTCTTTGGCATGAGCTGGGACCTTCTGCTCTGAGCCCTTACCTGATGCTAAATAT 911
Db 873 CTTTCTTTGGCATGAGCTGGGACCTTCTGCTCTGAGCCCTTACCTGATGCTAAATAT 932
Qy 912 GTGCTTGGCCCAAAAAGCATGCAAGTCAATGTTTAAACAGGATCTACAGAACTAT 971
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Qy 972 TTCACACAGATATGACTAGTTTATTTATTTCTGGGAGGAAATGAAATTCATATAGAA 1031
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Qy 1092 ATGAACAAGTAAATCTATCTTCAAGAATATTTGAAGTTGGGAAAAATTCATGTGA 1151
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QY 1332 AGTCTATCCCAACATATCCACATCTTATATTCACAATAATTAAGCTGTAGTATGACCTTA 1391
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QY 1392 AGAGCTGTCTAATGACCTGCGACCTTGCGAAGCTCAGGGGGGGCTGATTTAGTAAATGGGT 1451
Db 1413 AGAGCTGTCTAATGACCTGCGACCTTGCGAAGCTCAGGGGGGGCTGATTTAGTAAATGGGT 1472
QY 1452 CAATGATTCATCTTTTATGATGCTTCCAAAGGTGCTTGCCTTCTTCCCACTGACA 1511
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QY 1632 GATGATGTTTCATCCGTGAATGGTCCAGGAGAGACCTTTCACCTTGAATATGACATTA 1691
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QY 1692 TGTCATCACAAGCTCTGAGGCTTCTCTTCTTCACTCTGCTGAGACAGCTAAGACCTCACT 1751
Db 1713 TGTCATCACAAGCTCTGAGGCTTCTCTTCTTCACTCTGCTGAGACAGCTAAGACCTCACT 1772
QY 1752 TTTCAATGAGCATCTAGAGAGTGGAGCTCAGCTGGGGGTGATTTGCGCCCGCCATCTCGGG 1811
Db 1773 TTTCAATGAGCATCTAGAGAGTGGAGCTCAGCTGGGGGTGATTTGCGCCCGCCATCTCGGG 1832
QY 1812 GGAATGTCGGAAGACAATTTTGGTTACCTCAATGAGGAGTGGAGAGAGATACAGTGTCTA 1871
Db 1833 GGAATGTCGGAAGACAATTTTGGTTACCTCAATGAGGAGTGGAGAGAGATACAGTGTCTA 1892
QY 1872 CTACCAACTAGTGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTCACTGTAACAGAGAGT 1931
Db 1893 CTACCAACTAGTGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTCACTGTAACAGAGAGT 1952
QY 1932 CTCCCATTTACCAACTACCAATCCGAAGTGTCAACCTGTGTGAGACTAAGAAACCTGTGT 1991
Db 1953 CTCCCATTTACCAACTACCAATCCGAAGTGTCAACCTGTGTGAGACTAAGAAACCTGTGT 2012
QY 1992 TTTGAGTGAAGAAAGGCGCTGGAAGAGGGGAGCCAAACAATCTGTCTGCTT-CTCACAT 2050
Db 2013 TTTGAGTGAAGAAAGGCGCTGGAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACAT 2072
QY 2051 AGTCAATTTGGAATTAAGCATTTCTGTCTCTTTGGCTGTCTGCTCAGACACAGAGAGCAGAA 2110
Db 2073 AGTCAATTTGGAATTAAGCATTTCTGTCTCTTTGGCTGTCTGCTCAGACACAGAGAGCAGAA 2132
QY 2111 CTCTATCGGGGACACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGGGAAA 2170
Db 2133 CTCTATCGGGGACACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGGGAAA 2192
QY 2171 TGCCGTGATGGATTAATCTTCACTGCTGTGAGCTTGAAGTTTCTTCCCTTCAATCTAAC 2230
Db 2193 TGCCGTGATGGATTAATCTTCACTGCTGTGAGCTTGAAGTTTCTTCCCTTCAATCTAAC 2252
QY 2231 CTGCAAGCCAGCTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGTA 2290
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QY 2291 ATTTAGATCTCGAGACCTTCTGCGCACATTCATAATTAAGGCAACAAATATACCTT 2350
Db 2313 ATTTAGATCTCGAGACCTTCTGCGCACATTCATAATTAAGGCAACAAATATACCTT 2372
QY 2351 CCATGAGCACACACAGACTTTTGAAGAACAGACATGACTGCTTGAATTTAGGCTTTG 2410
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Db 2493 TGCTTAAACCACTGCTTCTCTGACCTTGAAGCCAGGCTGACTGATTAATCATGTTGTTAT 2552
QY 2531 AGAAAACTGATTTTGAAGCTTCTGATGCTTCAAGAGATGATTAATTAATCAATTTCT 2587
Db 2553 AGAAAACTGATTTTGAAGCTTCTGATGCTTCAAGAGATGATTAATTAATCAATTTCT 2609

RESULT 6

US-10-010-742-207
; Sequence 207, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jlang, Yungli
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Reiter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010.742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-742-207

Query Match 99.1%; Score 2565; DB 13; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 12 GGCAGCTCAGCTCAGCCAGTACCCAGATACGCTGGAGAACTTCCAGACGATGCTTCC 71
Db 33 GGCAGCTCAGCTCAGCCAGTACCCAGATACGCTGGAGAACTTCCAGACGATGCTTCC 92
QY 72 TGGGGCAGATCCTCTTGTGAGCATTAATTAACATATCATTAATTTCTGGCTGGAGCAAT 131
Db 93 TGGGGCAGATCCTCTTGTGAGCATTAATTAACATATCATTAATTTCTGGCTGGAGCAAT 152
QY 132 CACTCATATTTGGCTTTGGTATTTTCAAGGAGACACTCAATACAGTACTACTCTGGCT 191
Db 153 CACTCATATTTGGCTTTGGTATTTTCAAGGAGACACTCAATACAGTACTACTCTGGCT 212
QY 192 CAGCTGGGACATTTGGGAGAGTGAATCTGAGCTGACATTTTGAACCTGACATCAAAC 251
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Db 273 TTTCTGATATCGTATGATCAATGGCTGAAGGAAGGTGTTTAGAGCTTGTCATGATGTCA 332
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Db 333 AAGAGGCAAAAGATAGCTGTGCGAGCAGATGAATGTTTCAGAGCCGGAACAGACTGT 392
Qy 372 TTGCTGATCAAGATAGTGGCAATGCCCTTTGGCGGCTGAAAAAGCTCACTCAG 431
Db 393 TTGCTGATCAAGATAGTGGCAATGCCCTTTGGCGGCTGAAAAAGCTCACTCAG 452
Qy 432 ATGCTGGACCTTCAAAATGTTATATCATCTTCTTAAGGCAAGGGAGTCTAACCTTG 491
Db 453 ATGCTGGACCTTCAAAATGTTATATCATCTTCTTAAGGCAAGGGAGTCTAACCTTG 512
Qy 492 AGTATAAACTGGAACCTTCAGACATGCCGGAAGTGAATGTGACTATATATGCCAGCTCAG 551
Db 513 AGTATAAACTGGAACCTTCAGACATGCCGGAAGTGAATGTGACTATATATGCCAGCTCAG 572
Qy 552 AGACCTTGGGCTGTGAGAGCTCCCCGATGTTCCCCGACCAAGTGTCTGGGCACTCC 611
Db 573 AGACCTTGGGCTGTGAGAGCTCCCCGATGTTCCCCGACCAAGTGTCTGGGCACTCC 632
Qy 612 AAGTTGACAGAGGACCACTTCTCGGAAGTCTCAATACAGCTTTGAGCTGAACCTTG 671
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Db 693 AGAATGTGACATGAAAGTGTGTGTGCTGTGCTCTACAAATGTTACGATCAACAACATACT 752
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Qy 972 TTGACCAACAGATATGACTAGTATTATTTCTGGGAGGAAATGAATTCATATCTAGAA 1031
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Qy 1032 GTCTGAGTGAAGCAACAGAGCAAGAAACAAAAGAGCCAAAAGCAGAAAGGCTCCAT 1091
Db 1053 GTCTGAGTGAAGCAACAGAGCAAGAAACAAAAGAGCCAAAAGCAGAAAGGCTCCAT 1112
Qy 1092 ATGAAACAAGTAAATCTATCTTCAAGAATATTTAAGAGTTGGGAAATTAATTCATGTGA 1151
Db 1113 ATGAAACAAGTAAATCTATCTTCAAGAATATTTAAGAGTTGGGAAATTAATTCATGTGA 1172
Qy 1152 ACTAGACAAGTGTTAAGAGTATAAGTAAATATGACGTGAGAGCAAGTGCATCCGAG 1211
Db 1173 ACTAGACAAGTGTTAAGAGTATAAGTAAATATGACGTGAGAGCAAGTGCATCCGAG 1232
Qy 1212 ATCTCAGGGAACCTCCCTGCTGTCACTGGGGAAGTGAAGAGACAGATATGTCATGTT 1271
Db 1233 ATCTCAGGGAACCTCCCTGCTGTCACTGGGGAAGTGAAGAGACAGATATGTCATGTT 1292
Qy 1272 CTTTGTCTCTGAATTTTAAATTAATGTGTGCTGTAATCTTCTGAGGGAAGCCCTGGAA 1331
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Qy 1332 AGTCTATCCCAATATCAATCTTATATTTCCAAATTAAGCTGATGATGATCCCTTA 1391

Db 1353 AGTCTATCCCAATATCAATCTTATATTTCCAAATTAAGCTGATGATGATCCCTTA 1412
Qy 1392 AGAGCTGCTTAATTGACTGCACTTGGCAACTAGAGGGGGGCTGCAATTTAGTAATGGGT 1451
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Qy 1452 CAATGATTCACCTTTTAAATTAATGATGCTTCAAAAGGTGCTTGGCTTCTTCCCACTGACA 1511
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Qy 1512 AATGCCAAAGTTGAGAAAAATGATCAATATTTAGCATAAACAGACAGTGGCGACACC 1571
Db 1533 AATGCCAAAGTTGAGAAAAATGATCAATATTTAGCATAAACAGACAGTGGCGACACC 1592
Qy 1572 GATTTTAAATTAATCTGAGCACTTCTTTTAAACAAACAAATGCGGCTTATTTCTCA 1631
Db 1593 GATTTTAAATTAATCTGAGCACTTCTTTTAAACAAACAAATGCGGCTTATTTCTCA 1652
Qy 1632 GATGATGTTCAATCCGGAATGATCCAGGGGAAGGACCTTTCACCTGACTATATGGGACTTA 1691
Db 1653 GATGATGTTCAATCCGGAATGATCCAGGGGAAGGACCTTTCACCTGACTATATGGGACTTA 1712
Qy 1692 TGTCAATCAAGCTCTGAGGCTTCTCTTTCATCTCGGTGAGCAGTAAAGACTCAGT 1751
Db 1713 TGTCAATCAAGCTCTGAGGCTTCTCTTTCATCTCGGTGAGCAGTAAAGACTCAGT 1772
Qy 1752 TTTCAATAGCATTTAAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGG 1811
Db 1773 TTTCAATAGCATTTAAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGG 1832
Qy 1812 GGAATGTCGAAGCAATTTTGGTTACTCAATGAAGGGAAGTGAAGGATACAGTGCTA 1871
Db 1833 GGAATGTCGAAGCAATTTTGGTTACTCAATGAAGGGAAGTGAAGGATACAGTGCTA 1892
Qy 1872 CTACCAATAGTGAATAAAGGCGCAGAGGATGCTGCTCAACTCTCTCACTATACAGACGT 1931
Db 1893 CTACCAATAGTGAATAAAGGCGCAGAGGATGCTGCTCAACTCTCTCACTATACAGACGT 1952
Qy 1932 CTGCCCATTTACAACTTACCAATCCGAAGTGTCAACTGTGTCAAGACTTAAGAAACCTGGT 1991
Db 1953 CTGCCCATTTACAACTTACCAATCCGAAGTGTCAACTGTGTCAAGACTTAAGAAACCTGGT 2012
Qy 1992 TTTGATGAGAAAAGGCGCTGGAAGGGGAGGCAAAATGCTGTGCTT-CTGCAATT 2050
Db 2013 TTTGATGAGAAAAGGCGCTGGAAGGGGAGGCAAAATGCTGTGCTTCTTCTCAATT 2072
Qy 2051 AGTCATTTGGCAAAATAGCAATTCGTCTCTTGGCTGCTGCTCAGACAGAGCCAGAA 2110
Db 2073 AGTCATTTGGCAAAATAGCAATTCGTCTCTTGGCTGCTGCTCAGACAGAGCCAGAA 2132
Qy 2111 CTCTATCGGCAACAGAGATPACTCTCAAGTGAACAGAGTTGACAAGGCTTATGGGAAA 2170
Db 2133 CTCTATCGGCAACAGAGATPACTCTCAAGTGAACAGAGTTGACAAGGCTTATGGGAAA 2192
Qy 2171 TGCCGTATGGGANTTACTTCAAGCTTGTGAGCTTCAAGTTTCTTCCCTCAATTTTAC 2230
Db 2193 TGCCGTATGGGANTTACTTCAAGCTTGTGAGCTTCAAGTTTCTTCCCTCAATTTTAC 2252
Qy 2231 CTGCAAGCCAAAGTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAAAGTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTTCTTACTCTGA 2312
Qy 2291 ATTTAGATCTCCAGACCTTCTGCGCACAATTCAAATTAAGGCAACAAATATATCTT 2350
Db 2313 ATTTAGATCTCCAGACCTTCTGCGCACAATTCAAATTAAGGCAACAAATATATCTT 2372
Qy 2351 CCAATGAAGCACACAGACTTTTGAAGCAAGAACTGCTTGAATTAAGGCTTG 2410
Db 2373 CCAATGAAGCACACAGACTTTTGAAGCAAGAACTGCTTGAATTAAGGCTTG 2432
Qy 2411 AGGAATGAAGCTTTGAAGGAAAGATATCTTTGTTTCCAGCCCTTCCCAACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGGAAAGATATCTTTGTTTCCAGCCCTTCCCAACTCTTCA 2492

Db 1653 GATGATGTCATCCGTAATGTCACAGGAAGACCTTTCACCTTGACATATAGGACATTA 1712
Qy 1692 TGTGATACCAAGCTCTGAGGCTTCTCTTTCATCTCGCTGAGCACTTAAGACTAGT 1751
Db 1713 TGTGATACCAAGCTCTGAGGCTTCTCTTTCATCTCGCTGAGCACTTAAGACTAGT 1772
Qy 1752 TTTCAATAGACTCTAGAGCACTGAGGACTCAGCTGAGGCTGATTTTGGCCCCCATCTCCGG 1811
Db 1773 TTTCAATAGACTCTAGAGCACTGAGGACTCAGCTGAGGCTGATTTTGGCCCCCATCTCCGG 1832
Qy 1812 GGAATGTCGAAGCAATTTTGGTTTACCTCAATGAGGAGTGAAGAGATACAGTCTTA 1871
Db 1833 GGAATGTCGAAGCAATTTTGGTTTACCTCAATGAGGAGTGAAGAGATACAGTCTTA 1892
Qy 1872 CTACCAACTGATGATTAAGGCGAGGATGCTGTCACCTCTCACTGATACAGAGCT 1931
Db 1893 CTACCAACTGATGATTAAGGCGAGGATGCTGTCACCTCTCACTGATACAGAGCT 1952
Qy 1932 CTCCCATTAACACTACCCCAATCCGAAGTGTCAACTGTCTCAGGACTTAAGAAACCTGGT 1991
Db 1953 CTCCCATTAACACTACCCCAATCCGAAGTGTCAACTGTCTCAGGACTTAAGAAACCTGGT 2012
Qy 1992 TTTGAGTAGAAAAGGCGCTGAAAAGAGGAGGCCAACAAATCTGTCTGCTT-CTCACTT 2050
Db 2013 TTTGAGTAGAAAAGGCGCTGAAAAGAGGAGGCCAACAAATCTGTCTGCTTCTCACTT 2072
Qy 2051 AGTCAATTTGGCAATTAAGCAATTTCTGTCTTCTTGTGCTGCTCTCAGCAAGAGGCCGAA 2110
Db 2073 AGTCAATTTGGCAATTAAGCAATTTCTGTCTTCTTGTGCTGCTCTCAGCAAGAGGCCGAA 2132
Qy 2111 CTCTATCGGCGCACAGGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGAAA 2170
Db 2133 CTCTATCGGCGCACAGGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGAAA 2192
Qy 2171 TGCCTGATGGGATTAATCTTCACTGTGTGAGCTTCTTAAGTTTCTTCCCTTCAATTCACC 2230
Db 2193 TGCCTGATGGGATTAATCTTCACTGTGTGAGCTTCTTAAGTTTCTTCCCTTCAATTCACC 2252
Qy 2231 CTGCAAGCCCAAGTTCTGTGAAGAAATGCTGAGTTTACTCAGGTTTCTTAATCTGA 2290
Db 2253 CTGCAAGCCCAAGTTCTGTGAAGAAATGCTGAGTTTACTCAGGTTTCTTAATCTGA 2312
Qy 2291 ATTAGTCTCGAAGCCTTCTGCGCAACAATTCAAATTAAGCAACAACATTAACCTT 2350
Db 2313 ATTAGTCTCGAAGCCTTCTGCGCAACAATTCAAATTAAGCAACAACATTAACCTT 2372
Qy 2351 CCATGAAGCACACACAGACTTTTGAAGCAAGAGCAATGACTGTTGAATTTGAAGGCTTG 2410
Db 2373 CCATGAAGCACACACAGACTTTTGAAGCAAGAGCAATGACTGTTGAATTTGAAGGCTTG 2432
Qy 2411 AGGAATGAAGCTTTGAAGAAAGAAATCTTGTTCACACCCCTTCCCACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAAAGAAATCTTGTTCACACCCCTTCCCACTCTTCA 2492
Qy 2471 TGTGTTAAACCACTGCTCTGAGACCTTGAAGCCAGGCTGACTGATTAATCATGTTGAT 2530
Db 2493 TGTGTTAAACCACTGCTCTGAGACCTTGAAGCCAGGCTGACTGATTAATCATGTTGAT 2552
Qy 2531 AGAAAACTGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATTAATTAATTCCT 2587
Db 2553 AGAAAACTGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATTAATTAATTCCT 2609

RESULT 8
US-10-714-389-207
; Sequence 207, Application US/10714389
; Publication No. US20040101899A1

; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Jiang, Yuguu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer

; APPLICANT: Wang, Tongrong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491D1
; CURRENT APPLICATION NUMBER: US/10/714,389
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-389-207
Query Match 99.1%; Score 2565; DB 18; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 12 GGCAGCTCCAGCTGAGCAGATACCCAGATAGCTGGGAACCTTCCGAGCATGGCTTCCC 71
Db 33 GGCAGCTCCAGCTGAGCAGATACCCAGATAGCTGGGAACCTTCCGAGCATGGCTTCCC 92
Qy 72 TGGGCGAGATCTCTCTGAGCATTAATAGCATCATTAATTTCTGCTGAGCAATTG 131
Db 93 TGGGCGAGATCTCTCTGAGCATTAATAGCATCATTAATTTCTGCTGAGCAATTG 152
Qy 132 CACTCATATGCTGCTTGTGATTTTCAGGAGACATCCATCACTCACTGACTGCTGCT 191
Db 153 CACTCATATGCTGCTTGTGATTTTCAGGAGACATCCATCACTCACTGACTGCTGCT 212
Qy 192 CAGCTGGGAACCTGGGAGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGGAACCTGGGAGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAAC 272
Qy 252 TTTCTGATATCGATATACATGCTGAAGAAAGTGTGAGCTTGTGCTGCTGCTGCTGCT 311
Db 273 TTTCTGATATCGATATACATGCTGAAGAAAGTGTGAGCTTGTGCTGCTGCTGCTGCT 332
Qy 312 AAGAGGCAAGATGAGCTGTGAGCAGAGATGAATGTTTCAGAGGCCGAGCAGAGTGT 371
Db 333 AAGAGGCAAGATGAGCTGTGAGCAGAGATGAATGTTTCAGAGGCCGAGCAGAGTGT 392
Qy 372 TTGCTGATCAAGATGATGGAATGCTGCTTGTGAGCTGGAAGAAAGTGAATCTGACAG 431
Db 393 TTGCTGATCAAGATGATGGAATGCTGCTTGTGAGCTGGAAGAAAGTGAATCTGACAG 452
Qy 432 ATGCTGGCACTTAACAATGTTATATCATCACTTCTAAAGCAAGGGAATGCTAACCTTG 491
Db 453 ATGCTGGCACTTAACAATGTTATATCATCACTTCTAAAGCAAGGGAATGCTAACCTTG 512
Qy 492 AGTATTAATCTGAGGCTTTCAGCATGCGGAAAGTGAATGGAATGAATGCAAGCTCAG 551
Db 513 AGTATTAATCTGAGGCTTTCAGCATGCGGAAAGTGAATGGAATGAATGCAAGCTCAG 572
Qy 552 AGACCTTGGGCTGAGGCTTCCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
Db 573 AGACCTTGGGCTGAGGCTTCCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
Qy 612 AAGTTGACAGGAGGCACTTCTCGAAGTCTCAATATCCAGACTTGAAGCTGAGCTGAG 671
Db 633 AAGTTGACAGGAGGCACTTCTCGAAGTCTCAATATCCAGACTTGAAGCTGAGCTGAG 692
Qy 672 AGAATGTGACATGAAGGTTGTGTCTGCTCTCAATGTGAAGATCAACCAACTACT 731
Db 693 AGAATGTGACATGAAGGTTGTGTCTGCTCTCAATGTGAAGATCAACCAACTACT 752
Qy 732 CCGTATGATTTGAATATGACATTTGCAAGCAAGGAGATTCAAAGGAGACAGATCGG 791
Db 753 CCGTATGATTTGAATATGACATTTGCAAGCAAGGAGATTCAAAGGAGACAGATCGG 812
Qy 792 AGATCAAAAGGCGAGTCACTACAGCTCTAAACTCAAGGCTTCTGTGTGTCTCTT 851

Db 813 AGATCAAAAAGCGAGTCACTACAGCTGTAACTCAAAAGGCTTCTGTGTCTCTT 872
Qy 882 CTTTCTTTGGCCATGAGCTGGGCACTTTCGCCCTCAAGCCCTTAAGTATGTAATAAT 911
Db 873 CTTTCTTTGGCCATGAGCTGGGCACTTTCGCCCTCAAGCCCTTAAGTATGTAATAAT 932
Qy 912 GTGCTTGGCCACAAAAAGCATGCAAAAGTCATTTGTAACAAGAGATCTACAGAACTAT 971
Db 933 GTGCTTGGCCACAAAAAGCATGCAAAAGTCATTTGTAACAAGAGATCTACAGAACTAT 992
Qy 972 TTCAACACCAAGATATGACTAGTTTATATTTCTGGAGGAAATGTAATTCATATCTAGAA 1031
Db 993 TTCAACACCAAGATATGACTAGTTTATATTTCTGGAGGAAATGTAATTCATATCTAGAA 1052
Qy 1032 GTCTGAGAGGACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1091
Db 1053 GTCTGAGAGGACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1112
Qy 1092 ATGAACAAGATATCTATCTTCAAAAGCATATTAAGATTTGGGAAATATTCATGTGA 1151
Db 1113 ATGAACAAGATATCTATCTTCAAAAGCATATTAAGATTTGGGAAATATTCATGTGA 1172
Qy 1152 ACTAGAACAAGTGTATAGAGATATGTAATAATGACGCTGAGACAAAGTATCCGAG 1211
Db 1173 ACTAGAACAAGTGTATAGAGATATGTAATAATGACGCTGAGACAAAGTATCCGAG 1232
Qy 1212 ATCTAGAGGAGCTCCCGCTGCTGACCTGGGAGTGAAGAGACAGATATGATGATGT 1271
Db 1233 ATCTAGAGGAGCTCCCGCTGCTGACCTGGGAGTGAAGAGACAGATATGATGATGT 1292
Qy 1272 CTTTGTCTGTGAATTTTATGTAATATGCTGTAAATGTTGCTGTGAGAGAGCCCTGAA 1331
Db 1293 CTTTGTCTGTGAATTTTATGTAATATGCTGTAAATGTTGCTGTGAGAGAGCCCTGAA 1352
Qy 1332 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATGTAATGCTTA 1391
Db 1353 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATGTAATGCTTA 1412
Qy 1392 AAGCGTGTATATGACCTGCACTTCCGCACTCAAGGAGGCGCTGCACTTTATGTAATGGGT 1451
Db 1413 AAGCGTGTATATGACCTGCACTTCCGCACTCAAGGAGGCGCTGCACTTTATGTAATGGGT 1472
Qy 1452 CAATGATTCACCTTTTATGATGCTTCAAAAGTGTGCTTCTCTTCCCACTGACA 1511
Db 1473 CAATGATTCACCTTTTATGATGCTTCAAAAGTGTGCTTCTCTTCCCACTGACA 1532
Qy 1512 AATGCCAAGTTGAGAAAAATGATCAATAATTTAGATTAACAAGACAGTCCGCAACCC 1571
Db 1533 AATGCCAAGTTGAGAAAAATGATCAATAATTTAGATTAACAAGACAGTCCGCAACCC 1592
Qy 1572 GATTTTATTAATAAAGCTGAGCACTTCTTTTAAACAAATGCGGGTTTATTTCTCA 1631
Db 1593 GATTTTATTAATAAAGCTGAGCACTTCTTTTAAACAAATGCGGGTTTATTTCTCA 1652
Qy 1632 GATGATGTTTATCCGTAATGTGTCAGGAGAGAGACCTTTACCTTGATATATGACATTA 1691
Db 1653 GATGATGTTTATCCGTAATGTGTCAGGAGAGAGACCTTTACCTTGATATATGACATTA 1712
Qy 1692 TGTTCATCAAGCTGAGGCTTCTCTTTCATCTCGGTGAGACAGTCAAGACTCAGT 1751
Db 1713 TGTTCATCAAGCTGAGGCTTCTCTTTCATCTCGGTGAGACAGTCAAGACTCAGT 1772
Qy 1752 TTTTCAATAGCATCTGAGAGAGTGGGAGCTGAGCTGGGGTATTTTCCGCCCACTCCGGG 1811
Db 1773 TTTTCAATAGCATCTGAGAGAGTGGGAGCTGAGCTGGGGTATTTTCCGCCCACTCCGGG 1832
Qy 1812 GGAATGTCGAAGACAAATTTGGTTACTCAATGAGGAGTGGAGAGAGTACAGTGTCTA 1871
Db 1833 GGAATGTCGAAGACAAATTTGGTTACTCAATGAGGAGTGGAGAGAGTACAGTGTCTA 1892
Qy 1872 CTACCAACTAGTGTAAAGGCGAGGAGTGTCTGTCACACTCTTACATATACAGAGAGT 1931
Db 1893 CTACCAACTAGTGTAAAGGCGAGGAGTGTCTGTCACACTCTTACATATACAGAGAGT 1952

Qy 1932 CTCCCATTTAACAACCTAACCTCCGAAGTGTCAACTGTGTGAGACTAAGAAACCTGGT 1991
Db 1953 CTCCCATTTAACAACCTAACCTCCGAAGTGTCAACTGTGTGAGACTAAGAAACCTGGT 2012
Qy 1992 TTTGATGAAAAAGGCGCTGGAAAAGAGGAGCCCAACATCTGTCTGCTT-CTCACTT 2050
Db 2013 TTTGATGAAAAAGGCGCTGGAAAAGAGGAGCCCAACATCTGTCTGCTTCTCACTT 2072
Qy 2051 AGTCATTTGGCAAAATGAGCATCTGTCTTTGGGCTGCTGCTGACAGAGAGAGAGAA 2110
Db 2073 AGTCATTTGGCAAAATGAGCATCTGTCTTTGGGCTGCTGCTGACAGAGAGAGAGAA 2132
Qy 2111 CTCTATCGGAGCAGAGATTAACATCTCTCACTGTAACAAGATTGACAAAGCCTATGGGAA 2170
Db 2133 CTCTATCGGAGCAGAGATTAACATCTCTCACTGTAACAAGATTGACAAAGCCTATGGGAA 2192
Qy 2171 TGCTGATGGGATTAATCTTCAAGCTTTGAGCTTTAAAGTTTCTTCCCTTCACTTACC 2230
Db 2193 TGCTGATGGGATTAATCTTCAAGCTTTGAGCTTTAAAGTTTCTTCCCTTCACTTACC 2252
Qy 2231 CTGAGAGCAAGTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
Db 2253 CTGAGAGCAAGTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
Qy 2291 ATTTAGATCTCCAGACCTTCTGCGCAATTCAAATTAAGGCAACAAATATACCTT 2350
Db 2313 ATTTAGATCTCCAGACCTTCTGCGCAATTCAAATTAAGGCAACAAATATACCTT 2372
Qy 2351 CCATGAGCAGACACAGACTTTTGAAGAGACAAATGATCTGTTGAATGAGGCTTG 2410
Db 2373 CCATGAGCAGACACAGACTTTTGAAGAGACAAATGATCTGTTGAATGAGGCTTG 2432
Qy 2411 AGGAATGAGGCTTTGAAGAAAGATATCTTGTGTTCCAGGCCCCCTCCACACTCTCA 2470
Db 2433 AGGAATGAGGCTTTGAAGAAAGATATCTTGTGTTCCAGGCCCCCTCCACACTCTCA 2492
Qy 2471 TGTGTTAACCACTGCTTCTGAGACTTTGAGCAGCAGGCTGACTGATATGATGTTTAT 2530
Db 2493 TGTGTTAACCACTGCTTCTGAGACTTTGAGCAGCAGGCTGACTGATATGATGTTTAT 2552
Qy 2531 AGAAAACTGATTTTGAAGTTCTGATCTTCAAGAGATGATTAATATACATTTCT 2587
Db 2553 AGAAAACTGATTTTGAAGTTCTGATCTTCAAGAGATGATTAATATACATTTCT 2609

RESULT 9
US-10-717-296-207
; Sequence 207, Application US/10717296
; Publication No. US20040142361A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Davin C.
; APPLICANT: Jilang, Yutian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C8
; CURRENT APPLICATION NUMBER: US/10/717.296
; CURRENT FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: fastseq For Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-296-207

Query Match 99.1%; Score 2565; DB 18; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2566; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCAAGCAATGGCTTCC 71
Db 33 GGCAGCTCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCAAGCAATGGCTTCC 92

Db 2253 CTGCAAGCAATGTTGTAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
Qy 2291 ATTTGATGTCAGACCTTCTCTGCGCAATTTCAATTAAGCAACAATATACCTT 2350
Db 2313 ATTTGATGTCAGACCTTCTCTGCGCAATTTCAATTAAGCAACAATATACCTT 2372
Qy 2351 CCATAGACACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGG 2410
Db 2373 CCATAGACACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGG 2432
Qy 2411 AGAAATGAAGCTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGG 2470
Db 2433 AGAAATGAAGCTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGG 2492
Qy 2471 TGTGTTAACCACTGCTTCTGAGCTTGGAGCCAGGAGTGTATATCATGTTGTTAT 2530
Db 2493 TGTGTTAACCACTGCTTCTGAGCTTGGAGCCAGGAGTGTATATCATGTTGTTAT 2552
Qy 2531 AGAAATGAAGCTTTGAAGCTTGTATGCTTCAAGAGATGATTAATATCATTTGCT 2587
Db 2553 AGAAATGAAGCTTTGAAGCTTGTATGCTTCAAGAGATGATTAATATCATTTGCT 2609

RESULT 10
US-10-860-790-391
; Sequence 391, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-860-790-391

Query Match 99.1%; Score 2565; DB 19; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTCACTCAGCCAGTACCCAGATAGCGTGGGAACCTTCCCAGCCATGAGCTTCCC 71
Db 33 GGCAGCTCACTCAGCCAGTACCCAGATAGCGTGGGAACCTTCCCAGCCATGAGCTTCCC 92
Qy 72 TGGGGCAGATCTCTCTGAGGATTAATAGCATCATCTATTCTGCTGGAGCAATGG 131
Db 93 TGGGGCAGATCTCTCTGAGGATTAATAGCATCATCTATTCTGCTGGAGCAATGG 152
Qy 132 CACTCATCATTTGGCTTTGTAATTTCAAGGAGACCTCATCAAGTCACTACTGTCGCT 191
Db 153 CACTCATCATTTGGCTTTGTAATTTCAAGGAGACCTCATCAAGTCACTACTGTCGCT 212
Qy 192 CAGCTGGGAACTTTGGGGAGGATGGAATCTGAGCTGCACTTTTGAACCTGCATCAAC 251
Db 213 CAGCTGGGAACTTTGGGGAGGATGGAATCTGAGCTGCACTTTTGAACCTGCATCAAC 272
Qy 252 TTTTGTATTCGTATACATGAGCTGGAAGAGTGTATTTAGGCTTGTCTCATGAGTTCA 311
Db 273 TTTTGTATTCGTATACATGAGCTGGAAGAGTGTATTTAGGCTTGTCTCATGAGTTCA 332
Qy 312 AAGAAAGCAAGATGAGCTGTGCGAGCAGAGATGAATGTTCAAGAGCGCGGACAGAGTGT 371
Db 333 AAGAAAGCAAGATGAGCTGTGCGAGCAGAGATGAATGTTCAAGAGCGCGGACAGAGTGT 392

Qy 372 TTGCTGATCAAGTATAGTTGGCAATGCTCTTTTGGCGCTGAAAAAGGTGCACTCAAG 431
Db 393 TTGCTGATCAAGTATAGTTGGCAATGCTCTTTTGGCGCTGAAAAAGGTGCACTCAAG 452
Qy 432 ATGCTGGACCTTCAAAATGTTATATCATCACTTTTAAAGCAAGGGATGCTTAACCTTG 491
Db 453 ATGCTGGACCTTCAAAATGTTATATCATCACTTTTAAAGCAAGGGATGCTTAACCTTG 512
Qy 492 AGTATTAACCTGGAGCTTGCAGATGCCGGAAGTGAATGTGGAATATATGCAAGCTCAG 551
Db 513 AGTATTAACCTGGAGCTTGCAGATGCCGGAAGTGAATGTGGAATATATGCAAGCTCAG 572
Qy 552 AGACCTTGGGTGAGGCTCCCGATGTTTCCCGAGCCCAAGTGTCTGGCATCCC 611
Db 573 AGACCTTGGGTGAGGCTCCCGATGTTTCCCGAGCCCAAGTGTCTGGCATCCC 632
Qy 612 AAGTTGACCAAGGAGCCAACTTCTCGGAAGTCTCAATTACAGCTTTGAGCTGAATCTTG 671
Db 633 AAGTTGACCAAGGAGCCAACTTCTCGGAAGTCTCAATTACAGCTTTGAGCTGAATCTTG 692
Qy 672 AGAATGAGCAATGAAGTTGTGTGCTGTCTCAATGTTAGATCAACAACATCACT 731
Db 693 AGAATGAGCAATGAAGTTGTGTGCTGTCTCAATGTTAGATCAACAACATCACT 752
Qy 732 CCTGTATGATTAAGTGAATGACATTCGCAAGCAAGGAGATATCAAGTGAACAGATTCGG 791
Db 753 CCTGTATGATTAAGTGAATGACATTCGCAAGCAAGGAGATATCAAGTGAACAGATTCGG 812
Qy 792 AGATCAAAAAGCGGAGTCACTCAAGCTGCTTAACTCAAAAGCTTCTGTGTCTCTT 851
Db 813 AGATCAAAAAGCGGAGTCACTCAAGCTGCTTAACTCAAAAGCTTCTGTGTCTCTT 872
Qy 852 CTTTCTTTGCGATGAGTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTTAAATAT 911
Db 873 CTTTCTTTGCGATGAGTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTTAAATAT 932
Qy 912 GTGCTTTGGCCCAAAAAGCATGCAAAAGTATTTTCAACAAGGATCTACAGAACTAT 971
Db 933 GTGCTTTGGCCCAAAAAGCATGCAAAAGTATTTTCAACAAGGATCTACAGAACTAT 992
Qy 972 TTCACCAACAGATATGACTTATGTTTATTTTCTGGAGGAAATGAAATTCATATCTAGAA 1031
Db 993 TTCACCAACAGATATGACTTATGTTTATTTTCTGGAGGAAATGAAATTCATATCTAGAA 1052
Qy 1032 GTCTGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1091
Db 1053 GTCTGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1112
Qy 1092 ATGAACAAGATTAATCTATCTTCAAAAGCATATTTAGAGTTGGGAAATTAATTCATGTA 1151
Db 1113 ATGAACAAGATTAATCTATCTTCAAAAGCATATTTAGAGTTGGGAAATTAATTCATGTA 1172
Qy 1152 ACTAGCAAGTGTGTTAAGAGTATAGTAAATGCAAGTGTGAGACAAAGTCAATCCCAG 1211
Db 1173 ACTAGCAAGTGTGTTAAGAGTATAGTAAATGCAAGTGTGAGACAAAGTCAATCCCAG 1232
Qy 1212 ATTCAGGAGCCTCCCTGCTGTCACTGAGGAGTGAAGAGCAGGATAGTGATGTT 1271
Db 1233 ATTCAGGAGCCTCCCTGCTGTCACTGAGGAGTGAAGAGCAGGATAGTGATGTT 1292
Qy 1272 CTTTGTCTCTGAATTTTATGTTATATGCTGTATATGTTGCTTGAAGAGCCCTGGAA 1331
Db 1293 CTTTGTCTCTGAATTTTATGTTATATGCTGTATATGTTGCTTGAAGAGCCCTGGAA 1352
Qy 1332 AGTCTATCCCAACATATCCATCTTATATTCACAAATTAAGCTTATGTAATCCCTTA 1391
Db 1353 AGTCTATCCCAACATATCCATCTTATATTCACAAATTAAGCTTATGTAATCCCTTA 1412
Qy 1392 AGAGCTCTTAATTTGACGCACTTGGCACTCGAGGCGGCTGATTTTGTATAGGAT 1451
Db 1413 AGAGCTCTTAATTTGACGCACTTGGCACTCGAGGCGGCTGATTTTGTATAGGAT 1472

QY 1452 CAATGATGACTTTTATGATGCTTCCAAAGTGCTGCTGCTTCCCACTGACA 1511
| | | | |
DB 1473 CAATGATGACTTTTATGATGCTTCCAAAGTGCTTGGCTTCTTCCCACTGACA 1532
| | | | |
QY 1512 AATGCCAAAGTTGAGAAAAATGATCATATTTTATGCTAAACAGAGCATGGGACACC 1571
| | | | |
DB 1533 AATGCCAAAGTTGAGAAAAATGATCATATTTTATGCTAAACAGAGCATGGGACACC 1592
| | | | |
QY 1572 GATTTTATTAATTAACCTGAGACCTCTCTTTTAAACAAAGTGGGGTTTATTTCTCA 1631
| | | | |
DB 1593 GATTTTATTAATTAACCTGAGACCTCTCTTTTAAACAAAGTGGGGTTTATTTCTCA 1652
| | | | |
QY 1632 GATGATGTTTATCCTGATGATGCTTCAAGGAGGACCTTTCACTTGAATATGACATTA 1691
| | | | |
DB 1653 GATGATGTTTATCCTGATGATGCTTCAAGGAGGACCTTTCACTTGAATATGACATTA 1712
| | | | |
QY 1692 TGTTCATCAAGAGCTCTGAGGCTTCTCTTTTCATCTGCGTGAACAGCTAAGACTGAGT 1751
| | | | |
DB 1713 TGTTCATCAAGAGCTCTGAGGCTTCTCTTTTCATCTGCGTGAACAGCTAAGACTGAGT 1772
| | | | |
QY 1752 TTTTCATTAAGATCTAGAGCATGGGACTCAGCTGGGGTATTTTGGCCCCCATCTCGGG 1811
| | | | |
DB 1773 TTTTCATTAAGATCTAGAGCATGGGACTCAGCTGGGGTATTTTGGCCCCCATCTCGGG 1832
| | | | |
QY 1812 GGAATGCTCTGAAGACATTTTGGTTTACCTCAATGAGGAGGATGAGAGATACAGTCTCA 1871
| | | | |
DB 1833 GGAATGCTCTGAAGACATTTTGGTTTACCTCAATGAGGAGGATGAGAGATACAGTCTCA 1892
| | | | |
QY 1872 CTACCAACTAGTGGATTAAGAGCCAGAGGACTGCTCAACCTCTTACCATGTACAGAGCGT 1931
| | | | |
DB 1893 CTACCAACTAGTGGATTAAGAGCCAGAGGACTGCTCAACCTCTTACCATGTACAGAGCGT 1952
| | | | |
QY 1932 CTCCCCATTTCAACTACCACTCCGAAGTGTCAACTGTGTCAAGATCTAAGAAACCTGTGT 1991
| | | | |
DB 1953 CTCCCCATTTCAACTACCACTCCGAAGTGTCAACTGTGTCAAGATCTAAGAAACCTGTGT 2012
| | | | |
QY 1992 TTTGAGTGAAGAAAGGGCTGGAAGAGGGAGCCAACTGTCTGCTTCTCACTT 2050
| | | | |
DB 2013 TTTGAGTGAAGAAAGGGCTGGAAGAGGGAGCCAACTGTCTGCTTCTCACTT 2072
| | | | |
QY 2051 AGTCATTGGCAATTAAGCATTTCTGTCTTTTGGCTGCTGCTCAGACAGAGAGCCAGAA 2110
| | | | |
DB 2073 AGTCATTGGCAATTAAGCATTTCTGTCTTTTGGCTGCTGCTCAGACAGAGAGCCAGAA 2132
| | | | |
QY 2111 CTCTATCGGGCACCAGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTATGGGAAA 2170
| | | | |
DB 2133 CTCTATCGGGCACCAGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTATGGGAAA 2192
| | | | |
QY 2171 TGCCTGATGGGATTTATCTTCAAGCTGTGAGCTTCTAAGTTTCTTCCCTCACTTACCT 2230
| | | | |
DB 2193 TGCCTGATGGGATTTATCTTCAAGCTGTGAGCTTCTAAGTTTCTTCCCTCACTTACCT 2252
| | | | |
QY 2231 CTGCAAGCCAAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
| | | | |
DB 2253 CTGCAAGCCAAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
| | | | |
QY 2291 ATTTAAGTCTCAGAGCTTCTGCGCCAACTTCAATTAAGGCAACAACTATATACCTT 2350
| | | | |
DB 2313 ATTTAAGTCTCAGAGCTTCTGCGCCAACTTCAATTAAGGCAACAACTATATACCTT 2372
| | | | |
QY 2351 CCAATGAAGCACAAGAGCTTTTGAAGCAAGAGCAATGACTGTTGAATTTGAGGCTTG 2410
| | | | |
DB 2373 CCAATGAAGCACAAGAGCTTTTGAAGCAAGAGCAATGACTGTTGAATTTGAGGCTTG 2432
| | | | |
QY 2411 AGGAATGAAGCTTTGAAGAAAGAAATCTTGTTCACAGCCCTTCCCACTCTTCA 2470
| | | | |
DB 2433 AGGAATGAAGCTTTGAAGAAAGAAATCTTGTTCACAGCCCTTCCCACTCTTCA 2492
| | | | |
QY 2471 TGTGTTTAACCACTGCTTCTCTGACCTTGGAGCAGGCTGATTAATCACTGTTGTTAT 2530
| | | | |
DB 2493 TGTGTTTAACCACTGCTTCTCTGACCTTGGAGCAGGCTGATTAATCACTGTTGTTAT 2552
| | | | |
QY 2531 AGAAACTGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATATATTCCT 2587
| | | | |

DB 2553 AGAAACTGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATATATTCCT 2609
| | | | |
RESULT 11
US-10-023-339-2
; Sequence 2, Application US/10023339
; Publication No. US20030208058A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: B7-Like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT124P1
; CURRENT APPLICATION NUMBER: US/10/023,339
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/20917
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3357
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-339-2
Query Match 99.1%; Score 2563.4; DB 17; Length 3357;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2575; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 12 GGGAGCTCCACTCAGCAGTATCCAGATACGCTGGGAACCTTCCAGCCATGGCTTCCC 71
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DB 369 GGGAGCTCCACTCAGCAGTATCCAGATACGCTGGGAACCTTCCAGCCATGGCTTCCC 428
| | | | |
QY 72 TGGGGAGATCCCTTCTGAGCATTAATAGCATCATTTATTTCTGGCTGAGCAATTG 131
| | | | |
DB 429 TGGGGAGATCCCTTCTGAGCATTAATAGCATCATTTATTTCTGGCTGAGCAATTG 488
| | | | |
QY 132 CACTCATATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAAGTCACTACTGTGCGCT 191
| | | | |
DB 489 CACTCATATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAAGTCACTACTGTGCGCT 548
| | | | |
QY 192 CAGCTGGGAACATTTGGGAGATGAGATCTTGAAGTCTGCACTTTTGAACCTGACATCAAC 251
| | | | |
DB 549 CAGCTGGGAACATTTGGGAGATGAGATCTTGAAGTCTGCACTTTTGAACCTGACATCAAC 608
| | | | |
QY 252 TTTCTGATATCGTATGATGATGAGTGGTGAAGAGTGTTTTGAAGCTTGTGCTGATGATCA 311
| | | | |
DB 609 TTTCTGATATCGTATGATGATGAGTGGTGAAGAGTGTTTTGAAGCTTGTGCTGATGATCA 668
| | | | |
QY 312 AAGAAAGCAAAATGAGCTGTGAGCAGAGATGAATGTTTCAGAGCCGGAAGCAGAGTGT 371
| | | | |
DB 669 AAGAAAGCAAAATGAGCTGTGAGCAGAGATGAATGTTTCAGAGCCGGAAGCAGAGTGT 728
| | | | |
QY 372 TTGCTGATCAAGTATGATTTGGCAATGCTTTTGGCGCTGAAGAAAGTGAACCTCAAG 431
| | | | |
DB 729 TTGCTGATCAAGTATGATTTGGCAATGCTTTTGGCGCTGAAGAAAGTGAACCTCAAG 788
| | | | |
QY 432 ATGCTGGCCTTACAAATGTTTATATCACTTCTTAAAGGCAAGGGAATGCTAATCTTG 491
| | | | |
DB 789 ATGCTGGCCTTACAAATGTTTATATCACTTCTTAAAGGCAAGGGAATGCTAATCTTG 848
| | | | |
QY 492 AGATTAACCTGAGGCTTCAAGATGCGGAAGTGAATGAGCTTATATGCAAGCTCAG 551
| | | | |
DB 849 AGATTAACCTGAGGCTTCAAGATGCGGAAGTGAATGAGCTTATATGCAAGCTCAG 908
| | | | |
QY 552 AGACCTTGGGCTGTGAGGCTCCCGATGTTTCCCAAGCCCAAGTGTCTGGGATGCC 611
| | | | |
DB 909 AGACCTTGGGCTGTGAGGCTCCCGATGTTTCCCAAGCCCAAGTGTCTGGGATGCC 968
| | | | |
QY 612 AAGTTGACCAAGGAGCAGCACTTCTGGAGTCTCCAAATACAGCTTGAAGTGAAGTCTG 671
| | | | |

NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2603
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (53)..(901)
US-09-896-738-1

Query Match 99.1%; Score 2563; DB 9; Length 2603;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2574; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 12 GGCAGCTCCACTGACCCAGATACCCAGATAGCGTGGAACTTCCCGACCATGGCTTCCC 71
DB 3 GGCAGCTCCACTGACCCAGATACCCAGATAGCGTGGAACTTCCCGACCATGGCTTCCC 62
QY 72 TGGGGGAGATCCTCTCTGAGGCAATATTAGCATCATATTCTGGCTGGAGCAATTG 131
DB 63 TGGGGGAGATCCTCTCTGAGGCAATATTAGCATCATATTCTGGCTGGAGCAATTG 122
QY 132 CACTCATATTGGCTTTGTAATTTCAAGAGACACTCCATCACAGTCACTACTGCGCT 191
DB 123 CACTCATATTGGCTTTGTAATTTCAAGAGACACTCCATCACAGTCACTACTGCGCT 182
QY 192 CAGCTGGGAACTTTGGGAGAGATGGAATCCTGAGCTGCACCTTTGAACTGACATCAAC 251
DB 183 CAGCTGGGAACTTTGGGAGAGATGGAATCCTGAGCTGCACCTTTGAACTGACATCAAC 242
QY 252 TTTCTGATCGTGATCAATGCTGTAAGAGAGGTGTTTAGCGTGGCTCATGAGTCA 311
DB 243 TTTCTGATCGTGATCAATGCTGTAAGAGAGGTGTTTAGCGTGGCTCATGAGTCA 302
QY 312 AAGAAGCAAGATGAGCTGTGGAGCAGAGATGAATGTTCAAGAGCCGGACAGAGTGT 371
DB 303 AAGAAGCAAGATGAGCTGTGGAGCAGAGATGAATGTTCAAGAGCCGGACAGAGTGT 362
QY 372 TTGCTGATCAAGTATGTTGGCAATGCTCTTTGCGGCTGMAAAAAGTGCMACTCAG 431
DB 363 TTGCTGATCAAGTATGTTGGCAATGCTCTTTGCGGCTGMAAAAAGTGCMACTCAG 422
QY 432 ATGCTGCACCTCAAAATGTTATATCATCTCTTAAGGCAAGGGAATGCTTAACCTTG 491
DB 423 ATGCTGCACCTCAAAATGTTATATCATCTCTTAAGGCAAGGGAATGCTTAACCTTG 482
QY 492 AGTATAAACTGAGCCTTCAGCATGCGGAAGTGAATGGAATATATATGAGCTCAG 551
DB 483 AGTATAAACTGAGCCTTCAGCATGCGGAAGTGAATGGAATATATATGAGCTCAG 542
QY 552 AGACCTTGGGCTGAGAGCTTCCCGATGTTCCCGACGCCCAAGTGTGGAGCATGCC 611
DB 543 AGACCTTGGGCTGAGAGCTTCCCGATGTTCCCGACGCCCAAGTGTGGAGCATGCC 602
QY 612 AAGTGAACGAGGACCACTTCTCGGAAGTCTCCATACCAAGTTTGAAGTGAAGCTTG 671
DB 603 AAGTGAACGAGGACCACTTCTCGGAAGTCTCCATACCAAGTTTGAAGTGAAGCTTG 662
QY 672 AGAATGACCATGAAGTGTGTCTGTGCTTACATGTTAGATCAAAAGCAACATATCT 731
DB 663 AGAATGACCATGAAGTGTGTGTGTGTGTCTGTCTACATGTTAGATCAAAAGCAACATATCT 722
QY 732 CCGTATGATTAAGAAATGACATTTGCCCAAGCAACAGGGGATATCAAGATACGGAATCGG 791
DB 723 CCGTATGATTAAGAAATGACATTTGCCCAAGCAACAGGGGATATCAAGATACGGAATCGG 782
QY 792 AGATCAAAAGGCGAGTCACTACAGTGTCTAACTCAAGGCTTCTGTGTGTCTCTT 851
DB 783 AGATCAAAAGGCGAGTCACTACAGTGTCTAACTCAAGGCTTCTGTGTGTGTCTCTT 842
QY 852 CTTTCTTTGCTCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATCTAAATAT 911

DB 843 CTTTCTTTGCTCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACTGATCTAAATAT 902
QY 912 GTGCTTTGGCCAAAGAAAGCATGCAAGTCAATTTGTTACAAAGGATCTACGAATCTAT 971
DB 903 GTGCTTTGGCCAAAGAAAGCATGCAAGTCAATTTGTTACAAAGGATCTACGAATCTAT 962
QY 972 TTCAACCAAGATGATGACCTAGTTTATATTTCTGGAGGAAATGAATTCATATCTAGAA 1031
DB 963 TTCAACCAAGATGATGACCTAGTTTATATTTCTGGAGGAAATGAATTCATATCTAGAA 1022
QY 1032 GTCTGAGTGAAGCAAAAGAGCAAGAAACAAAGAGCCAAAGCAGAGCTCCAT 1091
DB 1023 GTCTGAGTGAAGCAAAAGAGCAAGAAACAAAGAGCCAAAGCAGAGCTCCAT 1082
QY 1092 ATGAAACAAGTAAATCTATCTTCAAGACATATTAGAAGTTGGGAAATATATCTATGTA 1151
DB 1083 ATGAAACAAGTAAATCTATCTTCAAGACATATTAGAAGTTGGGAAATATATCTATGTA 1142
QY 1152 ACTAGCAAGTGTGTTAAGATGATTAAGTAAATGACGAGGAGCAAGTCCAG 1211
DB 1143 ACTAGCAAGTGTGTTAAGATGATTAAGTAAATGACGAGGAGCAAGTCCAG 1202
QY 1212 ATCTCAGGAGCTCCCTGCTGTCACCTGGGAGTGAAGAGCAGATATGATGTT 1271
DB 1203 ATCTCAGGAGCTCCCTGCTGTCACCTGGGAGTGAAGAGCAGATATGATGTT 1262
QY 1272 CTTTGTCTGGAATTTTATGTTATATGCTGTGATATGTTGCTTGAGAAAGCCCTGGAA 1331
DB 1263 CTTTGTCTGGAATTTTATGTTATATGCTGTGATATGTTGCTTGAGAAAGCCCTGGAA 1322
QY 1332 AGTCTATCCCAATATCCACATCTATATTTCCACAAATTAAGCTGATGATGACCTTA 1391
DB 1323 AGTCTATCCCAATATATCCACATCTTATTTCCACAAATTAAGCTGATGATGACCTTA 1382
QY 1392 AGACGCTGTAATTTGAATGCACTGCACTGCAAGGAGGAGCTGCAATTTAGTATGCT 1451
DB 1383 AGACGCTGTAATTTGAATGCACTGCACTGCAAGGAGGAGCTGCAATTTAGTATGCT 1442
QY 1452 CAATGATTCATTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1511
DB 1443 CAATGATTCATTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1502
QY 1512 AATGCCAAGTTGAGAAAATGATCATATTTTGAATTAAGATTAAGCAGACAGTGGGCAACC 1571
DB 1503 AATGCCAAGTTGAGAAAATGATCATATTTTGAATTAAGATTAAGCAGACAGTGGGCAACC 1562
QY 1572 GATTTTATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1631
DB 1563 GATTTTATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1622
QY 1632 GATGATGTTCAATCGGAATGCTCCAGGAAAGGACCTTTCACCTTGAATATGCAATTA 1691
DB 1623 GATGATGTTCAATCGGAATGCTCCAGGAAAGGACCTTTCACCTTGAATATGCAATTA 1682
QY 1692 TGTGATCAACAAGTCTGAGGCTTCTCTTTCATCTGTGGTGAAGAGCTTAAGACCTCAGT 1751
DB 1683 TGTGATCAACAAGTCTGAGGCTTCTCTTTCATCTGTGGTGAAGAGCTTAAGACCTCAGT 1742
QY 1752 TTTCAATAGCATCTAGAGAGTGGAGCTCAGCTGGGATATTTGCGCCCATCTCCGAG 1811
DB 1743 TTTCAATAGCATCTAGAGAGTGGAGCTCAGCTGGGATATTTGCGCCCATCTCCGAG 1802
QY 1812 GGAATGCTGAAGACAAATTTGGTTTCTTCATGAGGAGTGAAGAGATACAGTGTCTTA 1871
DB 1803 GGAATGCTGAAGACAAATTTGGTTTCTTCATGAGGAGTGAAGAGATACAGTGTCTTA 1862
QY 1872 CTACCAACTAGAGATTAAGAGGCGAGGAGTGTCTCAACTCTCTACATGTAAGAGCT 1931
DB 1863 CTACCAACTAGAGATTAAGAGGCGAGGAGTGTCTCAACTCTCTACATGTAAGAGCT 1922
QY 1932 CTCCCATTTAACAATCCCAATCCGAAGTGTCAACTGTGTCAAGATTAAGAAACCTGTGT 1991
DB 1923 CTCCCATTTAACAATCCCAATCCGAAGTGTCAACTGTGTCAAGATTAAGAAACCTGTGT 1982

| | | | |
|----|------|-----------------------------------------------------------------|------|
| OY | 1992 | TTTGAAGTAAAGAAAGGCGCTGGAAAAGAGGGAGCCAAACAATCTGTCTTCTTCTCAACTT | 2050 |
| Db | 1983 | TTTGAAGTAAAGAAAGGCGCTGGAAAAGAGGGAGCCAAACAATCTGTCTTCTTCTCAACTT | 2042 |
| OY | 2051 | AGTCATTGGCCAAATATAGCAATTCTGCTCTTTGGCTGCTGCTCTGACACAGAGAGCCAGAA | 2110 |
| Db | 2043 | AGTCATTGGCCAAATATAGCAATTCTGCTCTTTGGCTGCTGCTCTGACACAGAGAGCCAGAA | 2102 |
| OY | 2111 | CTCTATGGGGGACCACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAA | 2170 |
| Db | 2103 | CTCTATGGGGGACCACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAA | 2162 |
| OY | 2171 | TGCGGTATGGGATTAATCTTCAGCTTTGTAGCCTCTAAAGTTCTTCCCTCATTTTAC | 2230 |
| Db | 2163 | TGCGGTATGGGATTAATCTTCAGCTTTGTAGCCTCTAAAGTTCTTCCCTCATTTTAC | 2222 |
| OY | 2231 | CTGCAGGCCAAGTTCTGTATAGAGAAATCCCTGAGTTCTAGCTCAGGTTTTCTTACTCTGA | 2290 |
| Db | 2223 | CTGCAGGCCAAGTTCTGTATAGAGAAATCCCTGAGTTCTAGCTCAGGTTTTCTTACTCTGA | 2282 |
| OY | 2291 | ATTATGATCTTCAGACCCCTTCCTGGCCAAATTCAAATTAAGGCAACAAATATACCTT | 2350 |
| Db | 2283 | ATTATGATCTTCAGACCCCTTCCTGGCCAAATTCAAATTAAGGCAACAAATATATACCTT | 2342 |
| OY | 2351 | CCATGAGACACACACACACTTTTGAAAGCAAGACATGATCTGTTGAATTAGAGCCTTG | 2410 |
| Db | 2343 | CCATGAGACACACACACACTTTTGAAAGCAAGACATGATCTGTTGAATTAGAGCCTTG | 2402 |
| OY | 2411 | AGGATGAGGCTTTGAAGAAAAGATATCTTGTTCACGCCCCCTTCCACACTCTTCA | 2470 |
| Db | 2403 | AGGATGAGGCTTTGAAGAAAAGATATCTTGTTCACGCCCCCTTCCACACTCTTCA | 2462 |
| OY | 2471 | TGTGTTAACCACTGCCTTCTGGAACCTTGAAGCACGGTGACTGATTAACATGTTGTAT | 2530 |
| Db | 2463 | TGTGTTAACCACTGCCTTCTGGAACCTTGAAGCACGGTGACTGATTAACATGTTGTAT | 2522 |
| OY | 2531 | AGAAAACGTGATTTTATGAGTTCTGATCGTTCAAGAGAAATGATTAATATATACATTTCT | 2587 |
| Db | 2523 | AGAAAACGTGATTTTATGAGTTCTGATCGTTCAAGAGAAATGATTAATATATACATTTCT | 2579 |

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?      RESULT 13
?      US-09-850-178-23
?      Sequence 23, Application US/09850178
?      Patent No. US2002003479A1
?      GENERAL INFORMATION:
?      APPLICANT: Abbott Laboratories
?      APPLICANT: Billing-Medel, Patricia A.
?      APPLICANT: Cohen, Maurice
?      APPLICANT: Colipits, Tracey L.
?      APPLICANT: Friedman, Paula N.
?      APPLICANT: Russell, John C.
?      APPLICANT: Granados, Edward N.
?      APPLICANT: Hodges, Steven C.
?      APPLICANT: Klass, Michael R.
?      APPLICANT: Kratochvil, Jon D.
?      APPLICANT: Roberts-Rapp, Lisa
?      APPLICANT: Stroupe, Stephen D.
?      APPLICANT: Gordon, Julian
?      TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
?      TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
?      FILE REFERENCE: 6251 US P1
?      CURRENT APPLICATION NUMBER: US/09/850,178
?      CURRENT FILING DATE: 2001-05-07
?      PRIOR APPLICATION NUMBER: US 08/972,376
?      PRIOR FILING DATE: 1997-11-18
?      NUMBER OF SEQ ID NOS: 33
?      SOFTWARE: Fastseq for Windows Version 4.0
?      SEQ ID NO 23
?      LENGTH: 2591
?      TYPE: DNA
?      ORGANISM: Homo sapiens

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US-09-850-178-23

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|----------------------------|-------|---------------|-----------|--------------|
| Query Match | 98.7% | Score 2554; | DB 9; | Length 2591; |
| Best Local Similarity | 99.9% | Pred. No. 0; | | |
| Matches 2576; Conservative | 0; | Mismatches 0; | Indels 2; | Gaps 2 |

| | | | | | | | | |
|----|-----|---------------|---------------------------------------------------|-------------------------|----------------------------|--------|-------------|------|
| OY | 12 | GGCAGCTC | CACTCAGCCAGTACCCAGATACGCTGGAA | CC | TTCCCA | GGCCTT | CC | 71 |
| Db | 11 | GGCAGCTC | CACCTCAGCCAGTACCCAGATACGCTGGAA | CC | TTCCCA | GGCCTT | CC | 70 |
| OY | 72 | TGGGGCAGATCCT | CTTCTCGAGCATTAATTACATCATATTA | TTCTGAGTGGAGCAAT | TTG | | | 131 |
| Db | 71 | TGGGGCAGATCCT | CTTCTCGAGCATTAATTACATCATATTA | TTCTGAGTGGAGCAAT | TTG | | | 130 |
| OY | 132 | CAC | TCA | TG | CTTGGTGGTATTTTCAGGGAGACACT | CCATCA | CACTCACT | 191 |
| Db | 131 | CAC | TCA | TG | CTTGGTGGTATTTTCAGGGAGACACT | CCATCA | CACTCACT | 190 |
| OY | 192 | CAGCTGGGAA | CAATTGGGGAGATGGAA | TC | TGAGTGCATCTT | GAAC | CTGACATCAAC | 251 |
| Db | 191 | CAGCTGGGAA | CAATTGGGGAGATGGAA | TC | TGAGTGCATCTT | GAAC | CTGACATCAAC | 250 |
| OY | 252 | TTTCTGATATCGT | ATGATCAATAGGCTGAAAGAGGTGTT | TAAG | CGTTAGCTGATGAGTTCA | | | 311 |
| Db | 251 | TTTCTGATATCGT | ATGATCAATAGGCTGAAAGAGGTGTT | TAAG | CGTTAGCTGATGAGTTCA | | | 310 |
| OY | 312 | AAGAAAGCA | AGATGAGCTGTGCGACAGATGAAT | GTTCAGAGGCGGACAGCATGT | | | | 371 |
| Db | 311 | AAGAAAGCA | AGATGAGCTGTGCGACAGATGAAT | GTTCAGAGGCGGACAGCATGT | | | | 370 |
| OY | 372 | TTTGGATCA | AGTGAATGTTGGCAATGCTCTTTGGCGGTGAAAA | CGTGCACATCAAG | | | | 431 |
| Db | 371 | TTTGGATCA | AGTGAATGTTGGCAATGCTCTTTGGCGGTGAAAA | CGTGCACATCAAG | | | | 430 |
| OY | 432 | ATGCTGCACCTA | CAAAATGTTATATCATCACTTCTTAAAGCAAGGGGATGTA | CTTGG | | | | 491 |
| Db | 431 | ATGCTGCACCTA | CAAAATGTTATATCATCACTTCTTAAAGCAAGGGGATGTA | CTTGG | | | | 490 |
| OY | 492 | AGTATTA | AAACCTGAGCCCTTCAGCATCCGGGAAGTAATGTGACATATATG | CACATGACATG | | | | 551 |
| Db | 491 | AGTATTA | AAACCTGAGCCCTTCAGCATCCGGGAAGTAATGTGACATATATG | CACATGACATG | | | | 550 |
| OY | 552 | AGACCTTGCGGTG | TGAGGCTCCCGATGGTTCCCCAGCCCA | CAGTGGCTTGGGATCC | | | | 611 |
| Db | 551 | AGACCTTGCGGTG | TGAGGCTCCCGATGGTTCCCCAGCCCA | CAGTGGCTTGGGATCC | | | | 610 |
| OY | 612 | AA | GTTGACAGGGACCACTTCTTGGAAGTCTCAATACAGCTTTGA | GCTAACTCTG | | | | 671 |
| Db | 611 | AA | GTTGACAGGGACCACTTCTTGGAAGTCTCAATACAGCTTTGA | GCTAACTCTG | | | | 670 |
| OY | 672 | AGA | ATGACATGAAGGTGTGTGTGCTCTACATAGTTACGATCAACA | CACATCACT | | | | 731 |
| Db | 671 | AGA | ATGACATGAAGGTGTGTGTGCTCTACATAGTTACGATCAACA | CACATCACT | | | | 730 |
| OY | 732 | CCTGATATG | TGAATAATGACATTTGCCAAGCAACAGGGATATCAAA | ATGACAGATCGG | | | | 791 |
| Db | 731 | CCTGATATG | TGAATAATGACATTTGCCAAGCAACAGGGATATCAAA | ATGACAGATCGG | | | | 790 |
| OY | 792 | AGATTA | AAAGCGGAGTCACTACAGCTGCTAAACTCAAA | GGCTTCTGTGTGTCTCT | | | | 851 |
| Db | 791 | AGATTA | AAAGCGGAGTCACTACAGCTGCTAAACTCAAA | GGCTTCTGTGTGTCTCT | | | | 850 |
| OY | 852 | CTTTCTTTG | CCATCGCTGGGCACTTCTGCGCTCAGGCCCTTACCTGATGCTAAATAT | | | | | 911 |
| Db | 851 | CTTTCTTTG | CCATCGCTGGGCACTTCTGCGCTCAGGCCCTTACCTGATGCTAAATAT | | | | | 910 |
| OY | 912 | GTG | CCCTTGCCCAAAAAAGCATGCAAAAGTATGT | TACACAGGGATCTACAGAACTAT | | | | 971 |
| Db | 911 | GTG | CCCTTGCCCAAAAAAGCATGCAAAAGTATGT | TACACAGGGATCTACAGAACTAT | | | | 970 |
| OY | 972 | TTTCA | CCACGATATGACCTAGTTTATATTTCTGGGAGGAATGAATTCATATCTA | TAAC | | | | 1031 |
| Db | 971 | TTTCA | CCACGATATGACCTAGTTTATATTTCTGGGAGGAATGAATTCATATCTA | TAAC | | | | 1030 |

Db 71 TGGGGAGATCTCTTCTTGAGCATATATTAGCATCATATATTCTGCTGGAGCAATTG 130
Qy 132 CACTCATCTTTGGCTTTGGTATTTTCAGGGAGACATCCCATCAAGACTACTGTCGCT 191
Db 131 CACTCATCTTTGGCTTTGGTATTTTCAGGGAGACATCCCATCAAGACTACTGTCGCT 190
Qy 192 CAGCTGGAGCACTTGGGGAGAGATGGAATCTGAGCTGCATCTTTGAACTGACATCAAC 251
Db 191 CAGCTGGAGCACTTGGGGAGAGATGGAATCTGAGCTGCATCTTTGAACTGACATCAAC 250
Qy 252 TTTTCGATATCGTGATACATAGCTGAGAGAAAGTGTGTTGAGCTTGGCTGATGAGTTCA 311
Db 251 TTTTCGATATCGTGATACATAGCTGAGAGAAAGTGTGTTGAGCTTGGCTGATGAGTTCA 310
Qy 312 AAGAGGGCAAAATGAGCTGTGGAGCAGAGATGAAATGTTCAAGGGCGGAGCAGAGT 371
Db 311 AAGAGGGCAAAATGAGCTGTGGAGCAGAGATGAAATGTTCAAGGGCGGAGCAGAGT 370
Qy 372 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGGCTGAAAAAGTGCATCAACAG 431
Db 371 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGGCTGAAAAAGTGCATCAACAG 430
Qy 432 ATGCTGGACCTTCAAAATGTTATATCATCTTAAAGGCAAGGGAAATGCTAACCTTG 491
Db 431 ATGCTGGACCTTCAAAATGTTATATCATCTTAAAGGCAAGGGAAATGCTAACCTTG 490
Qy 492 AGTATTAACCTGGAGCTTCAAGATGCGGAAAGTGAATGGAGCTAATATGCAAGCTGAG 551
Db 491 AGTATTAACCTGGAGCTTCAAGATGCGGAAAGTGAATGGAGCTAATATGCAAGCTGAG 550
Qy 552 AGACCTTGGCGTGTGAGGCTCCCGATGCTCCCGACCCCAAGTGTCTGGGCAATCCC 611
Db 551 AGACCTTGGCGTGTGAGGCTCCCGATGCTCCCGATGCTCCCGACCCCAAGTGTCTGGGCAATCCC 610
Qy 612 AAGTTGACCAAGGAGCCAACTTCTCGAAAGTCTCCAAATACAGCTTTGAGCTGAACCTG 671
Db 611 AAGTTGACCAAGGAGCCAACTTCTCGAAAGTCTCCAAATACAGCTTTGAGCTGAACCTG 670
Qy 672 AAGAAATGACCAAGGAGCTTGTGTGTCTGTCTCAAAATGTTTCAATCAACAACATCT 731
Db 671 AAGAAATGACCAAGGAGCTTGTGTGTCTGTCTCAAAATGTTTCAATCAACAACATCT 730
Qy 732 CCTGTATGATTAATAATGACATTTGCCAAAGCAACAGGGAGTATCAAAATGACAGATCCG 791
Db 731 CCTGTATGATTAATAATGACATTTGCCAAAGCAACAGGGAGTATCAAAATGACAGATCCG 790
Qy 792 AGATCAAAAGGCGGAGTCACTTACAGCTGTAAATCTCAAAAGCTTCTGTGTGTCTCT 851
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Qy 852 CTTTCTTGGCATCAGCTGGGAGCTTCTGCTCTGAGCCCTTACCTGATGCTAAATAT 911
Db 851 CTTTCTTGGCATCAGCTGGGAGCTTCTGCTCTCTGAGCCCTTACCTGATGCTAAATAT 910
Qy 912 GTGCTTGGCAAC-AAAAAGCATGCAAGTCAATTGTTTCAACAGGGATCTACAGAACTA 970
Db 911 GTGCTTGGCAACAAAAAAGCATGCAAGTCAATTGTTTCAACAGGGATCTACAGAACTA 970
Qy 971 TTTTCAACCAAGATATGACCTTGTATTTTATTTCTGGGAGAAATGAAATTCATCTTAA 1030
Db 971 TTTTCAACCAAGATATGACCTTGTATTTTATTTCTGGGAGAAATGAAATTCATCTTAA 1030
Qy 1031 AGTCTGAGTGAACAACAAGCAGAAACAAAAAGAGCCAAAAGCAGAAAGGCTCCAA 1090
Db 1031 AGTCTGAGTGAACAACAAGCAGAAACAAAAAGAGCCAAAAGCAGAAAGGCTCCAA 1090
Qy 1091 TATGAAACAAGATTAATCTTCTTCAAAAGCATATTTGAAGTTGGGAAAATTAATTCATG 1150
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Qy 1210 AACTAGACAAGTGTGTTAAAGTGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1210
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Qy 1211 GATCTCAGGAGACCTCCCTGCTGTCACTGGGAGTGAAGAGCAGGAATAGTCATGT 1270
Db 1210 GATCTCAGGAGACCTCCCTGCTGTCACTGGGAGTGAAGAGCAGGAATAGTCATGT 1269
Qy 1271 TCTTGTCTGTGAATTTTATGTTATATGCTGTATATGTTGCTGTGAGAAAGCCCTGGA 1330
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Qy 1331 AAGCTATCCCAACATATCCATCTATATTTCCCAAAATTAAGCTATGATATGATCCCT 1390
Db 1330 AAGCTATCCCAACATATCCATCTATATTTTCCCAAAATTAAGCTATGATATGATCCCT 1389
Qy 1391 AAGAGCTGTATATGATGCTGCACTTCCCACTCAGGGGCGGCTGCAATTTATGATGGG 1450
Db 1390 AAGAGCTGTATATGATGCTGCACTTCCCACTCAGGGGCGGCTGCAATTTATGATGGG 1449
Qy 1451 TCAAAATGATCACTTTTATGATGCTTCCAAAGGCTTGGCTTCTCTCCCACTGAC 1509
Db 1450 TCAAAATGATCACTTTTATGATGCTTCCAAAGGCTTGGCTTCTCTCTCCCACTGAC 1509
Qy 1511 AAATGCCAAAGTGAAGAAAAATGATCATATTTTATGATTAACAGAGAGTGGGCAAC 1570
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Qy 1571 CGATTTTATTAATTAACCTGAGCACCCTCTTTTAAACAAACAAATGCGGTTTATTTCTC 1630
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Qy 1691 ATGTCATCAAGGCTCTGAGGCTTCTCTTCCATCTGCGGAGCAGCTAAGACCTGAG 1750
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Db 1750 TTTTCAATAGCATCTTGAAGCAGTGGAGTCACTGCTGGGAGTGTGTTGGCCCCCATCTCCG 1809
Qy 1811 GGGAAATGCTGAAGCAATTTTGTCTTACCTCAATAGAGGAGTGAAGATACGCTCT 1870
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Qy 1871 ACTACCAATAGTGAATTAAGGCGAGGAGTGTCTCAACCTTCAACCATGTAACGAGAG 1930
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Qy 1931 TCTCCCATTAACCACTCAATCCCAATCCCAATGTCATCTGTGAGGACTAAGAAACCTGG 1990
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Db 2350 TCCATGAGACACACACAGACTTTTGAAGCAAGACAATGACTCTTGAATTGAGCCCTT 2409
Qy 2410 GAGGAATGAAGCTTTGAAGGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTC 2469
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Qy 2470 ATGTGTTAACCACTGCTTCTCTGAGCCTTGAGCCACGAGTACTGTATTACATGTTGTA 2529
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Qy 2530 TAGAAAATGATTTTGAAGTTCTGATCGTTCAAGAGAATGATTAATATACATTTCT 2587
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RESULT 15
US-10-023-339-9
; Sequence 9, Application US/10023339
; Publication No. US20030208058A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: B7-Like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: P1124P1
; CURRENT APPLICATION NUMBER: US/10/023,339
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/20917
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-339-9

Query Match 93.6%; Score 2421.8; DB 17; Length 2626;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2535; Conservative 0; Mismatches 7; Indels 11; Gaps 11;

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Db 57 GGAACCTTCCCGCAGCATGGCTTCCCTGGGGCAGATCCCTTCTGAGCATTAATTTAGC 116
Qy 104 ATCATCATTTATTCGTGCTGAGCAATTGCACTCATCATTTGGCTTTATTTTCAGGAGA 163
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Db 117 ATATATATTTATTCGTGCTGAGCAATTGCACTCATCATTTGGCTTTATTTTCAGGAGA 176
Qy 164 CACTTCATCAAGTCACTACTGCTGCTCAGCTGGGAACTTGGGAGAGATGAACTCTG 223
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Qy 224 AGCTGCATTTTGAACCTGACATCAAACTTTCGATATTCGATGATCAATGGCTGAAGAA 283
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Qy 343 TGAATGTTCAAGAGCC-GGACAGCAGTGTGTTGCTGATCAAGTATGTTGGCAATGCT 401
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Qy 402 C-TTGGCGGTGAAAAAGTGAACATCAAGATGCTGGACCTACAAATGTTATATATC 460
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Qy 461 ACTTTAAAGCAAGGGAAATGCTAACCTTGAATATTAACCTGAGCTTCAGCATGCC 520
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Db 477 ACTTTAAAGCAAGGGAAATGCTAACCTTGAATATTAACCTGAGCTTCAGCATGCC 536
Qy 521 GAAATGAAATGATCTTAATGCGAGTCAAGAACCTTGGGGGTGTAGAGCTCCCGCATG 580
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Qy 581 TTCCCGCAGCCACAGTGTCTGGGCAATCCCAAGTTGACCAAGGAGCAACTTCTGGAA 640
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Qy 641 GTCTCAATACAGCTTTGAGCTGAACCTGAGAAATGACATGAAGGTTGTCTGTG 700
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Qy 701 CTCTCAATGTTACGATCAACACACATCTCTGTTATGATTGAAATGACATTTGCCAA 760
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Qy 941 TCAATGTTAACAGGGGATATCAAGTGAAGAAATGGAGATCAAAAGGGGAGTCACTACAGCT 1000
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Qy 1061 CAAAAAGAACCAAAAGCAGAGAGCTCCATATGAAACAGATTAATCTATCTTCAAGAC 1120
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Qy 1361 TTCCAAATTAATGATGATGATGATCCCTAAGACCTGCTAATGATGCTCACTTGC 1420
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Qy 1481 AAGGTGCTTGGGCTTCTTCCCACTGACAAATGCC-AAAGTTGAGAAAAATGATCAT 1539

Db 1496 AAGTGCCTGGCTTCTTCCCACTGACAAATGCCAAAGTGGAGAAAAATGATCATA 1555
QY 1540 ATTTTAGCATTAACAGAGC-AGTCGGCGACACCGATTTTATTAATACTGAGCACCTTC 1598
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QY 1599 TTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCA-CCGTGAATGGTCCA 1657
Db 1616 TTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCA-CCGTGAATGGTCCA 1675
QY 1658 GGGAAAGACCTTTCACCTTGACTATATGSCATTATGTCAACAAGCTCTGAGGCTTCTC 1717
Db 1676 GGGAAAGACCTTTCACCTTGACTATATGSCATTATGTCAACAAGCTCTGAGGCTTCTC 1735
QY 1718 CTTTCATCTCGTGTGAGAGACTAAGACCTCAGTTTCAATAGCACTAGAGAGTGGGA 1777
Db 1736 CTTTCATCTCGTGTGAGAGACTAAGACCTCAGTTTCAATAGCACTAGAGAGTGGGA 1795
QY 1778 CTCAGCTGGGATATTTCCGCCCATCTCCGGGGAAATGTCGAAGCAATTTTGGTTA 1837
Db 1796 CTCAGCTGGGATATTTCCGCCCATCTCCGGGGAAATGTCGAAGCAATTTTGGTTA 1855
QY 1838 CCTCAATGAGGAGTGGAGAGATACAGTCTACTACCACTAGTGAATAAGGCCAGG 1897
Db 1856 CCTCAATGAGGAGTGGAGAGATACAGTCTACTACCACTAGTGAATAAGGCCAGG 1915
QY 1898 GATGCTGCTCAA-CCTCTACCATGTACAGAGAGCTCCGCCATTAACAACAATTTTCCG 1956
Db 1916 GATGCTGCTCAACCTCTACCATGTACAGAGAGCTCCGCCATTAACAACAATTTTCCG 1975
QY 1957 AAGTGTG-AACTGTGTCAAGACTAAGAAACCTGTGTTTGAAGTGAAGAGGCTGGAAA 2015
Db 1976 AAGTGTCAACTGTGTCAAGACTAAGAAACCTGTGTTTGAAGTGAAGAGGCTGGAAA 2035
QY 2016 GAGGGAGGCCAACAAATCTGTCTGCTT-CTCATTATGCTATGGCAATTAAGCATTTCTG 2074
Db 2036 GAGGGAGGCCAACAAATCTGTCTGCTTCTCATTATGCTATGGCAATTAAGCATTTCTG 2095
QY 2075 TCTCTTGGCTGTGCTGACGACAGAGAGCCAGAACTCATGCGGACACAGGATTAACAT 2134
Db 2096 TCTCTTGGCTGTGCTGACGACAGAGAGCCAGAACTCATGCGGACACAGGATTAACAT 2155
QY 2135 CTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTGATGGATTAATCTTCAGCT 2194
Db 2156 CTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTGATGGATTAATCTTCAGCT 2215
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QY 2255 AATGCTGAGTTCTACTCAGGTTTCTTACTGTAATTTAGATCTCCAGACCTTCCTG 2314
Db 2276 AATGCTGAGTTCTACTCAGGTTTCTTACTGTAATTTAGATCTCCAGACCTTCCTG 2335
QY 2315 GCCACAATTCAATTAAGGCAACAACATATACCTTCATGAAGCACACAGACTTTTG 2374
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QY 2375 AAAGCAAGACATGACTGCTGAATTGAGGCTTGAAGATGAAGCTTTGAAGGAAAG 2434
Db 2396 AAAGCAAGACATGACTGCTGAATTGAGGCTTGAAGATGAAGCTTTGAAGGAAAG 2455
QY 2435 AATACTTTGTTCCAGCCCCCTCCACAACCTTCATGTTTAAACAACCTGCTTCTGG 2494
Db 2456 AATACTTTGTTCCAGCCCCCTCCACAACCTTCATGTTTAAACAACCTGCTTCTGG 2515
QY 2495 CCTTGAGGACACGAGTACTGATATGATGTTGTTATAGAAAACGTGATTTAGAGTTCTGA 2554
Db 2516 CCTTGAGGACACGAGTACTGATATGATGTTGTTATAGAAAACGTGATTTAGAGTTCTGA 2575
QY 2555 TCGTTCAAGAGATGATTAATATACATTTCTT 2587

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Search completed: May 31, 2005, 10:07:34
Job time : 1781.97 secs

QY 191 TCAGCTGGGAAACATTTGGGGAGGATGGAAATCTGAGCTGCACTTTTGAACCTGACATCAAA 250
DB 61 TCAGCTGGGAAACATTTGGGGAGGATGGAAATCTGAGCTGCACTTTTGAACCTGACATCAAA 120
QY 251 CTTTCTGATATGCTGATACAAATGGCTGAAGAGGTGTTTAGGCTTGGTTCATGAGTTC 310
DB 121 CTTTCTGATATGCTGATACAAATGGCTGAAGAGGTGTTTAGGCTTGGTTCATGAGTTC 180
QY 311 AAAAGAGGCAAGATGAGCTGTGCGAGCAGATGAAATGTTCAGAGGCGGACAGCAGTG 370
DB 181 AAAAGAGGCAAGATGAGCTGTGCGAGCAGATGAAATGTTCAGAGGCGGACAGCAGTG 240
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QY 431 GATGCTGGACCTTACAAATGTTATATCATCATCTTCTTAAAGGCAMGGGAAATGCTAACCTT 490
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QY 491 GAGTATAAAACTGGAGCTTCAGCATGCGGAAAGTGAATGTGGACTATATATGCTCAGCTCA 550
DB 361 GAGTATAAAACTGGAGCTTCAGCATGCGGAAAGTGAATGTGGACTATATATGCTCAGCTCA 420
QY 551 GAGACCTTGGCGGTGAGAGGCTCCCGATGGTTCCCGACGCCACAGTGGTCTGGGCAATCC 610
DB 421 GAGACCTTGGCGGTGAGAGGCTCCCGATGGTTCCCGACGCCACAGTGGTCTGGGCAATCC 480
QY 611 CAAGTTGACCGAGGAGCCAACTTCTCGAAGTCTCCAAATACAGCTTTGAGCTGAACTCT 670
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QY 671 GAGAAATGTCACATGAAAGTTGTGTCTGTCTTACAAATGTTACATCAACAACATATAC 730
DB 541 GAGAAATGTCACATGAAAGTTGTGTCTGTCTTACAAATGTTACATCAACAACATATAC 600
QY 731 TCCGTGATGATTTGAAAAATGACATTTGGCAAAAGCAAGGGGATATCAAAGTGAAGAAATG 790
DB 601 TCCGTGATGATTTGAAAAATGACATTTGGCAAAAGCAAGGGGATATCAAAGTGAAGAAATG 660
QY 791 GAGATCAAAAAGCGGAGTCACTTACAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTCT 850
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QY 1031 AGTCTGAGTGAACAAAGAGACAGAAACAAAAAGAGCCAAAGCAGAGAGGCTTCCA 1090
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QY 1211 GATCTCAGGAGACCTCCCTGCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGT 1270
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DB 1861 TTTTGAATGAAAAAGGCTGAAAAAGGGAGGCCAACAAATCTGTCTGTCTCTCAAT 1920
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DB 1921 TATGCTATGGCAATTAAGATCTGTCTTGTGGCGTGCCTGAGCAGAGAGCCAGA 1980
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QY 2170 ATGCTGATGGAGTATCTTACGCTTGTGAGCTTCTAAATTTCTTTCTCTCATTTAC 2229
DB 2041 ATGCTGATGGAGTATCTTACGCTTGTGAGCTTCTAAATTTCTTTCTCTCATTTAC 2100
QY 2230 CCGCAGGCAAGTTCTGTAAAGAAATGCTGAGTCTGAGTCTGAGTTTCTTACTCTCG 2289
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QY 2290 AATTTAGATCTCAGACCTTCTCGGCACAATTCAAATTTAAGGCAACAATATACCT 2349
DB 2161 AATTTAGATCTCAGACCTTCTCGGCACAATTCAAATTTAAGGCAACAATATACCT 2220
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Db 2221 TCCATGAGACACACAGACTTTTGAAGACAGACATGACTCTGGAATGAGGCTT 2280
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Db 2281 GAGGATGAGACTTTGAAGGAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTC 2340
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RESULT 2
BX371687/c
LOCUS BX371687 939 bp mRNA linear EST 28-APR-2004
DEFINITION BX371687 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1039YG21 3-PRIME, mRNA sequence.
BX371687
ACCESSION BX371687.2 GI:46834026
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 939)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30459784.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
742.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DA1021ZB08_CS01978_1kc=742.r.
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/cissue_type="PLACENTA COT 25-NORMALIZED"
/clone_1b="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 32.8%; Score 849.4; DB 5; Length 939;
Best Local Similarity 98.7%; Pred. 1.9e-222;
Matches 927; Conservative 0; Mismatches 5; Indels 7; Gaps 7;
QY 1103 AAATCTATCTTCAAGACATA-TTGAAGTTGGGAAATTA-TTCATGTGAACATAGCAA 1160
Db 939 AAATCTATCTTCAAGACATA-TTGAAGTTGGGAAATTA-TTCATGTGAACATAGCAA 880
QY 1161 G-TGTGTTAGAGTGAATGAATGAATGACAGTGAAGCAAGTGCATCCAGATCTCAGG 1219
Db 879 GATGTGTTAGAGTGAATGAATGAATGACAGTGAAGCAAGTGCATCCAGATCTCAGG 820
QY 1220 GA-CTTCCCTGCTGCTGACCTGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGTC 1278
Db 1220 GA-CTTCCCTGCTGCTGACCTGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGTC 1278

ORIGIN
Query Match 32.8%; Score 849.4; DB 5; Length 939;
Best Local Similarity 98.7%; Pred. 1.9e-222;
Matches 927; Conservative 0; Mismatches 5; Indels 7; Gaps 7;
QY 1103 AAATCTATCTTCAAGACATA-TTGAAGTTGGGAAATTA-TTCATGTGAACATAGCAA 1160
Db 939 AAATCTATCTTCAAGACATA-TTGAAGTTGGGAAATTA-TTCATGTGAACATAGCAA 880
QY 1161 G-TGTGTTAGAGTGAATGAATGAATGACAGTGAAGCAAGTGCATCCAGATCTCAGG 1219
Db 879 GATGTGTTAGAGTGAATGAATGAATGACAGTGAAGCAAGTGCATCCAGATCTCAGG 820
QY 1220 GA-CTTCCCTGCTGCTGACCTGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGTC 1278
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Db 819 GACCCTCCCTGCTGCTGACCTGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGTC 760
QY 1279 TCTGAATTTTATGTTATGTTGCTGTAATGTTGCTCTGAGGAGCCCTTGAAGTCTAT 1338
Db 759 TCTGAATTTTATGTTATGTTGCTGTAATGTTGCTCTGAGGAGCCCTTGAAGTCTAT 700
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Db 699 CCCAATATCCATCTTATATTCACAAATTAAGCTGATATGTAACCTTAAGAGCT 640
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Db 639 GCTAATGAGTGGCACTTGGCACTAGAGGCGGCTGCAATTTTATGTAATGAGTCAATGA 580
QY 1459 TTCACCTTTTATGATGCTTCAAGAGGCTTGGCTTCTTCCCACTGACAAATGCCA 1518
Db 579 TTCACCTTTTATGATGCTTCAAGAGGCTTGGCTTCTTCCCACTGACAAATGCCA 520
QY 1519 AAGTTGAGAAAATGATCATATTTTATGATTAACAGAGCAGTGGGACACCGATTTTA 1578
Db 519 AAGTTGAGAAAATGATCATATTTTATGATTAACAGAGCAGTGGGACACCGATTTTA 460
QY 1579 TAAATTAAGTACGACCTCTTTTAAACAAACAAATGCGGTTTATTTCTCAGATGATG 1638
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QY 1759 AGCATCTAGAGCAGTGGGACTGAGTGGGCTGATTTTCCCTCATCTCCGCGGGAATGT 1818
Db 279 AGCATCTAGAGCAGTGGGACTGAGTGGGCTGATTTTCCCTCATCTCCGCGGGAATGT 220
QY 1819 CTGAAGACAAATTTGTTGTTCCCTCAATGAGGAGCTGAGAGGATACAGTCTACTCCAA 1878
Db 219 CTGAAGACAAATTTGTTGTTCCCTCAATGAGGAGCTGAGAGGATACAGTCTACTCCAA 160
QY 1879 CTAGTGAATTAAGGCGAGGATGCTGCTCAACCTCTACCATGTAGAGAGCTCTCCCA 1938
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Db 99 TTACAACTACCCCAATCCGAAGTGTCAACTGTGTGAGGACNTAAGAAACCTGTGTTGAG 40
QY 1998 TAGA-AAAGGCGCTGGAAG-AGGGAGGCCAACAATCT 2034
Db 39 TAGA-AAAGGCGCTGGAAG-AGGGAGGCCAACAATCT 1

RESULT 3
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LOCUS BX377228 1018 bp mRNA linear EST 08-APR-2004
DEFINITION BX377228 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1039YG21 3-PRIME, mRNA sequence.
BX377228
ACCESSION BX377228.2 GI:46283446
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1018)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:3046952.
COMMENT
Contact: Genoscope

Db 26 TGAATAAAGTGTGCACTGACAGATGCTGGACCTTCAAAATGTTATATGACACATTTCATAA 85
 Qy 470 GGGAAAGGGGAATGCTAACCCTTGAATATAAATCTGAGCTTCAACATGCCGGAATGAT 529
 Db 86 GGGAAAGGGGAATGCTAACCCTTGAATATAAATCTGAGCTTCAACATGCCGGAATGAT 145
 Qy 530 GTGAGACTATAATGCTGAGCTGAGAGACCTTGGGTGTGAGGCTCCCGATGGTTCCTCCAG 589
 Db 146 GTGAGACTATAATGCTGAGCTGAGAGACCTTGGGTGTGAGGCTCCCGATGGTTCCTCCAG 205
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 Qy 650 ACCAGCTTTGAGCTGGAATCTGAGAAATGTGACATGAAAGTGTGTCTGTGCTCTCAAT 709
 Db 266 ACCAGCTTTGAGCTGGAATCTGAGAAATGTGACATGAAAGTGTGTCTGTGCTCTCAAT 325
 Qy 710 GTTACGATCAACAACACATACCTCTGTATGATGTAATAATGATTCGCAAAAGCAACAGG 769
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 Qy 770 GATATCAAAGTGAAGAGATCGAGATCAAAAAGGCGAGTCACTACAGCTGTAACTCA 829
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 Qy 950 CAACAGGAGTCTACAGAACTATTTCACACAGATGATGACCTATTATATTTCTGGA 1009
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 Db 746 GTTGGGAAATTAATTCATGTAAGTGAACATGAGTGTG-TTAAAGTGAATGAATGCA 805
 Qy 1189 GTTGGGAGACAGTGCATCCCAAGATCTCAGGAGCTCCCTGTGCTCACTGGGG 1245
 Db 806 GTTGGGAGACAGTGCATCCCAAGATCTCAGGAGCTCCCTGTGCTCACTGGGG 862
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 LOCUS UI-CF-FNO-afj-a-01-0-UI.sj UI-CF-FNO Homo sapiens cDNA clone
 DEFINITION UI-CF-FNO-afj-a-01-0-UI 3', mRNA sequence.
 ACCESSION CA311913
 VERSION CA311913.1 GI:24530011
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 779)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477

PUBMED COMMENT

8889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul.mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.research.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

Location/Qualifiers
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 /issue_type="Human lung Epithelial cells"
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 /clone_1lb="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site: 1: Ecor I; Site 2: Not I;
 UI-CF-FNO is a subtracted cDNA library derived from two
 normalized Human lung epithelial cell libraries (EN1 and
 DU1) The library was subtracted according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 Bento-Soares@uiowa.edu
 TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
 6hr to LPS 24h
 TAG LIB=UI-CF-FNO
 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 29.7%; Score 769; DB 6; Length 779;
 Best Local Similarity 99.4%; Pred. No. 2,5e-209;
 Matches 772; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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 Qy 824 AACTCAAGGCTTCTGTGTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 883
 Db 719 AACTCAAGGCTTCTGTGTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
 Qy 884 CTCAGCCCTTACCTGATGCTAAATAATGTCCTTGGCCCAAAAAGCATGCAAGTCA 943
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 Db 539 CTGGGAGGAATTAATTCATATCTAGAACTCTGAGTGAAGCAAAAGCAAGCAAAACA 480
 Qy 1064 AAAGAAGCCAAAAGGAGGCTCCATATGAAACAATATCTATCTTCAAGACATA 1123
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 Db 419 TTGAAGTTGGGAAATTAATTCATGTAAGTGAACATGAGTGTGTTAAGTGAATGAATA 360
 Qy 1184 ATGCAAGTGAAGCAAGTGCATCCCAAGATCTCAGGAGCTCCCTGTGCTCACTGG 1243

Db 359 ATGCACTGGAGACAAGATGCATCCCCAGATCTCAGGAACTCCCCCTGCTGCACCTGG 300

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Db 299 GGAATGAGAGACAAGATAGTCATGTTCTTTGTCTCGAAATTTTAACTTAATATGTGCTG 240

QY 1304 TAAATGTCCTCTGAGGAAGCCCCCTGGAAAGTCATCCACAATATCCACATCTTAATATTC 1363

Db 239 TAAATGTCCTCTGAGGAAGCCCCCTGGAAAGTCATCCACAATATCCACATCTTAATATTC 180

QY 1364 CACAATTAAGCTGATGATGATACCTTAAGAAGCTGCAATATGCACTGCACCTGGCAACT 1423

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QY 1424 CAGGGGGCGGCTGATTTAGTAATAGGTGCAAAATGATTCATCTTTTATGATGCTTCCAAAG 1483

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| RESULT 6 | BM981657/c | LOCUS | BM981657 | 751 bp | mRNA | linear | EST 21-PEB-2003 |
|------------|----------------------------|-----------------------------------|--------------------------------------------|--------|------|--------|-----------------|
| DEFINITION | UI-CF-EN1-adi-m-02-0-UI.s1 | UI-CF-EN1 Homo sapiens cDNA clone | UI-CF-EN1-adi-m-02-0-UI 3', mRNA sequence. | | | | |

| | |
|-----------|----------------------|
| ACCESSION | BM981657 |
| VERSION | BM981657.1 |
| KEYWORDS | GI:19604370 |
| SOURCE | EST. |
| ORGANISM | Homo sapiens (human) |
| | Homo sapiens |

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 751)
Bonaldi, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

| | |
|---------|-----------------------------------|
| JOURNAL | Genome Res. 6 (9), 791-806 (1996) |
| MEDLINE | 97044477 |
| PUBMED | 8889548 |
| COMMENT | Contact: McCray, PB |

University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reesgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

| FEATURES | Location/Qualifiers |
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| source | 1. .751 |

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/mol_type="mRNA"
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Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pTT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the

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following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT. TAG_TISSUE=Human Lung Epithelial Cell lines untreated LPS 6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

| | | | | |
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| Query Match | 28.6% | Score 740.6 | DB 5 | Length 751 |
| Best Local Similarity | 99.3% | Pred. No. 3.6e-201 | | |
| Matches 743; Conservative | 0 | Mismatches 5 | Indels 0 | Gaps 0 |

322 AGATGACCTGTCGAGCAGATGAATCTTCAAGGCCCGACACAGAGTGTTCGATCA 381

Db 751 AGATGAGCTGCGAGCAGATGAATGTTCAAGGCCGACACAGAGTGTTCCTGATCA 692

382 AGTGATGTTGGCAATGCTCTTTGGCGGTGAAAAAGTGCACCTCACAGATGCTGGCAC 441

Db 691 AGTGATGTTGGCAATGCTCTNTGGCGCTGAAAAACGTGCACATCACAAGATGCTGGCAC 632

442 CTACAATGTTATATCATCATCTTAAGGCAGGGGATGCTAACCTTGATATAAAC 501

Db 631 CTACAATGTTATATCATCACTTCTAAGGCAAGGGAGTGCCTAAGTATATAAAC 572

502 TGAACCTTCAGCATGCCGAAGTGAATGTGACTATAATGCCACCTCAGACCACTTTGG 561

Db 571 TGGAGCTTCAGCATGCCGGAAGTGAATGTGACATAATAATGCCAGCTCAGAGACCTTCCG 512

562 GTGTGAAGCTCCCCGATGGTTCCCCCAGCCACAGTGGTCTGGGATCCCAAGTTGACCA 621

Db 511 GTGTGAGGCTCCCCGATGGTTCCCCCAGCCCAcAGTGGTCTGGGcATCCCAAGTTgACCA 452

622 GGGAGCCAACTTCTCGAAGTCTCCCAATACAGCTTTGAGCTGAACCTGTGGAATGGAC 681

Db 451 GGAAGCACTTCTCGAAGTCTCCAAATACCAGCTTTGAGCTGAACCTGTGGAATGTGAC 392

682 CATGAAGGTTGCTGCTACCAAGTACCAATCAACAACATACCTGATGAI 741

Db 391 CATTGAAGGTTGTCGTGCTACCAATGTTACGATCAACACACATACCTCCGATGAT 552

331 TCGAATTCGACAGGGTCTTTCAAGGTGACAGAATCCGATCAAAG 272
/42 TGAATAATGACATATGCCTAAAGCAGGGATATTAAGATGACAGATCGAGG
08

802 GCGGAGTCACTCCACAGCGCTTAACTTCAAAGGCGTTTCGCTGCTCTTCCTTTCTTTGCG 861

Ph 271 GCGGACCTACCAAGCTGCTAACTCAAGGCTTCTCTGTGTCTCTCTTCCTTTCTTTGC 212

862 CATCAGCTGGGACCTTCGCCCTCTCAGCCCTTACCTGATGCTAAAAATATGTGCTTGGC 921

Db 211 CATCAGCTGGGCACTTCGCTTCAGCCCTTACCTGATCTMAAATAATGCGCTGGCC 152

922 CACAAAAGCATGCNAAGTCATTGTTACACAGGATCTACAGACTATTCACCA 981

Db 151 CACAAAAGCATGCAAGTCATTGTTACAACAGGATCTACAGACTATTTCCACCACA 92

982 GATATGACCTAGTTTATATTTCTGGAGGAATGAATCATATCTAGAAGCTGGAGTG 1041

Db 91 GATATGACCTAGTTTATATTCTGGAGGAATGATTCATATCTAGAACTCTGAGTG 32

QY 1042 AGCAACAAAGCAAGAAACAAAAAGAA 1069

Db 31 AGCAACAGAGCAAAAAAAAAA 4


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Qy      147 TTGGATATTCAGGAGACACATCCATCAGATCACTAATCTGCTGAGTGGGAACTTTG
Db      120 TTGGATATTCAGGAGACACATCCATCAGATCACTAATCTGCTGAGTGGGAACTTTG
Qy      207 GGGAGATGGAATCCTGAGCTGACATTTTGAACCTGACATCAAACTTTCTGATATGTGA
Db      180 GGGAGATGGAATCCTGAGCTGACATTTTGAACCTGACATCAAACTTTCTGATATGTGA
Qy      267 TACAATGCTGAAGGAAGGTGTTTGGCTGGTGCATAGTTCAAAGAAGCAAGATG
Db      240 TACAATGCTGAAGGAAGGTGTTTGGCTGGTGCATAGTTCAAAGAAGCAAGATG
Qy      327 AGCTGTCGAGAGCAGATGAATGTTTCAAGAGCCGAGCAGAGTGTGCTGATCAAGTGA
Db      300 AGCTGTCGAGAGCAGATGAATGTTTCAAGAGCCGAGCAGAGTGTGCTGATCAAGTGA
Qy      387 TAGTTGGCAATGCTCTTTGGCGCTGAAAACCTGCACTCAGACATGCTGGCACTTACA
Db      360 TAGTTGGCAATGCTCTTTGGCGCTGAAAACCTGCACTCAGACATGCTGGCACTTACA
Qy      447 AATGTTATATCATCATCTTGAAGGAAGGAAGGAATCTAATCTGAGTGAATAAAGTGGAG
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Qy      507 CCTTCAGCATGCGGAGATGAATGTGACTATATATCCAGCTCAGACACTTGGCGTGTG
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Qy      567 AGGCTCCCGAGATGTTTCCCGCAGCCCAAGTGTCTGGGCTATCCAACTTGGACAGGAG
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RESULT 9
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DEFINITION UI-CF-FNO-sey-b-10-0-UI 3', mRNA sequence.
ACCESSION CA313445
VERSION CA313445.1 GI:24531543
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 737)
AUTHORS Bonaldo,M.F., Lennom,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab

```

```

FEATURES
source
    University of Iowa
    2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
    Tel: 319 356 4866
    Fax: 319 356 7171
    Email: paul-mccray@iowa.edu
    Tissue Procurement: Dr. M. J. Welsh, University of Iowa
    cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
    DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
    Clone Distribution: Researchers may obtain clones from Research
    Genetics (www.resgen.com) or from Open Biosystems
    (www.openbiosystems.com).
    The following repetitive elements were found in this cDNA
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    POLYA=yes.
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    /clone_lib="UI-CF-FNO"
    /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
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    UI-CF-FNO is a subtracted cDNA library derived from two
    normalized Human lung epithelial cell libraries (EN1
    and DUI) The library was subtracted according to
    Bonaldo, Lennom and Soares, Genome Research, 6:791-806,
    1996. For additional information, contact:
    bento-soares@uiowa.edu
    TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
    TAG_LIB=UI-CF-FNO
    TAG_SEQ=GCCTGTAGGC"

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ORIGIN

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Query Match      26.8%; Score 694; DB 6; Length 737;
Best Local Similarity 99.4%; Pred. No. 9,5e-186;
Matches 716; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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Qy      1869 CTACTACCAACTAGTGTGATTAAGGCGCAGGATGCTCTCAACCTCTCAATGTACAGA
Db      737 CTACTACCAACTAGT-GATTAAGGCGCAGGATGCTCTCAACCTCTCAATGTACAGA
Qy      1929 CGTCTCCCATTAACACATCCCAATCCGAAGGTCAACGTGTGAGACTAAGAAACCT
Db      678 CGTCTCCCATTAACACATCCCAATCCGAAGGTCAACGTGTGAGACTAAGAAACCT
Qy      1989 GGTTTTGAAGTAAAGAGGCGCTGAAAGAGGGAGCCCAAAATCTGTCTGCTT-CTGAC
Db      618 GGTTTTGAAGTAAAGAGGCGCTGAAAGAGGGAGCCCAAAATCTGTCTGCTTCTGAC
Qy      2048 ATTAGTCATTTGGCAATAATGAACATTTCTTTGGCTGCTGCTCTGAGCAGACAGAGCCA
Db      558 ATTAGTCATTTGGCAATAATGAACATTTCTTTGGCTGCTGCTCTGAGCAGACAGAGCCA
Qy      2108 GAACCTATATCGGGACCCGAGATTAACATCTTCAGAGTGAACAGATGACAGAGCCATGAG
Db      498 GAACCTATATCGGGACCCGAGATTAACATCTTCAGAGTGAACAGATGACAGAGCCATGAG
Qy      2168 AATAGCCTATGGAGTATATCTTCACTTGTGAGCTTCTAAGTTTCTTCCCTCATTTCT
Db      438 AATAGCCTATGGAGTATATCTTCACTTGTGAGCTTCTAAGTTTCTTCCCTCATTTCT
Qy      2228 ACCCTGCAAGCCCAAGTCTGTAAGAGAAATGCTGAGTCTGAGTCTGAGTTTCTTACTC
Db      378 ACCCTGCAAGCCCAAGTCTGTAAGAGAAATGCTGAGTCTGAGTCTGAGTTTCTTACTC
Qy      2288 TGAATTTAGATCTCCAGACCCCTTCTGCGCAAAATTTCAAATTAAGGCAACAAATATAC
Db      318 TGAATTTAGATCTCCAGACCCCTTCTGCGCAAAATTTCAAATTAAGGCAACAAATATAC

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QY 2348 CTTCCATGAGACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTGAGGCC 2407
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Db 258 CTTCCATGAGACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTGAGGCC 199
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QY 2408 TTGAGGAATGAGCTTTGAGAGAAAGATCTTTGTTTCCAGCCCTTCCACACTCT 2467
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Db 198 TTGAGGAATGAGCTTTGAGAGAAAGATCTTTGTTTCCAGCCCTTCCACACTCT 139
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QY 2468 TCATGTTGTAACCACTGCTTCTGAGACTTGGAGCCAGCTGACTGATTAATCATGTTGT 2527
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RESULT 10
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LOCUS 17000600041697 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259813
VERSION CN259813.1 GI:47276227
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 714)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 714 Std Error: 0.00.
Location/Qualifiers

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="Oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Query Match 26.7%; Score 690; DB 7; Length 714;
Best Local Similarity 99.7%; Pred. No. 1.3e-186;
Matches 712; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 110 ATTATTTCTGCTGAGCAATTGACATCATTTGCTTGGTATTTTCAGGAGACACTCC 169
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QY 170 ATCAGAGTCACTACTGCTGCTTCACTGAGCAATTTGGGAGAGATGGAATCTGAGCTGC 229
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Db 121 ATCAGAGTCACTACTGCTGCTTCACTGAGCAATTTGGGAGAGATGGAATCTGAGCTGC 180
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QY 230 ACTTTGAACTGACATCAAACTTTCTGATATGCTGATACATAGCTGAGAGAGGTGT 289
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Db 181 ACTTTGAACTGACATCAAACTTTCTGATATGCTGATACATAGCTGAGAGAGGTGT 240
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QY 290 TTAGGCTTGGTCCATGATGTTCAAGAAGCAAGATGAGCTGCGAGCAGATGAATG 349
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Db 241 TTAGGCTTGGTCCATGATGTTCAAGAAGCAAGATGAGCTGCGAGCAGATGAATG 300
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QY 350 TTGAGAGCCCGAGCAGAGTGTTCGATCAAGTATGTTGGCAATGCTTTGGCG 409
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Db 301 TTGAGAGCCCGAGCAGAGTGTTCGATCAAGTATGTTGGCAATGCTTTGGCG 360
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QY 470 GGCAGGGGGAATCTAACCTTGATATAAAATGAGCCCTTCAGATGCCGGAAGTAA 529
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QY 530 GTGACTATATATGCGAGCTCAGAGACTTCCGCTGAGAGCTCCCGATGTTCCCCAG 589
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Db 541 CCCACAGTGGTCTGGGCACTCCCAAGTTGACACAGAGCCCACTTCTCGAAGTCTCAAT 600
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QY 650 ACCAGCTTTGAGCTGAGCTCTGAGATGAGACCAAG-AGGTGTTCTGTGCTTACAA 708
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Db 601 ACCAGCTTTGAGCTGAGCTCTGAGATGAGACCAAGAGTTGTCTGTGCTTACAA 660
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QY 709 TGTTCAGATCAACAAACATAC-TCTGTATGATTTGAAATGATCATTTGCCAAG 761
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Db 661 TGTTCAGATCAACAAACATAC-TCTGTATGATTTGAAATGATCATTTGCCAAG 714
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RESULT 11
CN259812 698 bp mRNA linear EST 16-MAY-2004
LOCUS 17000600177307 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259812
VERSION CN259812.1 GI:47276226
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 698)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 698 Std Error: 0.00.
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="Oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in

Db 601 TTATGATGCTTCAAGAGTCCCTTGGCTTCTCTCCCACTGCAATGCGCAAGTTGA 660
Qy 1526 GA-AAATGATCATTAATTTTA 1545
Db 661 GACCACTGATCATTAATTTTA 681

RESULT 13
BU632767/c 700 bp mRNA linear EST 23-SEP-2002
LOCUS BU632767/c
DEFINITION UI-H-FEI-bdy-k-03-0-UI.s1 NCI CGAP FEI Homo sapiens cDNA clone
ACCESSION BU632767
VERSION BU632767.1 GI:23300022
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 700)
AUTHORS NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: James Martin
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soaresuiowa.edu
The following repetitive elements were found in this cDNA
sequence: 623-700, >MSR20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
1..700
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FEI-bdy-k-03-0-UI"
/issue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FEI"
/note="Organ: Chondrosarcoma; Vector: pRT3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP FEI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCTACGAC. The cell lines were provided by Dr James
Martin from the University of Iowa.
TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
TAG_LIB=UI-H-FEI
TAG_SEQ=CGCTACGAC"

ORIGIN
Query Match 25.7%; Score 665; DB 5; Length 700;
Best Local Similarity 99.9%; Pred. No. 2.1e-179;
Matches 676; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1912 TCCTACATGTACAGAGCTCTCCCATTAACAATCCGAATCGAAGTGTCACTGTG 1971

Db 700 TCCTACATGTACAGAGCTCTCCCATTAACAATCCGAATCGAAGTGTCACTGTG 641
Qy 1972 CAGACTAAGAAACCTGTTTGTAGTAGAAAAGGCGTGGAAAGAGGGAGCCAA 2031
Db 640 CAGACTAAGAAACCTGTTTGTAGTAGAAAAGGCGTGGAAAGAGGGAGCCAA 581
Qy 2032 TCTGTCTGCTT-CTCATTATGATTTGGAAATTAAGCATTTCTTGTGCTGCTG 2090
Db 580 TCTGTCTGCTTCTCATTATGATTTGGAAATTAAGCATTTCTTGTGCTGCTG 521
Qy 2091 CTCAGACAGAGAGCCAGAACTCTATCGGCGACAGAGATTAATCTCTCAGTAA 2150
Db 520 CTCAGACAGAGAGCCAGAACTCTATCGGCGACAGAGATTAATCTCTCAGTAA 461
Qy 2151 TTGACAAAGGCTTATGGAAATGCGTGAATGATTTATCTTCACTTGTGAGCTT 2210
Db 460 TTGACAAAGGCTTATGGAAATGCGTGAATGATTTATCTTCACTTGTGAGCTT 401
Qy 2211 TTCTTTCCCTTCAATTTCTACCTTCCAGCCAAAGCTTGTAGAGAAATGCTG 2270
Db 400 TTCTTTCCCTTCAATTTCTACCTTCCAGCCAAAGCTTGTAGAGAAATGCTG 341
Qy 2271 CTCAGGTTTCTTACTCTGATTTAGATCTCCAGACCCCTTCTGCGCAATTCAT 2330
Db 340 CTCAGGTTTCTTACTCTGATTTAGATCTCCAGACCCCTTCTGCGCAATTCAT 281
Qy 2331 AGGCAACAAACATATATCTTCCATGAGACACACAGACTTTTGAAGCAAGCA 2390
Db 280 AGGCAACAAACATATATCTTCCATGAGACACACAGACTTTTGAAGCAAGCA 221
Qy 2391 CTCCTGAATTTAGGCTTGAAGAAATGAGCTTTGAAGAAATTAATCTTTTCC 2450
Db 220 CTCCTGAATTTAGGCTTGAAGAAATGAGCTTTGAAGAAATTAATCTTTTCC 161
Qy 2451 CCCCCTTCCCACTCTTCAATGTTTAAACCACTGCTTCTGAGCTTGAAGCAGAG 2510
Db 160 CCCCCTTCCCACTCTTCAATGTTTAAACCACTGCTTCTGAGCTTGAAGCAGAG 101
Qy 2511 ACTGATATACATGTTTATAGAAACGATTTTAAAGTTCTGATCGTTCAAGAT 2570
Db 100 ACTGATATACATGTTTATAGAAACGATTTTAAAGTTCTGATCGTTCAAGAT 41
Qy 2571 TTTAATATACATTTCT 2587
Db 40 TTTAATATACATTTCT 24

RESULT 14
CB241729/c 691 bp mRNA linear EST 12-FEB-2003
LOCUS CB241729/c
DEFINITION UI-CF-FN0-efz-p-01-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
ACCESSION CB241729
VERSION CB241729.1 GI:28363373
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 691)
AUTHORS Bonaldi, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171

Email: paul-mccray@iowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-af2-p-01-0-UI"
 /issue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-FNO is a subtracted cDNA library derived from two
 normalized Human Lung epithelial cell libraries (EN1 and
 DU1) The library was subtracted according to according to
 Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@iowa.edu
 TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_LIB=UI-CF-FNO
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 25.6%; Score 661; DB 6; Length 691;
 Best Local Similarity 99.9%; Pired. No. 2.9e-178;
 Matches 672; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1916 ACCATGTACAGAGCGTCCGCCATCACTACCAATCCGAAGTGTCACTGTGACAG 1975
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 691 ACCATGTACAGAGCGTCCGCCATCACTACCAATCCGAAGTGTCACTGTGACAG 632
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 1976 ACTAAGAAACCCCTGTTTGTAGTAAAGAGGCGCTGAAAGAGGAGCCAAACAATCTG 2035
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 631 ACTAAGAAACCCCTGTTTGTAGTAAAGAGGCGCTGAAAGAGGAGCCAAACAATCTG 572
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 2036 TCTGCTT-CTCAGATAGTCAATGGCAATTAAGCATTCGTCTTGGCTGCTGCTCA 2094
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 571 TCTGCTTCTCAGATAGTCAATGGCAATTAAGCATTCGTCTTGGCTGCTGCTCA 512
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 2095 GCACAGAGAGCCAGAACTCATCGGACACCGAGATTAACATCTCTCAGTAAAGAGTTGA 2154
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 511 GCACAGAGAGCCAGAACTCATCGGACACCGAGATTAACATCTCTCAGTAAAGAGTTGA 452
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 2155 CAAGGCTATGGAAGATGCGCTGATGGAATTAATTCAGCTTGTGAGCTTCAAGTTTCT 2214
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 451 CAAGGCTATGGAAGATGCGCTGATGGAATTAATTCAGCTTGTGAGCTTCAAGTTTCT 392
 |||||
 2215 TTCCCTTCAATTCACCTCGCAAGCTTGTAAAGAAATGCTGAGTTCTTACTCA 2274
 |||||
 391 TTCCCTTCAATTCACCTCGCAAGCTTGTAAAGAAATGCTGAGTTCTTACTCA 332
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 2275 GGTTCCTTACTGTGAATTTAGATCTCAGAGACCCCTCTGSCCAATTCAAATTAAGGC 2334
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 331 GGTTCCTTACTGTGAATTTAGATCTCAGAGACCCCTCTGSCCAATTCAAATTAAGGC 272
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 2335 AACAAACATATACCTTCATGGAAGACACACAGACTTTTGAAGCAAGACAATGCTGC 2394
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 2395 TTGAATTGAGGCGCTTGAGAAATTAAGCTTTGAAGAAAGAAATTAATCTTTGTTCCAGCCCC 2454
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 211 TTGAATTGAGGCGCTTGAGAAATTAAGCTTTGAAGAAAGAAATTAATCTTTGTTCCAGCCCC 152

QY 2455 CTTCCACACTCTTCATGTTGTTAAACACCTGCTTCTGAGACCTTGAGCCAGGTGACTG 2514
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 DB 151 CTTCCACACTCTTCATGTTGTTAAACACCTGCTTCTGAGACCTTGAGCCAGGTGACTG 92
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 QY 2515 TATTACATGTTGTTTAAAGAAACATGATTTTGAAGTTCGATTCGTTCAAGACAATATTAA 2574
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 DB 91 TATTACATGTTGTTTAAAGAAACATGATTTTGAAGTTCGATTCGTTCAAGACAATATTAA 32
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 QY 2575 ATATACATTTCT 2587
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 DB 31 ATATACATTTCT 19
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RESULT 15
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 DEFINITION
 UI-CF-FNO-af1-e-12-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
 CA314865
 ACCESSION
 VERSION
 CA314865.1 GI:24532963
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 691)
 REFERENCE
 AUTHORS
 Ronaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL
 Genome Res. 6 (9), 791-806 (1996)
 MEDLINE
 97044477
 PUBMED
 8889548
 COMMENT
 Contact: McCray, PB
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@iowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

Location/Qualifiers
 1..691
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-af1-e-12-0-UI"
 /issue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-FNO is a subtracted cDNA library derived from two
 normalized Human Lung epithelial cell libraries (EN1 and
 DU1) The library was subtracted according to according to
 Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@iowa.edu
 TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_LIB=UI-CF-FNO
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 25.5%; Score 660; DB 6; Length 691;
Best Local Similarity 99.7%; Pred. No. 5.7e-178;
Matches 671; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1916 ACCATGTACAGAGAGCTCTCCCATTAACAATACCAATCCGAGTGTCAACTGTGCAGG 1975
|||
DB 691 ACCATGTACAGAGAGCTCTCCCATTAACAATCCGAGTGTCAACTGTGCAGG 632
|||

QY 1976 ACTAAGAAACCCCTGTTTGTAGTAAAGGCGCTGAGAAAGGGAGCCCAAAATCTG 2035
|||
DB 631 ACTAAGAAACCCCTGTTTGTAGTAAAGGCGCTGAGAAAGGGAGCCCAAAATCTG 572
|||

QY 2036 TCTGCTT-CTCAGATTAGTCAATTGCAAAATAGCATTCTGTCTTTGGCTGCTGCTCA 2094
|||
DB 571 TCTGCTTCTCAGATTAGTCAATTGCAAAATAGCATTCTGTCTTTGGCTGCTGCTCA 512
|||

QY 2095 GCACAGAGAGCCAGAACTCTATCGGGCCACAGATTAACATCTCTCAGTGAACAGAGTTGA 2154
|||
DB 511 GCACAGAGAGCCAGAACTCTATCGGGCCACAGATTAACATCTCTCAGTGAACAGAGTTGA 452
|||

QY 2155 CAAGGCTATGAGGAAATGCCGATGAGATTATCTTCAGCTTGTGAGCTTCTAGTTTCT 2214
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DB 451 CAAGGCTATGAGGAAATGCCGATGAGATTATCTTCAGCTTGTGAGCTTCTAGTTTCT 392
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QY 2215 TTCCCTTCATTCTACCCCTGCAAGGCCAAGTCTGTAGAGAAATGCTGAGTTCTAGCTCA 2274
|||
DB 391 TTCCCTTCATTCTACCCCTGCAAGGCCAAGTCTGTAGAGAAATGCTGAGTTCTAGCTCA 332
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QY 2275 GGTTTTCTTACTGAAATTTAGATCTCCAGACCCCTCTGSCCAATTCMAATTAAGGC 2334
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DB 331 GGTTTTCTTACTGAAATTTAGATCTCCAGACCCCTCTGSCCAATTCMAATTAAGGC 272
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QY 2335 AACAAATATTAATCTTCATGAGACACACAGACTTTTGAAGCAAGACATGACTGC 2394
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DB 271 AACAAATATTAATCTTCATGAGACACACAGACTTTTGAAGCAAGACATGACTGC 212
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QY 2395 TTGAATTGAGGCGCTTGAAGATGAAGCTTGAAGAAATACCTTTGTTCCAGCCCC 2454
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DB 211 TTGAATTGAGGCGCTTGAAGATGAAGCTTGAAGAAATACCTTTGTTCCAGCCCC 152
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QY 2455 CTTCCCACTCTTCATGTGTTAAACAATGCTTCTGAGCTTGAAGCCAGGTGACTG 2514
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DB 151 CTTCCCACTCTTCATGTGTTAAACAATGCTTCTGAGCTTGAAGCCAGGTGACTG 92
|||

QY 2515 TATTACATGTTGTATAGAAACGATTTTGAAGTTCTGATCGTTCAAGAAATGATTAA 2574
|||
DB 91 TATTACATGTTGTATAGAAACGATTTTGAAGTTCTGATCGTTCAAGAAATGATTAA 32
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QY 2575 ATATACATTTCCT 2587
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DB 31 ATATACATTTCCT 19
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Search completed: May 31, 2005, 00:10:46
Job time : 10066.7 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 07:16:54 ; Search time 2657.37 Seconds

(without alignments)
10502.938 Million cell updates/sec

Title: US-09-763-978B-10

Sequence: 1 ttcaagactatagaac.....ttcacctgacatagc 576

Scoring table:

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Gap 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 576 | 100.0 | 576 | 6 | BD235839 A novel m |
| 2 | 576 | 100.0 | 1567 | 6 | BD264689 Compositi |
| 3 | 576 | 100.0 | 1567 | 6 | AR238092 Sequence |
| 4 | 576 | 100.0 | 1567 | 6 | AR257633 Sequence |
| 5 | 576 | 100.0 | 1567 | 6 | AR283679 Sequence |
| 6 | 576 | 100.0 | 1567 | 6 | AR443353 Sequence |
| 7 | 576 | 100.0 | 1567 | 6 | AR478431 Sequence |
| 8 | 576 | 100.0 | 1567 | 6 | AX366307 Sequence |
| 9 | 576 | 100.0 | 1965 | 6 | CQ41191 Sequence |
| 10 | 576 | 100.0 | 2587 | 6 | BD235830 A novel m |
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| 14 | 576 | 100.0 | 2627 | 6 | AR478744 Sequence |
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| 32 | 491 | 85.4 | 625 | 6 | AX208278 Sequence |
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| 35 | 452 | 78.5 | 541 | 6 | AR257587 Sequence |
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ALIGNMENTS

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| DEFINITION | A novel method of diagnosing, monitoring, staging, imaging and treating various cancers. | | | | |
| ACCESSION | BD235839.1 | GI:33045609 | | | |
| VERSION | JP 2002523760-A/10. | | | | |
| KEYWORDS | Homo sapiens (human) | | | | |
| SOURCE | Homo sapiens | | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| REFERENCE | 1 (bases 1 to 576) | | | | |
| AUTHORS | Salceda,S., Sun,Y., Recipon,H. and Caffery,R. | | | | |
| TITLE | A novel method of diagnosing, monitoring, staging, imaging and treating various cancers | | | | |
| JOURNAL | Patent: JP 2002523760-A 10 30-JUL-2002; | | | | |
| DIADEXUS INC | | | | | |
| OS | Homo sapiens (human) | | | | |
| PN | JP 2002523760-A/10 | | | | |
| PD | 30-JUL-2002 | | | | |
| PF | 01-SEP-1999 JP 2000567741 | | | | |
| PR | 02-SEP-1998 US 60/098880 | | | | |
| PT | SUSANA SALCEDA, YONGMING SUN, HERVE RECIPON, ROBERT CAFFERY PC | | | | |
| GO1N33/574;A61K39/395;A61K39/395;A61K39/395 PC | | | | | |
| PC | A61K49/00;C07K16/32;C12N15/09;C12Q1/68;C12N15/00;A61K49/02 CC | | | | |
| A novel method of diagnosing, monitoring, staging, imaging and treating | | | | | |
| CC | various cancers | | | | |
| FT | Key | | | | |
| FT | source | | | | |
| FEATURES | Location/Qualifiers | | | | |
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| ORIGIN | 100.0%; Score 576; DB 6; Length 576; | | | | |
| Query Match | | | | | |

Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION Compositions and methods for the therapy and diagnosis of ovarian cancer.
ACCESSION BD264689.1 GI:33074457
VERSION BD264689.1
KEYWORDS JP 2002532093-A/74.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1567)
Mitcham, J.L., King, G.E., Algate, P.A. and Frudakis, T.N.
Compositions and methods for the therapy and diagnosis of ovarian cancer.
Patent: JP 2002532093-A 74 02-OCT-2002;
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OS Homo sapiens (human)
PN JP 2002532093-A/74
PD 02-OCT-2002
PR 17-DEC-1999 JP 2000588356
PR 17-DEC-1998 US 09/215681, 17-DEC-1998 US 09/216003 PR
23-JUN-1999 US 09/338933, 24-SEP-1999 US 09/404879 PI
JENNIFER L MITCHAM, GORDON B KING, PAUL A ALGATE, TONY N FRUDAKIS PC
C12N1/5/09, A61K31/7115, A61K35/14, A61K35/76, A61K39/00, A61K39/395, PC
A61K39/395,
PC A61K48/00, A61P35/00, A61P37/04, C07K14/82, C07K19/00, C12N1/15, PC
C12N1/19, PC

C12N1/21, C12N5/06, C12N5/10, C12Q1/68, G01N33/53, G01N33/53, G01N33/PC
566,
PC G01N33/574, G01N33/577, C12N15/00, C12N5/00, C12N5/00 CC
Compositions and methods for the therapy and diagnosis of CC
ovarian cancer
FH Key Location/Qualifiers
FT source 1.1567
FT location/Qualifiers
1.1567
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ORIGIN

Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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DEFINITION Sequence 74 from patent US 6468546.
ACCESSION AR238092.1 GI:27283056
VERSION AR238092.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham, J.L., King, G.E. and Algate, P.A.
TITLE Compositions and methods for therapy and diagnosis of ovarian

JOURNAL Patent: US 6468546-A 74 22-OCT-2002;
FEATURES Location/Qualifiers
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DEFINITION Sequence 74 from patent US 6468931.
ACCESSION AR257633
VERSION AR257633.1 GI:27307708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITL E Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6468931-A 74 03-DEC-2002;
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DEFINITION Sequence 74 from patent US 6528253.
ACCESSION AR283679
VERSION AR283679.1 GI:29720576
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITL E Compositions and methods for diagnosis of ovarian cancer
JOURNAL Patent: US 6528253-A 74 04-MAR-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No.1.9e-151;
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LOCUS
DEFINITION Sequence 74 from patent US 6670463.
ACCESSION AR443353
VERSION AR443353.1 GI:42671132
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Prudakis,T.N. and King,G.E.
TITLES Compositions and methods for therapy of ovarian cancer
JOURNAL Patent: US 6670463-A 74 30-DEC-2003;
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ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS
DEFINITION Sequence 74 from patent US 6699664.
ACCESSION AR478431
VERSION AR478431.1 GI:47237083
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W.,
Fanger,G.R., Reed,S.G., Vedvick,T.S. and Carter,D.
TITLES Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: US 6699664-A 74 02-MAR-2004;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Sequence 74 from Patent WO0206317.
DEFINITION AX366307
ACCESSION AX366307
VERSION AX366307.1 GI:18697733
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Mitcham, J.L., King, G.E., Algate, P.A., Fling, S.P., Retter, M.W.,
Fanger, G.R., Reed, S.G., Vedvick, T.S., Carter, D., Hill, P. and
Albone, E.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: WO 0206317-A 74 24-JAN-2002;
CORIXA CORPORATION (US)
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ORIGIN

Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 91 TTCAAGACATATTAGAAAGTTGGGAAATATATTCATGTGAATGAGCAAGTGTGTTAAGA 150
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CO412191 1965 bp DNA linear PAT 23-JAN-2004
LOCUS Sequence 19262 from Patent WO0170979.
DEFINITION CO412191
ACCESSION CO412191
VERSION CO412191.1 GI:41319972
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 19262 27-SEP-2001;
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Best Local Similarity 100.0%; Pred. No. 1.9e-151;
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| ACCESSION | BD235830 | | |
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| ORGANISM | Homo sapiens | | |
| REFERENCE | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| TITLE | Salceda,S., Sun,Y., Recipon,H. and Caffery,R. | | |
| JOURNAL | A novel method of diagnosing, monitoring, staging, imaging and | | |
| COMMENT | treating various cancers | | |
| | Patent: JP 2002523760-A 1 30-JUL-2002; | | |
| | DIADEXUS INC | | |
| | OS Homo sapiens (human) | | |
| | PN JP 2002523760-A/1 | | |
| | PD 30-JUL-2002 | | |
| | PF 01-SRP-1999 JP 2000567741 | | |
| | PR 02-SRP-1998 US 60/098880 | | |
| | PI SUSANA SALCEDA, YONGMING SUN, HERVE RECIPON, ROBERT CAFFERKEY PC | | |
| | G01N33/574, A61K39/395, A61K39/395, A61K39/395, A61K39/395 PC | | |
| | , A61K49/00, A61K49/00, | | |
| | PC A61K51/00, C07K16/32, C12N15/09, C12Q1/68, C12N15/00, A61K49/02 CC | | |
| | A novel method of diagnosing, monitoring, | | |
| | staging, imaging and | | |
| | treating | | |
| | CC various cancers | | |
| | CC key | | |
| | FT source | | |
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| Oy | 301 | CACCTTCGCACTCAGGGGCGGCTGCATTTTATGTATGGGTCAAATGATCACTTTTATG | 360 |
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| ACCESSION | AX403048 | | |
| VERSIONS | AX403048.1 GI:21388028 | | |
| KEYWORDS | | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| REFERENCE | 1 Fox, G., Sullivan, J. K. and Fang, M. B7-like molecules and uses thereof Patent: WO 0202624-A 1 10-JAN-2002; | | |
| AUTHORS | Fox, G., Sullivan, J. K. and Fang, M. | | |
| TITLE | B7-like molecules and uses thereof | | |
| JOURNAL | Patent: WO 0202624-A 1 10-JAN-2002; | | |
| FEATURES | Amgen, Inc. (US) | | |
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| ORIGIN | | | |
| | Query Match | 100.0%; Score 576; DB 6; Length 2603; | |
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DEFINITION Compositions and methods for the therapy and diagnosis of ovarian cancer.
ACCESSION BD265002.1 GI:33074770
VERSION BD265002.1
KEYWORDS JP 2002532093-A/387.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A. and Frudakis,T.N.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: JP 2002532093-A 387 02-OCT-2002;
CORIXA CORP
COMMENT OS Homo sapiens (human)
PN JP 2002532093-A/387
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588356
PR 17-DEC-1998 US 09/215681,17-DEC-1998 US 09/216003 PR
23-JUN-1999 US 09/338933, 24-SEP-1999 US 09/404879 PI
JENNIFER L MITCHAM, GORDON E KING, PAUL A ALGATE, TONY N FRUDAKIS PC
C12N15/09, A61K31/7115, A61K35/14, A61K35/76, A61K39/00, A61K39/395, PC
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PC A61K48/00, A61P35/00, A61P37/04, C07K14/82, C07K19/00, C12N1/15, PC
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FH Key Location/Qualifiers
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Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 13
LOCUS AR238405 2627 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 391 from patent US 6468546.
ACCESSION AR238405
VERSION AR238405.1 GI:27283369
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham,J.L., King,G.E. and Algate,P.A.
TITLE Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6468546-A 391 22-OCT-2002;
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QY 421 TGAATCATTAATTTTAGCATAAACAGAGCATGCGGACACCGATTTTAATAATAACTGAG 480
Db 1553 TGAATCATTAATTTTAGCATAAACAGAGCATGCGGACACCGATTTTAATAATAACTGAG 1612
QY 481 CACCTTCTTTTAAACAACAATGCGGTTTATTTCTCAAGATGATGTTCAATCCGTGAAT 540
Db 1613 CACCTTCTTTTAAACAACAATGCGGTTTATTTCTCAAGATGATGTTCAATCCGTGAAT 1672
QY 541 GGTCCAGGGAAGGACCTTGACCTTGACTATATGGC 576
Db 1673 GGTCCAGGGAAGGACCTTGACCTTGACTATATGGC 1708
```

Search completed: May 30, 2005, 17:54:03
Job time : 2659.37 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 05:15:03 ; Search time 353.272 Seconds
(without alignments)
9651.969 Million cell updates/sec

Title: US-09-763-978B-10
Perfect score: 576
Sequence: 1 ttcaagacatactagtagt.....ttccacctgacataatgac 576

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 576 | 100.0 | 576 | 3 | AAZ90479 |
| 2 | 576 | 100.0 | 1567 | 3 | AA69764 |
| 3 | 576 | 100.0 | 1567 | 6 | ABN72658 |
| 4 | 576 | 100.0 | 1567 | 9 | ADA08823 |
| 5 | 576 | 100.0 | 1567 | 10 | ADF08570 |
| 6 | 576 | 100.0 | 1567 | 10 | ADG46318 |
| 7 | 576 | 100.0 | 1596 | 11 | ACN92433 |
| 8 | 576 | 100.0 | 1965 | 5 | ADL45372 |
| 9 | 576 | 100.0 | 2587 | 3 | AAZ90470 |
| 10 | 576 | 100.0 | 2591 | 6 | ABL57354 |
| 11 | 576 | 100.0 | 2603 | 6 | AAZ90479 |
| 12 | 576 | 100.0 | 2627 | 3 | AAA70077 |
| 13 | 576 | 100.0 | 2627 | 4 | AAH55681 |
| 14 | 576 | 100.0 | 2627 | 6 | ABN72971 |
| 15 | 576 | 100.0 | 2627 | 9 | ADA08544 |
| 16 | 576 | 100.0 | 2627 | 10 | ADP08887 |
| 17 | 576 | 100.0 | 2627 | 10 | ADG46174 |
| 18 | 576 | 100.0 | 2627 | 12 | ADN40452 |
| 19 | 576 | 100.0 | 2690 | 12 | ADP81075 |
| 20 | 574.4 | 99.7 | 3357 | 6 | AAZ90479 |

| | | | | | |
|----|-------|------|------|----|----------|
| 21 | 550.8 | 95.6 | 2626 | 6 | ABL56582 |
| 22 | 549 | 95.3 | 595 | 5 | AD173905 |
| 23 | 549 | 95.3 | 595 | 5 | AD167515 |
| 24 | 549 | 95.3 | 643 | 5 | ADL39142 |
| 25 | 529.4 | 91.9 | 2626 | 4 | AAZ90479 |
| 26 | 529.4 | 91.9 | 2626 | 6 | AAZ90479 |
| 27 | 499.8 | 86.8 | 1657 | 3 | AAZ90479 |
| 28 | 499.8 | 86.8 | 1657 | 10 | ADP08887 |
| 29 | 499.8 | 86.8 | 1658 | 4 | AAZ90479 |
| 30 | 499.8 | 86.8 | 1658 | 4 | AAZ90479 |
| 31 | 499.8 | 86.8 | 1658 | 5 | AAZ90479 |
| 32 | 499.8 | 86.8 | 1658 | 6 | AAZ90479 |
| 33 | 499.8 | 86.8 | 1658 | 6 | AAZ90479 |
| 34 | 499.8 | 86.8 | 1658 | 6 | AAZ90479 |
| 35 | 499.8 | 86.8 | 1658 | 6 | AAZ90479 |
| 36 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 37 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 38 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 39 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 40 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 41 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 42 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 43 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 44 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |
| 45 | 499.8 | 86.8 | 1658 | 8 | AAZ90479 |

ALIGNMENTS

RESULT 1
AAZ90479
ID AAZ90479 standard; cDNA; 576 BP.
XX
AC AAZ90479;
DT 06-JUN-2000 (first entry)
XX
DE Cancer specific gene (clone ID 16656542) fragment #10.
XX
KW CCG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
KW endometrial; uterine; lung; cytotoxic; ss.
XX
OS Homo sapiens.
XX
PN W0200012758-A1.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US019655.
XX
PR 02-SEP-1998; 98US-0098880P.
XX
PA (DIAD-) DIADEXUS LLC.
XX
PI Salceda S, Sun Y, Recipon H, Catterkey R;
XX
DR WPI; 2000-256657/22.
XX
PT Diagnosing, staging, monitoring, imaging and treating cancer especially
PT gynecological cancers e.g. breast, ovarian cancer and lung cancer.
PT involves measuring cancer specific gene levels in cells and body fluids.
XX
PS Claim 9; Page 50-51; 58pp; English.
XX
CC The invention relates to detecting, diagnosing metastasis and staging
CC cancer by measuring levels of cancer specific genes (CSG) in cells,
CC tissues or body fluids. Their remission and progression, decreases and
CC increases in CSG levels, is also monitored, by periodic sample analysis.
CC The methods are useful for detecting cancers, especially gynecologic
CC cancers which include ovarian, breast, endometrial and uterine cancer and
CC lung cancer. Antibodies against the CSOs labeled with paramagnetic ions
CC or a radioisotope is useful for imaging cancer and when conjugated with a

CC cytotoxic agent are useful for treating cancer. The present sequence
CC represents a CCG (clone ID: 1656542 and gene ID: 234617) fragment
XX
SQ Sequence 576 BP; 169 A; 118 C; 122 G; 167 T; 0 U; 0 Other;

| | | | | |
|-----------------------|--------------|-----------|------------|------------|
| Query Match | 100.0% | Score 576 | DB 3 | Length 576 |
| Best Local Similarity | 100.0% | Pred. No. | 3.1e-172 | |
| Matches 576 | Conservative | 0 | Mismatches | 0 |
| | | | Gaps | 0 |

| | | | | | | | | | | | | |
|----|-----|---------|---------|---------|---------|--------|----------|----------|---------|--------|---------|-----|
| OY | 1 | TTCAAGA | CATVTTT | GAAGTTG | GGAAAAA | TAATTC | AGTCA | AGTCA | GTAGCA | CAAGT | GTGTTAA | 60 |
| Db | 1 | TTCAAGA | CATVTTT | GAAGTTG | GGAAAAA | TAATTC | AGTCA | AGTCA | GTAGCA | CAAGT | GTGTTAA | 60 |
| OY | 61 | GTGAT | TAAGT | AAAAAT | CGCTG | AGACAA | GTCAT | CCCGAG | ATCTCAG | GGAACT | CCCCCTG | 120 |
| Db | 61 | GTGAT | TAAGT | AAAAAT | CGCTG | AGACAA | GTCAT | CCCGAG | ATCTCAG | GGAACT | CCCCCTG | 120 |
| OY | 121 | CCGTG | CACCT | GGGGAG | TGAGAG | ACAGAT | ATGCGCAT | GTCTT | GTCTG | CTGAA | TTTTT | 180 |
| Db | 121 | CCGTG | CACCT | GGGGAG | TGAGAG | ACAGAT | ATGCGCAT | GTCTT | GTCTG | CTGAA | TTTTT | 180 |
| OY | 181 | TTATAT | GTGCT | TAATGT | TGCTCT | GTGAG | AAAGCC | CTCGAA | AGCTAT | ATCCAA | CATAT | 240 |
| Db | 181 | TTATAT | GTGCT | TAATGT | TGCTCT | GTGAG | AAAGCC | CTCGAA | AGCTAT | ATCCAA | CATAT | 240 |
| OY | 241 | CATCT | TATAT | TCACAA | TTAAGCT | GTATG | TATGT | ATGTA | CTTAAG | AGCGT | CTGTA | 300 |
| Db | 241 | CATCT | TATAT | TCACAA | TTAAGCT | GTATG | TATGT | ATGTA | CTTAAG | AGCGT | CTGTA | 300 |
| OY | 301 | CACCT | TGCA | CTCAG | GGGGCG | GCTGC | ATTTAG | TAAAGGGT | CAAAAT | ATACCT | TTT | 360 |
| Db | 301 | CACCT | TGCA | CTCAG | GGGGCG | GCTGC | ATTTAG | TAAAGGGT | CAAAAT | ATACCT | TTT | 360 |
| OY | 361 | ATGCT | TC | CAAAAG | TGCTTG | GCTTCT | CTCCCA | CTGACAA | ATATGCC | AAAGTT | GAGAAAA | 420 |
| Db | 361 | ATGCT | TC | CAAAAG | TGCTTG | GCTTCT | CTCCCA | CTGACAA | ATATGCC | AAAGTT | GAGAAAA | 420 |
| OY | 421 | TGAT | CAT | ATATTT | TAGAT | TAACAG | AGCA | GTGGCG | ACACCG | ATTTT | ATAATTA | 480 |
| Db | 421 | TGAT | CAT | ATATTT | TAGAT | TAACAG | AGCA | GTGGCG | ACACCG | ATTTT | ATAATTA | 480 |
| OY | 481 | CACCT | TC | TTTTT | AAACAA | CAAAAT | GC | GGGTTT | ATTTCT | CAATG | ATGTT | 540 |
| Db | 481 | CACCT | TC | TTTTT | AAACAA | CAAAAT | GC | GGGTTT | ATTTCT | CAATG | ATGTT | 540 |
| OY | 541 | GGT | CCAG | GAAG | ACCTT | CAC | CTTGA | CAATAT | GGC | | | 576 |
| Db | 541 | GGT | CCAG | GAAG | ACCTT | CAC | CTTGA | CAATAT | GGC | | | 576 |

RESULT 2
AAA69764
ID AAA69764 standard; cDNA; 1567 BP.

AC AAA69764;

DT 07-NOV-2000 (first entry)

DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:74.

KM Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KM tumour antigen; identification; cytostatic; gene therapy; vaccine; ss

OS Homo sapiens.

PN WO200036107-A2.

PD 22-JUN-2000 .

PF 17-DEC-1999; 99WO-US030270.

PR 17-DEC-1998; 98US-00215681.

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| 99 | 99 |
| 100 | 100 |

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|----|----------------------|----------------|
| PR | 23-JUN-1999; | 99US-00338933. |
| PR | 24-SEP-1999; | 99US-00404879. |
| XX | | |
| PA | (CORI-) CORIXA CORP. | |

PI Mitcham JL, King GE, Algate PA, Frudakis TN;

WPI; 2000-431589/37.

PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of PT cancer, preferably ovarian cancer.

PS Claim 1; Fig 2; 299pp; English.

CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AAB69691 to AAB70077 and AAB12552 to AAB12557, represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention

SQ Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other;

| | | | | |
|-----------------------|----------------|--------------|----------|-------------|
| Query Match | 100.0% | Score 576 | DB 3 | Length 1567 |
| Best Local Similarity | 100.0% | Pred. No. | 5e-172 | |
| Matches 576 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

| | | | |
|----|-----|--------------------------------------------------------------|-----|
| QY | 1 | TTCAAAGACATATTNCAACTGGGAAATTAATTCATGGAACCTGACAAAGGTTTAGA | 60 |
| Db | 91 | TTCAAAGACATATTNCAAGTTGGGAAATTAATTCATGGAACCTGACAAAGTGTTAGA | 150 |
| QY | 61 | GTGATAAGTAAATGCAACGTGAGACAAGATGCATCCAGATCTCAGGAGACTCCCTG | 120 |
| Db | 151 | GTGATAAGTAAATGCAACGTGAGACAAGATGCATCCAGATCTCAGGAGACTCCCTG | 210 |
| QY | 121 | CTGTGCACCTGGGAGTGAAGAGACAGATATGTGATGTTCTTTGTCTCTGAATTTTAG | 180 |
| Db | 211 | CTGTGCACCTGGGAGTGAAGAGACAGATATGTGATGTTCTTTGTCTCTGAATTTTAG | 270 |
| QY | 181 | TTTAAATGTGTGTAATGTGCTCTCAGAGAGCCCTGGAAAGTCTATCCCAACTATCCA | 240 |
| Db | 271 | TTTAAATGTGTGTAATGTGCTCTCAGAGAGCCCTGGAAAGTCTATCCCAACTATCCA | 330 |
| QY | 241 | CACCTTAATTCACCAAAATTAACTGTAGTATGTACCTTAAGACGCTGTAATTGACTGC | 300 |
| Db | 331 | CACCTTAATTCACCAAAATTAACTGTAGTATGTACCTTAAGACGCTGTAATTGACTGC | 390 |
| QY | 301 | CACCTTGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAAATGATTCACTTTTATG | 360 |
| Db | 391 | CACCTTGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAAATGATTCACTTTTATG | 450 |
| QY | 361 | ATGCTTCCAAAGGTGCTTGAGCTTCCTCCCAATGACCAATGCGCAAATGTGAGAAAA | 420 |
| Db | 451 | ATGCTTCCAAAGGTGCTTCGCTTCTCTTCCCACTGACCAATGCGCAAATGTGAGAAAA | 510 |
| QY | 421 | TGATCATTAATTTTAGCATTAACAGACAGATCGGCACACCGATTTTAAATAAACTGAG | 480 |
| Db | 511 | TGATCATTAATTTTAGCATTAACAGACAGATCGGCACACCGATTTTAAATAAACTGAG | 570 |
| QY | 481 | CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCAATGATGTTCAATCCGTGAAT | 540 |
| Db | 571 | CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCAATGATGTTCAATCCGTGAAT | 630 |
| QY | 541 | GGTCCAGGGAAGGACCTTTCACCTGACATATGCG 576 | |
| Db | 631 | GGTCCAGGGAAGGACCTTTCACCTGACATATGCG 666 | |

RESULT 3

ABN72658
ID ABN72658 standard; DNA; 1567 BP.
XX
AC ABN72658;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ovarian carcinoma antigen polynucleotide #74.
XX
KW Human; immunostimulant; cytotoxic; cancer; ovarian carcinoma; ds.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
XX (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX WPI; 2002-164781/21.
XX
DR
XX
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
PS Example 1; Page 115; 408pp; English.
XX
XX
CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytotoxic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents DNA related
CC to the invention
XX
SQ Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAACCTAGACAAAGTGTGTTAGA 60
DB 91 TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAACCTAGACAAAGTGTGTTAGA 150
QY 61 GTGATAGTAAATATGACGCTGGAGACAAAGTGCATCCCAAGTCTCAGGACCTCCCTG 120
DB 151 GTGATAGTAAATATGACGCTGGAGACAAAGTGCATCCCAAGTCTCAGGACCTCCCTG 210
QY 121 CCGTGCACCTGGGAGGAGAGACAGATAGTCATGTTCTTGTCTCGAATTTTAG 180
DB 211 CCGTGCACCTGGGAGGAGAGACAGATAGTCATGTTCTTGTCTCGAATTTTAG 270
QY 181 TTATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAAGTCTATCCCAACATATCA 240
DB 271 TTATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAAGTCTATCCCAACATATCA 330
QY 241 CATCTTATATTTCCCAAAATTAAGTGTAGTATGATACCTTAAGAGCGCTGTAATGATGC 300
DB 331 CATCTTATATTTCCCAAAATTAAGTGTAGTATGATACCTTAAGAGCGCTGTAATGATGC 390
QY 301 CATCTTGCACACTGAGGAGCGCTGCATTTTATGTAATGAGTCAATGATCACTTTTATG 360

DB 391 CACTTGCACACTGAGGAGCGCTGCATTTTATGTAATGAGTCAATGATCACTTTTATG 450
QY 361 ATGCTTCAAAAGTGCCTTGGCTTCTTCCCACTGACAAATGCCAAAGTGAAGAAA 420
DB 451 ATGCTTCAAAAGTGCCTTGGCTTCTTCCCACTGACAAATGCCAAAGTGAAGAAA 510
QY 421 TGATCATTAATTTTAAAGTAAACAGAGAGTGGCGACACCGATTTTAAATTAAGTAG 480
DB 511 TGATCATTAATTTTAAAGTAAACAGAGAGTGGCGACACCGATTTTAAATTAAGTAG 570
QY 481 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCAGATGATGTCGTTGAAT 540
DB 571 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCAGATGATGTCGTTGAAT 630
QY 541 GGTCCAGGAAAGACCTTTCACCTTGACTATATGAC 576
DB 631 GGTCCAGGAAAGACCTTTCACCTTGACTATATGAC 666
RESULT 4
ADA08823
ID ADA08823 standard; DNA; 1567 BP.
XX
AC ADA08823;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide #74.
XX
KW de; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PI (MITC/) MITCHAM J L.
PI (KING/) KING G E.
PI (ALGA/) ALGATE P A.
PI (FLIN/) FLING S P.
PI (RETT/) RETTER M W.
PI (FANG/) FANGER G R.
PI (REBD/) REED S G.
PI (VEDV/) VEDVICK T S.
PI (CART/) CARTER D.
PI (HILL/) HILL P.
PI (ALBO/) ALBONE E.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX WPI; 2003-532352/50.
XX
PT New isolated 0772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
PS Example 1; Fig 2; 371pp; English.
XX
XX The invention relates to an isolated 0772P polypeptide, which has the
XX structure fully defined in the specification. The composition containing
XX the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
XX or antigen presenting cells are useful for stimulating an immune response
XX and treating ovarian cancer. Detecting the presence of the
XX polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
XX carcinoma cDNAs and protein cDNAs were identified using microarray
XX technology. The present sequence represents a human ovarian carcinoma

CC antigen polynucleotide.

SQ Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other;

Query Match 100.0%; Score 576; DB 9; Length 1567;

Best Local Similarity 100.0%; Pred. No. 5e-172;

Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATTTTAAAGTGGGAAATTAATTCATGTAACTAGACAGTGGTTAAGA 60
 |||
 DB 91 TTCAAAGACATTTTAAAGTGGGAAATTAATTCATGTAACTAGACAGTGGTTAAGA 150
 |||
 QY 61 GTGATAGTAAATGACGCTGAGACAGTGCATCCCAATCTCAGGAGCCTCCCTCG 120
 |||
 DB 151 GTGATAGTAAATGACGCTGAGACAGTGCATCCCAATCTCAGGAGCCTCCCTCG 210
 |||
 QY 121 CCTGTACCTGGGAGTGAAGACAGATAGTGCATGTTCTTCTCTGTAATTTTATG 180
 |||
 DB 211 CCTGTACCTGGGAGTGAAGACAGATAGTGCATGTTCTTCTCTGTAATTTTATG 270
 |||
 QY 181 TTATATGTGCTGTATGTTGCTCTGAGGAAGCCCTGAAAGTCTATCCCAATATCA 240
 |||
 DB 271 TTATATGTGCTGTATGTTGCTCTGAGGAAGCCCTGAAAGTCTATCCCAATATCA 330
 |||
 QY 241 CATCTTATATTCACAATTAAGCTGTAGTATGTACCTTAAGAAGCTGTAAATGACTGC 300
 |||
 DB 331 CATCTTATATTCACAATTAAGCTGTAGTATGTACCTTAAGAAGCTGTAAATGACTGC 390
 |||
 QY 301 CACTTGGCACTCAGGGGGGGGCTGCAATTTAGTAAGGTCAAATGATTCATCTTTTATG 360
 |||
 DB 391 CACTTGGCACTCAGGGGGGGGCTGCAATTTAGTAAGGTCAAATGATTCATCTTTTATG 450
 |||
 QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCGCAAGTTGAGAAAA 420
 |||
 DB 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCGCAAGTTGAGAAAA 510
 |||
 QY 421 TGATCATTAATTTTAAAGTAAACAGACAGTGGCGACACCGATTTTATTAATTAAGTGA 480
 |||
 DB 511 TGATCATTAATTTTAAAGTAAACAGACAGTGGCGACACCGATTTTATTAATTAAGTGA 570
 |||
 QY 481 CACCTTCTTTTAAACAAATGCGGTTTATTTCTAGATGATGATTCATCCGTAAT 540
 |||
 DB 571 CACCTTCTTTTAAACAAATGCGGTTTATTTCTAGATGATGATTCATCCGTAAT 630
 |||
 QY 541 GGTCCAGGAGAGCCTTCACTTGAATATATGCG 576
 |||
 DB 631 GGTCCAGGAGAGCCTTCACTTGAATATATGCG 666
 |||

RESULT 5
 ADF08570
 ID ADF08570 standard; cDNA; 1567 BP.
 XX
 AC ADF08570;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE cDNA encoding secreted ovarian carcinoma antigen segid 74.
 XX
 KW gene therapy; protein therapy; vaccine; antibody inhibition;
 KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
 KW secreted ovarian carcinoma antigen; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003124140-A1.
 PD 03-JUL-2003.
 XX
 PF 17-JUL-2002; 2002US-00198053.
 XX
 PR 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.

PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00657857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00884441.
 PR 17-JUL-2001; 2001US-00907969.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Bangur CS, Retter MW, Fanger GR, Hill P;
 DR WPI; 2003-897152/82.
 PT Oncogenic nucleic acids useful for the prevention, diagnosis and
 PT treatment of breast cancer.
 XX
 PS Example 1; SEQ ID NO 74; 399pp; English.
 XX
 CC The invention describes nucleic acids (I) and the polypeptides (II) they
 CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
 CC treating diseases related to their aberrant expression i.e. breast
 CC cancers. For example, (I) and (II) may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of (II) by expressing
 CC inactive proteins or to supplement the patient's own production of (II).
 CC Additionally, (I) may be used to produce (II), by inserting (I) into a
 CC host cell and culturing the cell to express the protein (II). (I) And its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. The host cell may also be used as antigens in the production of
 CC antibodies against (II) and in assays to identify modulators of (II)'s
 CC expression and activity. The anti-(II) antibodies, agonists and
 CC antagonists may be used to regulate expression and activity and as
 CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
 CC immunoassay). This sequence represents a polynucleotide encoding a
 CC secreted ovarian carcinoma antigen.
 XX
 SQ Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other;
 Query Match 100.0%; Score 576; DB 10; Length 1567;
 Best Local Similarity 100.0%; Pred. No. 5e-172;
 Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATTTTAAAGTGGGAAATTAATTCATGTAACTAGACAGTGGTTAAGA 60
 |||
 DB 91 TTCAAAGACATTTTAAAGTGGGAAATTAATTCATGTAACTAGACAGTGGTTAAGA 150
 |||
 QY 61 GTGATAGTAAATGACGCTGAGACAGTGCATCCCAATCTCAGGAGCCTCCCTCG 120
 |||
 DB 151 GTGATAGTAAATGACGCTGAGACAGTGCATCCCAATCTCAGGAGCCTCCCTCG 210
 |||
 QY 121 CCTGTACCTGGGAGTGAAGACAGATAGTGCATGTTCTTCTCTGTAATTTTATG 180
 |||
 DB 211 CCTGTACCTGGGAGTGAAGACAGATAGTGCATGTTCTTCTCTGTAATTTTATG 270
 |||
 QY 181 TTATATGTGCTGTATGTTGCTCTGAGGAAGCCCTGAAAGTCTATCCCAATATCA 240
 |||
 DB 271 TTATATGTGCTGTATGTTGCTCTGAGGAAGCCCTGAAAGTCTATCCCAATATCA 330
 |||
 QY 241 CATCTTATATTCACAATTAAGCTGTAGTATGTACCTTAAGAAGCTGTAAATGACTGC 300
 |||
 DB 331 CATCTTATATTCACAATTAAGCTGTAGTATGTACCTTAAGAAGCTGTAAATGACTGC 390
 |||
 QY 301 CACTTGGCACTCAGGGGGGGGCTGCAATTTAGTAAGGTCAAATGATTCATCTTTTATG 360
 |||
 DB 391 CACTTGGCACTCAGGGGGGGGCTGCAATTTAGTAAGGTCAAATGATTCATCTTTTATG 450
 |||
 QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCGCAAGTTGAGAAAA 420
 |||
 DB 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCGCAAGTTGAGAAAA 510
 |||

| | | | |
|---------------------------|---------------------------------------------------------------------------|-----------------------------------------------------------------|-----|
| OY | 421 | TCATCATATATTTTACATTTAAACAGAGCAGTGGCGACACCCGATTTTATTAATTAACCTGAG | 480 |
| DB | 511 | TCATCATATATTTTACATTTAAACAGAGCAGTGGCGACACCCGATTTTATTAATTAACCTGAG | 570 |
| OY | 481 | CACCTTCCTTTTAAACCAACCAATGCGGGTTATTTCTTCAGATGATGTTATCCGTGAAT | 540 |
| DB | 571 | CACCTTCCTTTTAAACCAACCAATGCGGGTTATTTCTTCAGATGATGTTATCCGTGAAT | 630 |
| OY | 541 | GGTCCAGGAGACCTTCACCTTGACATATATGCG | 576 |
| DB | 631 | GGTCCAGGAGACCTTCACCTTGACATATATGCG | 666 |
| RESULT 6 | | | |
| ID | ADG46318 | standard; cDNA; 1567 BP. | |
| XX | ADG46318; | | |
| XX | ADG46318; | | |
| XX | 26-FEB-2004 | (first entry) | |
| XX | | | |
| DE | Human ovarian carcinoma polynucleotide #74. | | |
| XX | | | |
| KX | Human; ovarian carcinoma; gene; 88; O8E; ovarian cancer; | | |
| KW | secreted tumour antigen; cytosolatic; 0772P. | | |
| XX | | | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | US2003165504-A1. | | |
| XX | | | |
| PD | 04-SEP-2003. | | |
| XX | | | |
| PF | 04-APR-2001; 2001US-00827271. | | |
| XX | | | |
| PR | 17-DEC-1998; 98US-00215681. | | |
| PR | 17-DEC-1998; 98US-00216003. | | |
| PR | 23-JUN-1999; 99US-00338933. | | |
| PR | 24-SEP-1999; 99US-00404879. | | |
| PR | 17-JUL-2000; 2000US-00617747. | | |
| PR | 10-AUG-2000; 2000US-00636801. | | |
| PR | 20-SEP-2000; 2000US-00667857. | | |
| XX | | | |
| PA | (RETT/) RETTER M W. | | |
| PA | (FANG/) FANGER G R. | | |
| PI | Retter MW, Fanger GR; | | |
| PI | | | |
| DR | WPI; 2003-098035/82. | | |
| XX | | | |
| PT | New isolated O8E or 0772P polypeptides, useful for diagnosing, | | |
| PT | preventing, treating and monitoring cancer, e.g. ovarian cancer, | | |
| PT | stimulating the immune response in patient. | | |
| PS | Example 1; SEQ ID NO 74; 290bp; English. | | |
| XX | | | |
| CC | The invention relates to human ovarian carcinoma polypeptides, designated | | |
| CC | O8E or 0772P, and the polynucleotides encoding them. The invention also | | |
| CC | relates to methods for inhibiting the development of cancer, e.g. ovarian | | |
| CC | cancer in a patient, methods for stimulating and/or expanding T cells and | | |
| CC | methods for identifying secreted tumour antigens. The polypeptides, | | |
| CC | compositions, antibodies to the polypeptides and methods are useful for | | |
| CC | diagnosing, preventing, treating and monitoring cancer, e.g. ovarian | | |
| CC | cancer. The composition is particularly useful for stimulating an immune | | |
| CC | response in patient. This sequence represents a human ovarian carcinoma | | |
| CC | polynucleotide of the invention. | | |
| XX | | | |
| XX | | | |
| XX | Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other; | | |
| Query Match | 100.0%; Score 576; DB 10; Length 1567; | | |
| Best Local Similarity | 100.0%; Pred. No. 5e-172; | | |
| Matches 576; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | | |

| | | | |
|----------|----------------------------------------------------------------------|---------------------------------------------------------|-----|
| QY | 1 | TTCAAAGCATATTAGAAGTTGGGAAAATATTCATGTGAACATGAGCAAGGTGTAA | 60 |
| Db | 91 | TTCAAAGCATATTAGAAGTTGGGAAAATATTCATGTGAACATGAGCAAGGTGTAA | 150 |
| QY | 61 | GTGATTAAGTAAATATGACAGTGGAGACAAGTGCATCCCGAGATCTCAGGGA | 120 |
| Db | 151 | GTGATTAAGTAAATATGACAGTGGAGACAAGTGCATCCCGAGATCTCAGGGA | 210 |
| QY | 121 | CTGTGACCTGGGAGTGGAGAGACAGAGATATGTCATGTTCTTTGCTCTGAA | 180 |
| Db | 211 | CTGTGACCTGGGAGTGGAGAGACAGAGATATGTCATGTTCTTTGCTCTGAA | 270 |
| QY | 181 | TTATATGTCGTATATGTGCTCTGAGGAAGCCCTGGAAAGTCTATCCACA | 240 |
| Db | 271 | TTATATGTCGTATATGTGCTCTGAGGAAGCCCTGGAAAGTCTATCCACA | 330 |
| QY | 241 | CATCTTAATATCCACAATTAAGCTGTATGATGATACCCCTAAGACGCTGA | 300 |
| Db | 331 | CATCTTAATATCCACAATTAAGCTGTATGATGATACCCCTAAGACGCTGA | 390 |
| QY | 301 | CACTTGCGCACTCGAGGCGCGCTGCATTTTATGATATGATGATTCAC | 360 |
| Db | 391 | CACTTGCGCACTCGAGGCGCGCTGCATTTTATGATATGATGATTCAC | 450 |
| QY | 361 | ATGCTTCCAAAGTGGCTTGGCTTCTCTCCCACTGACAAATGCCCAAT | 420 |
| Db | 451 | ATGCTTCCAAAGTGGCTTGGCTTCTCTCCCACTGACAAATGCCCAAT | 510 |
| QY | 421 | TGATCATATATTTAGCATTAACAGAGAGTCCGCGCACCGATTTTAA | 480 |
| Db | 511 | TGATCATATATTTAGCATTAACAGAGAGTCCGCGCACCGATTTTAA | 570 |
| QY | 481 | CACCTTCTTTTAAACAAACAATGCGGTTTATTTCTCAGATGATGTTCA | 540 |
| Db | 571 | CACCTTCTTTTAAACAAACAATGCGGTTTATTTCTCAGATGATGTTCA | 630 |
| QY | 541 | GGTCCAGGAAAGACCTTTCACTTGACTATATGGC | 576 |
| Db | 631 | GGTCCAGGAAAGACCTTTCACTTGACTATATGGC | 666 |
| RESULT 7 | | | |
| ACN92433 | | | |
| ID | ACN92433 | standard; DNA; 1596 BP. | |
| AC | ACN92433; | | |
| XX | | | |
| DT | 02-DEC-2004 | (first entry) | |
| XX | | | |
| DE | Breast cancer related marker, seq id 13583. | | |
| XX | | | |
| KW | Cancer; breast; tumour; cytostatic; marker; detection; therapy; db. | | |
| XX | | | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | US2003099974-A1. | | |
| XX | | | |
| PD | 29-MAY-2003. | | |
| XX | | | |
| PF | 18-JUL-2002; 2002US-00198846. | | |
| XX | | | |
| PR | 18-JUL-2001; 2001US-0306220P. | | |
| XX | | | |
| PA | (MILL-) MILLENNIUM PHARM INC. | | |
| XX | | | |
| PI | Lillie J, Xu Y, Wang Y, Steinmann K; | | |
| XX | | | |
| DR | WPI; 2003-787014/74. | | |
| XX | | | |
| PT | Novel isolated polypeptide associated with breast cancer, useful for | | |
| XX | detecting presence of polypeptide in sample, as a marker for breast | | |
| XX | cancer. | | |

PS Disclosure; SEQ ID NO 13583; 36bp; English.
XX
XX The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (SI). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?docID=20030099974
XX
SQ Sequence 1596 BP; 457 A; 354 C; 340 G; 424 T; 0 U; 21 Other;
Query Match 100.0%; Score 576; DB 11; Length 1596;
Best Local Similarity 100.0%; Pred. No. 5,1e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAAAGTTGGGAAATTAATTCAGTGAAGTGTGTTAAGA 60
DB 267 TTCAAGACATATTAAAGTTGGGAAATTAATTCAGTGAAGTGTGTTAAGA 326
QY 61 GTGATAGTAAATATGACGTGAGACAGATGATCCCAAGTCTCAGGACCTCCCTCG 120
DB 327 GTGATAGTAAATATGACGTGAGACAGATGATCCCAAGTCTCAGGACCTCCCTCG 386
QY 121 CCTGTACCTGGGAGTGAAGACAGATGATGATGTTCTTGTCTCTGAATTTTAG 180
DB 387 CCTGTACCTGGGAGTGAAGACAGATGATGATGTTCTTGTCTCTGAATTTTAG 446
QY 181 TTATATGCTGTGAATGTTGCTGTGAGAAAGCCCTGGAAGTCTATCCCAATATCA 240
DB 447 TTATATGCTGTGAATGTTGCTGTGAGAAAGCCCTGGAAGTCTATCCCAATATCA 506
QY 241 CATCTTATATTCACAAATTAAGCTGTAGATGATCCCTAAGACGTGTAATTTGACTGC 300
DB 507 CATCTTATATTCACAAATTAAGCTGTAGATGATCCCTAAGACGTGTAATTTGACTGC 566
QY 301 CACTTGGCAACTGACGGGCGGCTGCAATTTAGTAAATGGTCAATGATTCACCTTTTAG 360
DB 567 CACTTGGCAACTGACGGGCGGCTGCAATTTAGTAAATGGTCAATGATTCACCTTTTAG 626
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCCCAACTGACAAATGCAAAAGTTGAGAAAA 420
DB 627 ATGCTTCCAAAGGTGCTTGGCTTCTCCCAACTGACAAATGCAAAAGTTGAGAAAA 686
QY 421 TGATCATTAATTTAGATTAACAGACAGTCCGCGACACCGATTTTAAATTAACCTGAG 480
DB 687 TGATCATTAATTTAGATTAACAGACAGTCCGCGACACCGATTTTAAATTAACCTGAG 746
QY 481 CACCTTCTTTTAAACAAATGCGGTTTATTTCTCAGATGATGTTGATCCGTAAT 540
DB 747 CACCTTCTTTTAAACAAATGCGGTTTATTTCTCAGATGATGTTGATCCGTAAT 806
QY 541 GGTCCAGGAAAGGACCTTTCACCTGACTATATAGGC 576
DB 807 GGTCCAGGAAAGGACCTTTCACCTGACTATATAGGC 842

RESULT 8
ADL45372
ID ADL45372 standard; DNA; 1965 BP.
XX
XX ADL45372;
XX
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #19262.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
KW

XX
OS Homo sapiens.
XX
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
XX WPI; 2001-611502/70.
XX
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 19262; 106bp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
SQ Sequence 1965 BP; 557 A; 450 C; 452 G; 503 T; 0 U; 3 Other;
Query Match 100.0%; Score 576; DB 5; Length 1965;
Best Local Similarity 100.0%; Pred. No. 5,6e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAAAGTTGGGAAATTAATTCATGTAAGTGAAGTGTGTTAAGA 60
DB 1130 TTCAAGACATATTAAAGTTGGGAAATTAATTCATGTAAGTGAAGTGTGTTAAGA 1189
QY 61 GTGATAGTAAATATGACGTGAGACAGATGATCCCAAGTCTCAGGACCTCCCTCG 120
DB 1190 GTGATAGTAAATATGACGTGAGACAGATGATCCCAAGTCTCAGGACCTCCCTCG 1249

QY 121 CCTGTGACCTGGGAGTGAAGAGACAGAGATAGTCATGTTCTTTGCTGTAATTTTAG 180
DB 1250 CCTGTGACCTGGGAGTGAAGAGACAGAGATAGTCATGTTCTTTGCTGTAATTTTAG 1309
QY 181 TTATATGCTGTATATGTTGCTGTAGAGAAACCCCTGGAAAGTCTATCCCAACATATCCA 240
DB 1310 TTATATGCTGTATATGTTGCTGTAGAGAAACCCCTGGAAAGTCTATCCCAACATATCCA 1369
QY 241 CATCTTATATTTCCCAATTAAGCTGTATGTATGTAACCTTAAGACGCTGTATTTGACTGC 300
DB 1370 CATCTTATATTTCCCAATTAAGCTGTATGTATGTAACCTTAAGACGCTGTATTTGACTGC 1429
QY 301 CACTTGGCACTGAGGGGGCGCTGCATTTTATAGTAATGGTCAAAATGATGACTTTTATG 360
DB 1430 CACTTGGCACTGAGGGGGCGCTGCATTTTATAGTAATGGTCAAAATGATGACTTTTATG 1489
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAA 420
DB 1490 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAA 1549
QY 421 TGATCATATTTTGAATTAACAGAGAGTCGCGGACACCGATTTTAAATAAATCTGAG 480
DB 1550 TGATCATATTTTGAATTAACAGAGAGTCGCGGACACCGATTTTAAATAAATCTGAG 1609
QY 481 CACCTTCTTTTAAACAAAGGAGGTTTATTTCTCAGATGATGTCATCCGTAAT 540
DB 1610 CACCTTCTTTTAAACAAAGGAGGTTTATTTCTCAGATGATGTCATCCGTAAT 1669
QY 541 GGTCCAGGAGGAGCCTTTGACCTTGAATATGCG 576
DB 1670 GGTCCAGGAGGAGCCTTTGACCTTGAATATGCG 1705

RESULT 9
AA290470
ID AA290470 standard; cDNA; 2587 BP.

XX AA290470;

DT 06-JUN-2000 (first entry)

DE Cancer specific gene (CSG) sequence (clone ID 16656542).

KM CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
endometrial; uterine; lung; cytotoxic; ss.

OS Homo sapiens.

PN W0200012758-A1.

PD 09-MAR-2000.

PF 01-SEP-1999; 99WO-US019655.

PR 02-SEP-1998; 98US-0098880P.

PA (DIAD-) DIADEXUS LLC.

PI Salceda S, Sun Y, Recipon H, Cafferkey R;

XX WPI; 2000-256657/22.

DR
XX
XX
PT Diagnosing, staging, monitoring, imaging and treating cancer especially
PT gynecological cancers e.g. breast, ovarian cancer and lung cancer.
XX Involves measuring cancer specific gene levels in cells and body fluids.
PS Claim 9; Page 44-45; 58pp; English.

CC The invention relates to detecting, diagnosing metastasis and staging
CC cancer by measuring levels of cancer specific genes (CSG) in cells,
CC tissues or body fluids. Their remission and progression, decreases and
CC increases in CSG levels, is also monitored, by periodic sample analysis.

CC The methods are useful for detecting cancers, especially gynecologic
CC cancers which include ovarian, breast, endometrial and uterine cancer and
CC lung cancer. Antibodies against the CSGs labeled with paramagnetic ions
CC or a radioisotope is useful for imaging cancer and when conjugated with a
CC cytotoxic agent are useful for treating cancer. The present sequence
CC represents a CSG sequence (clone ID: 16656542 and gene ID: 234617)
XX

SO Sequence 2587 BP; 737 A; 588 C; 580 G; 682 T; 0 U; 0 Other;

Query Match 100.0%; Score 576; DB 3; Length 2587;
Best Local Similarity 100.0%; Pred. No. 6,4e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAAAGACATATTAAGTTGGGAAATTAATTCATGTGAACATGAGTGTGTTAGA 60
DB 1112 TTGAAAGACATATTAAGTTGGGAAATTAATTCATGTGAACATGAGTGTGTTAGA 1171
QY 61 GTGATAAGTAAATATGACGAGAGACAGATGATCCCAATCTCAGGACCTCCCTG 120
DB 1172 GTGATAAGTAAATATGACGAGAGACAGATGATCCCAATCTCAGGACCTCCCTG 1231
QY 121 CCTGTCACTGGGAGTGAAGAGACAGATGATGTCATGTTCTTGTCTGAAATTTTAG 180
DB 1232 CCTGTCACTGGGAGTGAAGAGACAGATGATGTCATGTTCTTGTCTGAAATTTTAG 1291
QY 181 TTATATGCTGTATATGTTGCTGTAGAGAAACCCCTGGAAAGTCTATCCCAATATCCA 240
DB 1292 TTATATGCTGTATATGTTGCTGTAGAGAAACCCCTGGAAAGTCTATCCCAATATCCA 1351
QY 241 CATCTTATATTTCCCAATTAAGCTGTATGTATGTAACCTTAAGACGCTGTATTTGACTGC 300
DB 1352 CATCTTATATTTCCCAATTAAGCTGTATGTATGTAACCTTAAGACGCTGTATTTGACTGC 1411
QY 301 CACTTGGCACTGAGGGGGCGCTGCATTTTATAGTAATGGTCAAAATGATGACTTTTATG 360
DB 1412 CACTTGGCACTGAGGGGGCGCTGCATTTTATAGTAATGGTCAAAATGATGACTTTTATG 1471
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAA 420
DB 1472 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAA 1531
QY 421 TGATCATATTTTGAATTAACAGAGAGTCGCGGACACCGATTTTAAATAAATCTGAG 480
DB 1532 TGATCATATTTTGAATTAACAGAGAGTCGCGGACACCGATTTTAAATAAATCTGAG 1591
QY 481 CACCTTCTTTTAAACAAAGGAGGTTTATTTCTCAGATGATGTCATCCGTAAT 540
DB 1592 CACCTTCTTTTAAACAAAGGAGGTTTATTTCTCAGATGATGTCATCCGTAAT 1651
QY 541 GGTCCAGGAGGAGCCTTTGACCTTGAATATGCG 576
DB 1652 GGTCCAGGAGGAGCCTTTGACCTTGAATATGCG 1687

RESULT 10
ABL57354
ID ABL57354 standard; cDNA; 2591 BP.

XX ABL57354;

DT 12-AUG-2002 (first entry)

DE Breast BS265 gene EST clone 3038129.

KM BS265; human; breast; cancer; tumour; metastasis; diagnosis;

XX gene therapy; expressed sequence tag; EST; gene; ss.

OS Homo sapiens.

XX
XX
FH Key Location/Qualifiers
FT CDS 61..909
FT /tag= a
FT /product= "BS265"

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XX US2002034749-A1.
XX
XX
XX 21-MAR-2002.
XX
XX 07-MAY-2001; 2001US-00850178.
XX
XX 18-NOV-1997; 97US-00972376.
XX 18-NOV-1998; 98US-00193944.
XX
XX (BILL/) BILLINGEL P A.
XX (COHE/) COHEN M.
XX (COLE/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (GORD/) GORDON J.
XX (GRAN/) GRANADOS E N.
XX (HODG/) HODGES S C.
XX (KLAS/) KLAS M R.
XX (KRAT/) KRATOCHVIL J D.
XX (ROBE/) ROBERTS-RAPP L A.
XX (RUSS/) RUSSELL J C.
XX (STRO/) STROUPE S D.
XX
XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
XX Granados EN, Hodges SC, Klatos MR, Kratochvil JD, Roberts-Rapp LA,
XX Russell JC, Stroupe SD;
XX
XX MPI: 2002-403712/43.
XX P-PSDB; ABB76274.
XX
XX New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
XX staging, monitoring, prognosticating, in vivo imaging, preventing,
XX treating, or determining the predisposition of an individual to breast
XX cancer.
XX
XX Claim 52; Page 41-42; 52pp; English.
XX
XX The present sequence is of human breast BS265 gene expressed sequence tag
XX (EST) clone 3038129. ESTs were derived from cDNA libraries made from
XX breast tumour tissues, breast non-tumour tissues and numerous other
XX tissues, and entered into a database as gene transcript images. They were
XX then evaluated to identify EST sequences that were representative
XX primarily of the breast tissue libraries, and were ranked according to
XX their abundance in the target libraries and absence from background
XX libraries. 4 Partial clones (see ABL57345-48) represented the minimum
XX number of clones that, together with the full-length sequence of clone
XX 3090752H1 (see ABL57349), were needed to form a contig and from which a
XX consensus sequence (see ABL57350) for BS265 was derived. Other clones
XX appeared at positions in the assembly upstream of the above sequences.
XX Clone 3038129 spanned the entire assembly, and encoded the protein given
XX in ABB76274. The set of contiguous and partially overlapping cDNA
XX sequences, designated as BS265 and transcribed from breast tissue, and
XX the polypeptides encoded by them, are useful for detecting, diagnosing,
XX staging, monitoring, prognosticating, in vivo imaging, preventing,
XX treating, or determining the predisposition of an individual to diseases
XX and conditions of the breast, especially tumours and metastases
XX
XX Sequence 2591 BP; 739 A; 591 C; 579 G; 682 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 576; DB 6; Length 2591;
XX Best Local Similarity 100.0%; Pred. No. 6; 5e-172;
XX Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTCAAAGACATATTAGAGTGGGAAATATTCATGTGAACAGCAAGTGTGTTAAGA 60
XX |||||
XX 1111 TTCAAAGACATATTAGAGTGGGAAATATTCATGTGAACAGCAAGTGTGTTAAGA 1170
XX |||||
XX
XX 61 GTGATAAGTAAATGACGCTGAGACAGTGCATCCCAAGTCTCAGGACCTCCCTG 120
XX |||||
XX 1171 GTGATAAGTAAATGACGCTGAGACAGTGCATCCCAAGTCTCAGGACCTCCCTG 1230
XX |||||
XX
XX 121 CCTGTCACTGGGAGTGAAGGACAGATAGTGCATGTTCTTGTCTGAAATTTTAA 180
XX |||||

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Db 1231 CCTGTCACTGGGAGTGAAGGACAGATAGTGCATGTTCTTGTCTCTGAATTTTAA 1290
Qy 181 TTATATGCTGTATATGTTGCTCTGAGAGACCCCTGGAAAGTCAATCCAAATATCCA 240
Db 1291 TTATATGCTGTATATGTTGCTCTGAGAGACCCCTGGAAAGTCAATCCAAATATCCA 1350
Qy 241 CATCTTAATATTCACAAATTAAGCTGTATGTATACCTTAAGACGCTCTAATGACTGCG 300
Db 1351 CATCTTAATATTCACAAATTAAGCTGTATGTATACCTTAAGACGCTCTAATGACTGCG 1410
Qy 301 CACTTGGACACTCAGGGGGGGCTGCATTTTGTATATGGGTCAAAATGATTCATTTTAA 360
Db 1411 CACTTGGACACTCAGGGGGGGCTGCATTTTGTATATGGGTCAAAATGATTCATTTTAA 1470
Qy 361 ATGCTTCCAAAGAGTGCTTGGCTTCTCTTCCCACTGACAAATGCAAGTTGAGAAAA 420
Db 1471 ATGCTTCCAAAGAGTGCTTGGCTTCTCTTCCCACTGACAAATGCAAGTTGAGAAAA 1530
Qy 421 TGATCATATATTTTACATTAACAGACAGTGGGACACCGATTTTATTAATTAACCTGAG 480
Db 1531 TGATCATATATTTTACATTAACAGACAGTGGGACACCGATTTTATTAATTAACCTGAG 1590
Qy 481 CACCTTCTTTTAAACAACAATGCGGTTTATTTCTCAGATGATGTCATCCGTGAAT 540
Db 1591 CACCTTCTTTTAAACAACAATGCGGTTTATTTCTCAGATGATGTCATCCGTGAAT 1650
Qy 541 GGTCCAGGAGGAAGACCTTTCACCTTGACTATATAGC 576
Db 1651 GGTCCAGGAGGAAGACCTTTCACCTTGACTATATAGC 1686

RESULT 11
AAB29253
ID AAB29253 standard; DNA; 2603 BP.
XX
XX AAB29253;
XX
XX 07-MAY-2002 (first entry)
XX
XX Human B7-like protein (B7-L) DNA.
XX
XX Human; B7-like protein; B7-L; reproductive disorder; autoimmune disease;
XX proliferative disorder; infertility; hyperplasia; cancer; lung; breast;
XX brain; seminal vesicle; haematopoietic system; tumour; diabetes mellitus;
XX rheumatoid arthritis; systemic lupus erythematosus; toxic shock syndrome;
XX inflammatory bowel disease; psoriasis; allergy; Crohn's disease; vaccine;
XX Grave's disease; arteriosclerosis; multiple sclerosis; hypersensitivity;
XX nephropathy; skin disorder; endocrinopathy; vasculopathy; gynaecological;
XX myasthenia gravis; anaemia; lymphoproliferative disorder; neuroprotective;
XX cytotoxic; multiple myeloma; tissue-degenerating disease; nephrotropic;
XX immunosuppressive; asthma; virucide; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 53..901
XX FT /*tag= a
XX FT /product= "Human B7-L protein"
XX FT sig_peptide 53..124
XX FT /*tag= b
XX FT mat_peptide 125..898
XX FT /*tag= c
XX FT /product= "Human mature B7-L protein"
XX
XX WO200202624-A2.
XX
XX 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US021297.
XX
XX 30-JUN-2000; 2000US-0215645P.
XX
XX (AMGE-) AMGEN INC.

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XX Fox M, Sullivan JK, Fang M;
PI WPI, 2002-171639/22.
DR P-PSDB; AAE18336.
XX
PT Novel B7-1-like polypeptides, polynucleotides and their modulators useful
PT for prevention and treatment of reproductive, immune and proliferative
PT disorders, e.g. cancer, arteriosclerosis.
XX
PS Claim 1; Fig 1A-1C; 133pp; English.
XX
CC The present invention relates to an isolated B7-1-like (B7-L) polypeptide
CC and its polynucleotide. B7-1 and its modulators are useful for treating
CC reproductive disorders (e.g. infertility, miscarriage, preterm labour and
CC delivery and endometriosis) and proliferative disorders. Antibodies,
CC soluble proteins comprising extracellular domains and other regulators of
CC B7-L are useful for enhancing the immune response to tumours. B7-1 plays
CC a role in growth and maintenance of cancer cells based on the observation
CC of seminal vesicle hyperplasia in transgenic mice overexpressing B7-1.
CC Modulators of B7-1 are useful for the treatment of cancer e.g. seminal
CC vesicle, lung, brain, breast, ovarian, testicular cancer and cancers of
CC haematopoietic system. B7-1 and their modulators are useful to treat
CC autoimmune diseases such as systemic lupus erythematosus, rheumatoid
CC arthritis, immune thrombocytopenic purpura and psoriasis, chronic
CC inflammatory disease such as inflammatory bowel disease (Crohn's disease
CC and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and
CC diabetes mellitus. They are also useful as immunosuppressive agents for
CC bone marrow and organ transplantation or to prolong graft survival.
CC Modulators of B7-L are also useful for diagnosis and treatment of
CC diseases involving abnormal cell proliferation, arteriosclerosis and
CC vascular restenosis. Soluble B7-L serves as vaccine adjuvants.
CC Antagonists of B7-L are useful for alleviation of toxic shock syndrome or
CC alloimmunisation due to blood transfusions, and for treatment of
CC multiple sclerosis, allergy, asthma and hypersensitivity reactions,
CC nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and
CC pemphigoid), endocrinopathies, various neuropathies, vasculopathies,
CC coeliac disease, anaemia, thrombocytopenia, Guillain-Barre syndrome and
CC myasthenia gravis, and lymphoproliferative disorders such as multiple
CC myeloma. B7-L gene is useful in gene therapy and to map the locations of
CC B7-L gene and related genes on chromosomes, as hybridisation probes in
CC diagnostic assays, for isolating corresponding chromosomal B7-L genes,
CC and to identify heritable tissue-degenerating diseases. The present
CC sequence is human B7-L protein DNA
XX
SQ Sequence 2603 BP; 758 A; 589 C; 573 G; 682 T; 0 U; 1 Other;
Query Match 100.0%; Score 576; DB 6; Length 2603;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTCAAGACATATTAGAGTTGGGAAATATTCATGTCAGTACAGCAAGTGTGTTAAGA 60
DB 1103 TTCAAGACATATTAGAGTTGGGAAATATTCATGTCAGTACAGCAAGTGTGTTAAGA 1162
XX
QY 61 GTGATAGTAAATGACCGTGGAGACAGATGCCCATCTCAGGAGCTCCGCCCTG 120
DB 1163 GTGATAGTAAATGACCGTGGAGACAGATGCCCATCTCAGGAGCTCCGCCCTG 1222
XX
QY 121 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTGTCTGTAATTTTAA 180
DB 1223 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTGTCTGTAATTTTAA 1282
XX
QY 181 TTATATGTGCTGTAATGTGCTCTGAGGAAGCCCTTGAAAGTCTATCCCAATATCCA 240
DB 1283 TTATATGTGCTGTAATGTGCTCTGAGGAAGCCCTTGAAAGTCTATCCCAATATCCA 1342
XX
QY 241 CACTTATATTTCCAAATTAAGCTGTATGATACCTTAAGACGCTGCTAATTTGACTGC 300
DB 1343 CACTTATATTTCCAAATTAAGCTGTATGATACCTTAAGACGCTGCTAATTTGACTGC 1402
XX
QY 301 CACTTGCACATCGAGGGGGCGGTGCAATTTAGTAATGGGCAATGATTCACCTTTTAA 360

DB 1403 CACTTGCACATCGAGGGGGCGGTGCAATTTAGTAATGGGCAATGATTCACCTTTTAA 1462
QY 361 ATGCTTCCAAAGGTGCTTGCTGCTTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
DB 1463 ATGCTTCCAAAGGTGCTTGCTGCTTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1522
QY 421 TGAATCATATTTTAAAGTAAAGACAGACATGCGGCGACCGATTTTATTAATTAACCTGAG 480
DB 1523 TGAATCATATTTTAAAGTAAAGACAGACATGCGGCGACCGATTTTATTAATTAACCTGAG 1582
QY 481 CACTTCTTTTAAACAAACAAATGCGGTTTATTTCTGATGATGATGTTTATTCATCGTAAT 540
DB 1583 CACTTCTTTTAAACAAACAAATGCGGTTTATTTCTGATGATGATGTTTATTCATCGTAAT 1642
QY 541 GGTCCAGGGAAGACCTTTACCTTGATATGTC 576
DB 1643 GGTCCAGGGAAGACCTTTACCTTGATATGTC 1678
XX
RESULT 12
AAAT0077
ID AAA70077 standard; cDNA; 2627 BP.
XX
AC AAA70077;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:391.
XX
KM Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KM tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200036107-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US030270.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Frudakis TN;
PI WPI, 2000-431589/37.
XX
DR WPI, 2000-431589/37.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
PS Claim 1; Page 204-205; 299pp; English.
XX
CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AA69691 to AA70077 and AAB12552 to AAB12557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 100.0%; Score 576; DB 3; Length 2627;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTCAAAGCATATTGAAGTTGGGAAAAATTAATTCATGTGACTAGACAAGTGTGTAAGA 60
XX |||
DB 1133 TTCAAAGCATATTGAAGTTGGGAAAAATTAATTCATGTGACTAGACAAGTGTGTAAGA 1192
QY 61 GTGATTAAGTAAATGACGTGGAGACAGTGCATCCCAATCTCAGGAGCTCCCCCTG 120
XX |||
DB 1193 GTGATTAAGTAAATGACGTGGAGACAGTGCATCCCAATCTCAGGAGCTCCCCCTG 1252
QY 121 CCTGTCACCTGGGGAGTGAAGAGACAGATAGTGCATGTTCTTGGCTCTGTAATTTTAA 180
XX |||
DB 1253 CCTGTCACCTGGGGAGTGAAGAGACAGATAGTGCATGTTCTTGGCTCTGTAATTTTAA 1312
QY 181 TTATATGTCGTGTAATGTTCTCTGAGGAAGCCCTGGAAGTCTATCCCAATATCCA 240
XX |||
DB 1313 TTATATGTCGTGTAATGTTCTCTGAGGAAGCCCTGGAAGTCTATCCCAATATCCA 1372
QY 241 CATCTTATATTCACAAATTAAAGCTGTAGTATGATACCTTAAGACGTGTATTTGACTGC 300
XX |||
DB 1373 CATCTTATATTCACAAATTAAAGCTGTAGTATGATACCTTAAGACGTGTATTTGACTGC 1432
QY 301 CACTTGGCAACTCAGGGGGGGGCGCATTTTAGTAATGGGTCAATGATTCACCTTTTATG 360
XX |||
DB 1433 CACTTGGCAACTCAGGGGGGGGCGCATTTTAGTAATGGGTCAATGATTCACCTTTTATG 1492
QY 361 ATGCTTCCAAAGAGTGCCTTGCTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
XX |||
DB 1493 ATGCTTCCAAAGAGTGCCTTGCTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
QY 421 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATAAACTGAG 480
XX |||
DB 1553 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATAAACTGAG 1612
QY 481 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCACTCCGTAAT 540
XX |||
DB 1613 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCACTCCGTAAT 1672
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 576
XX |||
DB 1673 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 1708

RESULT 13
AAH55681
ID AAH55681 standard; DNA; 2627 BP.
XX
AC AAH55681;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human ovarian tumour-derived antigen O8E DNA sequence.
XX
KM Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;
XX antigen; O8E; ds.
XX
OS Homo sapiens.
XX
PN MO200140269-A2.
XX
PD 07-JUN-2001.
XX
PF 29-NOV-2000; 2000WO-US032520.
XX
PR 30-NOV-1999; 99US-00451651.
XX 22-FEB-2000; 2000US-00510662.
XX 10-MAR-2000; 2000US-00523586.
XX 07-APR-2000; 2000US-00545068.
XX 15-MAY-2000; 2000US-00571025.
XX
PA (CORI-) CORIXA CORP.
PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
XX WPI; 2001-356154/37.
DR

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DR N-PSDB; AAB99204; AAB99205.
XX
XX Breast tumor polypeptides and the nucleic acids that encode them, useful
PT for the prevention, diagnosis and treatment of breast cancer.
XX
XX Claim 24; Page 189; 221pp; English.
XX
XX The present invention relates to human breast tumour protein coding
CC sequences (see AAH5479-AAH5513, AAH5517-AAH55679 and AAH55682-
CC AAH55762). The breast tumour protein DNA sequences may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the breast tumour protein e.g. breast cancer.
CC The present sequence is a human ovarian tumour-derived antigen coding
CC sequence, which was used in an example from the present invention
SQ
Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 100.0%; Score 576; DB 4; Length 2627;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGCATATTGAAGTTGGGAAAAATTAATTCATGTGACTAGACAAGTGTGTAAGA 60
DB 1133 TTCAAAGCATATTGAAGTTGGGAAAAATTAATTCATGTGACTAGACAAGTGTGTAAGA 1192
QY 61 GTGATTAAGTAAATGACGTGGAGACAGTGCATCCCAATCTCAGGAGCTCCCCCTG 120
DB 1193 GTGATTAAGTAAATGACGTGGAGACAGTGCATCCCAATCTCAGGAGCTCCCCCTG 1252
QY 121 CCTGTCACCTGGGGAGTGAAGAGACAGATAGTGCATGTTCTTGGCTCTGTAATTTTAA 180
DB 1253 CCTGTCACCTGGGGAGTGAAGAGACAGATAGTGCATGTTCTTGGCTCTGTAATTTTAA 1312
QY 181 TTATATGTCGTGTAATGTTCTCTGAGGAAGCCCTGGAAGTCTATCCCAATATCCA 240
DB 1313 TTATATGTCGTGTAATGTTCTCTGAGGAAGCCCTGGAAGTCTATCCCAATATCCA 1372
QY 241 CATCTTATATTCACAAATTAAAGCTGTAGTATGATACCTTAAGACGTGTATTTGACTGC 300
DB 1373 CATCTTATATTCACAAATTAAAGCTGTAGTATGATACCTTAAGACGTGTATTTGACTGC 1432
QY 301 CACTTGGCAACTCAGGGGGGGGCGCATTTTAGTAATGGGTCAATGATTCACCTTTTATG 360
DB 1433 CACTTGGCAACTCAGGGGGGGGCGCATTTTAGTAATGGGTCAATGATTCACCTTTTATG 1492
QY 361 ATGCTTCCAAAGAGTGCCTTGCTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
DB 1493 ATGCTTCCAAAGAGTGCCTTGCTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
QY 421 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATAAACTGAG 480
DB 1553 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATAAACTGAG 1612
QY 481 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCACTCCGTAAT 540
DB 1613 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCACTCCGTAAT 1672
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 576
DB 1673 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 1708

RESULT 14
ABN72971
ID ABN72971 standard; DNA; 2627 BP.
XX
AC ABN72971;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ovarian carcinoma polynucleotide O8E.
XX
KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
DR

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XX OS Homo sapiens.
XX PN MO200206317-A2.
XX PD 24-JAN-2002.
XX PF 17-JUL-2001; 2001WO-US022635.
XX PR 17-JUL-2000; 2000US-00617747.
XX PR 10-AUG-2000; 2000US-00636801.
XX PR 20-SEP-2000; 2000US-00667857.
XX PR 04-APR-2001; 2001US-00827271.
XX PR 18-JUN-2001; 2001US-00884441.
XX PA (CORI-) CORIXA CORP.
XX PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR,
XX PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX DR WPI; 2002-164781/21.
XX DR P-PSDB; ABP30900, ABP30901.
XX PS Polypeptides comprising an immunogenic portion of an ovarian carcinoma
XX PT protein or its variants, useful for stimulating an immune response in a
XX PT patient and treating ovarian cancer.
XX PS Example 2; Page 319-320; 408pp; English.
XX CC This invention relates to polypeptides comprising an immunogenic portion
XX CC of an ovarian carcinoma protein which acts as an immunostimulant and is
XX CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
XX CC proteins, T cell populations and antigen presenting cells that express
XX CC the polypeptides are useful for stimulating an immune response in a
XX CC patient and treating ovarian cancer. This sequence represents DNA related
XX CC to the invention
XX CC
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 100.0%; Score 576; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAGAGTTGGGAAATTAATTCATGTAAGTACAGACAGTGTGTTAGA 60
DB 1133 TTCAAGACATATTAGAGTTGGGAAATTAATTCATGTAAGTACAGACAGTGTGTTAGA 1192
QY 61 GTGATTAAGTAAATGACAGTGAAGACAAAGTGCATCCCAATCTCAGAGGACTCCCTCG 120
DB 1193 GTGATTAAGTAAATGACAGTGAAGACAAAGTGCATCCCAATCTCAGAGGACTCCCTCG 1252
QY 121 CCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTCTGAAATTTTAA 180
DB 1253 CCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTCTGAAATTTTAA 1312
QY 181 TTATATGTGTGTAATGTTCTCTGAGAGAGCCCTGGAAAGCTATCCCAATCAATCCA 240
DB 1313 TTATATGTGTGTAATGTTCTCTGAGAGAGCCCTGGAAAGCTATCCCAATCAATCCA 1372
QY 241 CATCTTATATTCACAATTAAGCTGATGATGTAACCTTAAGAGCGTCTAATTTGATGC 300
DB 1373 CATCTTATATTCACAATTAAGCTGATGATGTAACCTTAAGAGCGTCTAATTTGATGC 1432
QY 301 CACTTGCAACCTGACGGGCGGCTGCAATTTTAAATGAGTCAATGATTCATTTTAA 360
DB 1433 CACTTGCAACCTGACGGGCGGCTGCAATTTTAAATGAGTCAATGATTCATTTTAA 1492
QY 361 ATGCTTCGAAAGGCTGCTGCTTCTTCCCAATGACAAATGCCAAATGTAGAGAAAA 420
DB 1493 ATGCTTCGAAAGGCTGCTTCTTCTTCCCAATGACAAATGCCAAATGTAGAGAAAA 1552
QY 421 TGATCATTAATTTAGCATAAACAGAGAGTGGCGAGACCCGATTTTAAATTAACCTGAG 480

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DB 1553 TGATCATTAATTTAGCATAAACAGAGAGTGGCGAGACCCGATTTTAAATTAACCTGAG 1612
QY 481 CACCTTCTTTTAAACAAATGCGGCTTTATTTCTCGATGATGTTATCGGTAAAT 540
DB 1613 CACCTTCTTTTAAACAAATGCGGCTTTATTTCTCGATGATGTTATCGGTAAAT 1672
QY 541 GGTCCAGGAGGAGACCTTCACCTTGACTATATAGG 576
DB 1673 GGTCCAGGAGGAGACCTTCACCTTGACTATATAGG 1708

RESULT 15
ADA08544
ID ADA08544 standard; cDNA; 2627 BP.
XX AC ADA08544;
XX DT 06-NOV-2003 (first entry)
XX DE Human ovarian carcinoma polynucleotide OBE.
XX KW ss; human; gene therapy; ovarian cancer; cancer.
XX OS Homo sapiens.
XX PN US2003091580-A1.
XX PD 15-MAY-2003.
XX PF 17-JUL-2001; 2001US-00907969.
XX PR 18-JUN-2001; 2001US-00884441.
XX PA (MITC/) MITCHAM J L.
XX PA (KING/) KING G E.
XX PA (ALGA/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PA (RETT/) RETTER M W.
XX PA (FANG/) FANGER M R.
XX PA (VEDV/) VEDVICK T S.
XX PA (CART/) CARTER D.
XX PA (HILL/) HILL P.
XX PA (ALBO/) ALBONE E.
XX PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR,
XX PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX DR WPI; 2003-532352/50.
XX PT New isolated O772P polypeptides and polynucleotides, useful in gene
XX PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
XX PT cancer.
XX PS Example 2; SEQ ID NO 391; 371pp; English.
XX CC The invention relates to an isolated O772P polypeptide, which has the
XX CC structure fully defined in the specification. The composition containing
XX CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
XX CC or antigen presenting cells are useful for stimulating an immune response
XX CC and treating ovarian cancer. Detecting the presence of the
XX CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
XX CC carcinoma cDNAs and protein cDNAs were identified using microarray
XX CC technology. The present sequence represents a human ovarian carcinoma
XX CC antigen polynucleotide.
XX CC
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 100.0%; Score 576; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAGAGTTGGGAAATTAATTCATGTAAGTACAGACAGTGTGTTAGA 60

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Db 1133 TTCAAGACATATTTAGAACTTGGGAAAATAATTCATGTGACTAGACAAGTGATTAGA 1192
QY 61 GTGATTAAGTAAATGACGTGAGACAAATGCAATCCCGAATCTCAGGGACCTCCCCCTG 120
Db 1193 GTGATTAAGTAAATGACGTGAGACAAATGCAATCCCGAATCTCAGGGACCTCCCCCTG 1252
QY 121 CCTGTCACCTGGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGCTCTGAAATTTTAG 180
Db 1253 CCTGTCACCTGGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGCTCTGAAATTTTAG 1312
QY 181 TTATATGTCGTGAATGTTGCTCTGAGAAAGCCCTGAAAGTCTATCCCAATATCCA 240
Db 1313 TTATATGTCGTGAATGTTGCTCTGAGAAAGCCCTGAAAGTCTATCCCAATATCCA 1372
QY 241 CATCTTAATTTCCAAATTAAGCTAGTATGTAACCTTAAGACGCTGCTAATTTGACTGC 300
Db 1373 CATCTTAATTTCCAAATTAAGCTAGTATGTAACCTTAAGACGCTGCTAATTTGACTGC 1432
QY 301 CACTTGCACACTCAGGGGGGCGCTGCATTTTAAATGGTCAATGATTCACCTTTTATG 360
Db 1433 CACTTGCACACTCAGGGGGGCGCTGCATTTTAAATGGTCAATGATTCACCTTTTATG 1492
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Db 1493 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
QY 421 TGATCTAATTTTAAAGATAAACAGACAGTCCGGCGACACGATTTAATAAATACTGAG 480
Db 1553 TGATCTAATTTTAAAGATAAACAGACAGTCCGGCGACACGATTTAATAAATACTGAG 1612
QY 481 CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTAAT 540
Db 1613 CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTAAT 1672
QY 541 GGTCCAGGGAAGACCTTTCACCTTGACTATATGTC 576
Db 1673 GGTCCAGGGAAGACCTTTCACCTTGACTATATGTC 1708
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OM nucleic - nucleic search, using sw model

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18: /cgn2_6/prodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 576 | 100.0 | 1567 | 9 | US-09-884-441-74 |
| 2 | 576 | 100.0 | 1567 | 10 | US-09-907-969-74 |
| 3 | 576 | 100.0 | 1567 | 10 | US-09-827-271-74 |
| 4 | 576 | 100.0 | 1567 | 15 | US-10-198-053-74 |
| 5 | 576 | 100.0 | 1567 | 19 | US-10-860-790-74 |
| 6 | 576 | 100.0 | 1567 | 14 | US-10-860-790-74 |
| 7 | 576 | 100.0 | 1567 | 14 | US-10-860-790-74 |
| 8 | 576 | 100.0 | 1567 | 10 | US-09-814-353-19262 |
| 9 | 576 | 100.0 | 2591 | 9 | US-09-850-178-23 |
| 10 | 576 | 100.0 | 2627 | 9 | US-09-896-738-1 |
| 11 | 576 | 100.0 | 2627 | 9 | US-09-778-320-207 |
| | | | | 9 | US-09-910-689-207 |

| | | | | | | |
|----|-------|-------|------|----|---------------------|--------------------|
| 12 | 576 | 100.0 | 2627 | 9 | US-09-884-441-391 | Sequence 391, App |
| 13 | 576 | 100.0 | 2627 | 10 | US-09-907-969-391 | Sequence 391, App |
| 14 | 576 | 100.0 | 2627 | 10 | US-09-827-271-391 | Sequence 391, App |
| 15 | 576 | 100.0 | 2627 | 13 | US-10-010-742-207 | Sequence 207, App |
| 16 | 576 | 100.0 | 2627 | 15 | US-10-198-053-391 | Sequence 391, App |
| 17 | 576 | 100.0 | 2627 | 18 | US-10-714-389-207 | Sequence 207, App |
| 18 | 576 | 100.0 | 2627 | 18 | US-10-717-296-207 | Sequence 207, App |
| 19 | 576 | 100.0 | 2627 | 19 | US-10-860-790-391 | Sequence 391, App |
| 20 | 574.4 | 99.7 | 3357 | 17 | US-10-023-339-2 | Sequence 2, Appl1 |
| 21 | 550.8 | 95.6 | 2626 | 9 | US-09-877-065-7 | Sequence 7, Appl1 |
| 22 | 549 | 95.3 | 595 | 10 | US-09-814-353-257 | Sequence 257, App |
| 23 | 549 | 95.3 | 595 | 10 | US-09-814-353-6647 | Sequence 6647, App |
| 24 | 549 | 95.3 | 643 | 10 | US-09-814-353-13032 | Sequence 13032, A |
| 25 | 529.4 | 91.9 | 2626 | 17 | US-10-023-339-9 | Sequence 9, Appl1 |
| 26 | 499.8 | 86.8 | 1658 | 9 | US-09-989-722-290 | Sequence 290, App |
| 27 | 499.8 | 86.8 | 1658 | 9 | US-09-989-723-290 | Sequence 290, App |
| 28 | 499.8 | 86.8 | 1658 | 9 | US-09-989-727-290 | Sequence 290, App |
| 29 | 499.8 | 86.8 | 1658 | 9 | US-09-989-731-290 | Sequence 290, App |
| 30 | 499.8 | 86.8 | 1658 | 9 | US-09-989-732-290 | Sequence 290, App |
| 31 | 499.8 | 86.8 | 1658 | 9 | US-09-991-073-290 | Sequence 290, App |
| 32 | 499.8 | 86.8 | 1658 | 9 | US-09-991-163-290 | Sequence 290, App |
| 33 | 499.8 | 86.8 | 1658 | 9 | US-09-990-442-290 | Sequence 290, App |
| 34 | 499.8 | 86.8 | 1658 | 9 | US-09-991-163-290 | Sequence 290, App |
| 35 | 499.8 | 86.8 | 1658 | 9 | US-09-993-604-290 | Sequence 290, App |
| 36 | 499.8 | 86.8 | 1658 | 9 | US-09-990-456-290 | Sequence 290, App |
| 37 | 499.8 | 86.8 | 1658 | 9 | US-09-989-721-290 | Sequence 290, App |
| 38 | 499.8 | 86.8 | 1658 | 9 | US-09-992-598-290 | Sequence 290, App |
| 39 | 499.8 | 86.8 | 1658 | 9 | US-09-989-293A-290 | Sequence 290, App |
| 40 | 499.8 | 86.8 | 1658 | 9 | US-09-989-735-290 | Sequence 290, App |
| 41 | 499.8 | 86.8 | 1658 | 9 | US-09-990-444-290 | Sequence 290, App |
| 42 | 499.8 | 86.8 | 1658 | 9 | US-09-991-181-290 | Sequence 290, App |
| 43 | 499.8 | 86.8 | 1658 | 9 | US-09-989-731-290 | Sequence 290, App |
| 44 | 499.8 | 86.8 | 1658 | 9 | US-09-990-436-290 | Sequence 290, App |
| 45 | 499.8 | 86.8 | 1658 | 9 | US-09-993-687-290 | Sequence 290, App |

ALIGNMENTS

RESULT 1

US-09-884-441-74

Sequence 74, Application US/09884441

Patent No. US2002019158A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Carter, Darrick

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C7

CURRENT APPLICATION NUMBER: US/09/884,441

CURRENT FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 489

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 74

LENGTH: 1567

TYPE: DNA

ORGANISM: Homo sapien

US-09-884-441-74

| | | | | |
|-----------------------|-----------------|------------------------------------------------------------|-----------|--------------|
| Query Match | 100.0%; | Score 576; | DB 9; | Length 1567; |
| Best Local Similarity | 100.0%; | Pred. No. 1.5e-164; | | |
| Matches 576; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | TTCAAGACATATTAGAGTTGGGAAATATTCATGTGAACCTAGACAAGTGTGTTAGAGA | 60 | |
| DB | 91 | TTCAAGACATATTAGAGTTGGGAAATATTCATGTGAACCTAGACAAGTGTGTTAGAGA | 150 | |
| QY | 61 | GTCATAGTAATGACAGTGTGAGACAAAGTGCATCCCGATTCAGGACCTCCCTG | 120 | |
| DB | 151 | GTCATAGTAATGACAGTGTGAGACAAAGTGCATCCCGATTCAGGACCTCCCTG | 210 | |
| QY | 121 | CTGTACCTGGGAGTGAAGAGACAGATAGCATGTTCTTGTCTGAAATTTTAA | 180 | |

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Db 211 CCTGTACCTGGGAGTGAAGACAGATAGTGTCTTCTGTGAATTTTAG 270
QY 181 TTATATGCTGTATATGTTGCTCTGAGAGAGCCCTGAAAGCTATCCCAATATCCA 240
Db 271 TTATATGCTGTATATGTTGCTCTGAGAGAGCCCTGAAAGCTATATCCCAATATCCA 330
QY 241 CATCTTATATTCACAAATTTAAGCTGTATGTATCCCTAAGACGCTGTAAATTGACTGC 300
Db 331 CATCTTATATTCACAAATTTAAGCTGTATGTATCCCTAAGACGCTGTAAATTGACTGC 390
QY 301 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATATGGGTCAATATGATCACTTTTAG 360
Db 391 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATATGGGTCAATATGATCACTTTTAG 450
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Db 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 510
QY 421 TGATCATATTTTATGATTAACAGAGACAGTGGCGACACCGATTTTATTAATTAACCTGAG 480
Db 511 TGATCATATTTTATGATTAACAGAGACAGTGGCGACACCGATTTTATTAATTAACCTGAG 570
QY 481 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTGATGATGTTTCATCCGTGAT 540
Db 571 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTGATGATGTTTCATCCGTGAT 630
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 576
Db 631 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 666
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RESULT 2

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US-09-907-969-74
; Sequence 74, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-969-74
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Query Match 100.0%; Score 576; DB 10; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATATTAGAAGTTGGGAAAAATTAATTCATGTGAACATGACAGTGTGTTAAGA 60
Db 91 TTCAAAGACATATTAGAAGTTGGGAAAAATTAATTCATGTGAACATGACAGTGTGTTAAGA 150
QY 61 GTGATTAAGTAAATGACAGTGAAGACAGATGCCAGATCTCGGGACCTCCCTCG 120
Db 151 GTGATTAAGTAAATGACAGTGAAGACAGATGCCAGATCTCGGGACCTCCCTCG 210
QY 121 CCTGTACCTGGGAGTGAAGACAGATAGTGTCTTCTGTGAATTTTAG 180
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Db 211 CCTGTACCTGGGAGTGAAGACAGATAGTGTCTTCTGTGAATTTTAG 270
QY 181 TTATATGCTGTATATGTTGCTCTGAGAGAGCCCTGAAAGCTATCCCAATATCCA 240
Db 271 TTATATGCTGTATATGTTGCTCTGAGAGAGCCCTGAAAGCTATATCCCAATATCCA 330
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Db 331 CATCTTATATTCACAAATTTAAGCTGTATGTATCCCTAAGACGCTGTAAATTGACTGC 390
QY 301 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATATGGGTCAATATGATCACTTTTAG 360
Db 391 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATATGGGTCAATATGATCACTTTTAG 450
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Db 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 510
QY 421 TGATCATATTTTATGATTAACAGAGACAGTGGCGACACCGATTTTATTAATTAACCTGAG 480
Db 511 TGATCATATTTTATGATTAACAGAGACAGTGGCGACACCGATTTTATTAATTAACCTGAG 570
QY 481 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTGATGATGTTTCATCCGTGAT 540
Db 571 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTGATGATGTTTCATCCGTGAT 630
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 576
Db 631 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 666
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RESULT 3

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US-09-827-271-74
; Sequence 74, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-827-271-74
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Query Match 100.0%; Score 576; DB 10; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATATTAGAAGTTGGGAAAAATTAATTCATGTGAACATGACAGTGTGTTAAGA 60
Db 91 TTCAAAGACATATTAGAAGTTGGGAAAAATTAATTCATGTGAACATGACAGTGTGTTAAGA 150
QY 61 GTGATTAAGTAAATGACAGTGAAGACAGATGCCAGATCTCGGGACCTCCCTCG 120
Db 151 GTGATTAAGTAAATGACAGTGAAGACAGATGCCAGATCTCGGGACCTCCCTCG 210
QY 121 CCTGTACCTGGGAGTGAAGACAGATAGTGTCTTCTGTGAATTTTAG 180
Db 211 CCTGTACCTGGGAGTGAAGACAGATAGTGTCTTCTGTGAATTTTAG 270
QY 181 TTATATGCTGTATATGTTGCTCTGAGAGAGCCCTGAAAGCTATCCCAATATCCA 240
Db 271 TTATATGCTGTATATGTTGCTCTGAGAGAGCCCTGAAAGCTATCCCAATATCCA 330
QY 241 CATCTTATATTCACAAATTTAAGCTGTATGTATCCCTAAGACGCTGTAAATTGACTGC 300
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Db 331 CATCTATATATCCACAATTAAGCTAGATAGTACCTTAAGCGCTGTAATGATGCG 390
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Qy 361 ATGCTTCCAAAGGCGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTGGAGAAAA 420
Db 451 ATGCTTCCAAAGGCGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTGGAGAAAA 510
Qy 421 TGATCATATATTTTATGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATAACTGAG 480
Db 511 TGATCATATATTTTATGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATAACTGAG 570
Qy 481 CACCTTCTTTTAAACAACAATATCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 540
Db 571 CACCTTCTTTTAAACAACAATATCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 630
Qy 541 GGTCCAGGAGGACCTTTCACCTTGACTATATGCG 576
Db 631 GGTCCAGGAGGACCTTTCACCTTGACTATATGCG 666
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RESULT 4

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US-10-198-053-74
; Sequence 74, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Panger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-053-74
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Query Match 100.0%; Score 576; DB 15; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;

Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TTCAAAGACATATTAGAAGTTGGAAAAATTAATTCATGTGAACCTAGACAAGTGTGTTAAGA 60
Db 91 TTCAAAGACATATTAGAAGTTGGAAAAATTAATTCATGTGAACCTAGACAAGTGTGTTAAGA 150
Qy 61 GTGATAAGTAAATGACGCTGAGAGACAAGTGCATCCCGAGATCCAGAGACCTCCCGCTG 120
Db 151 GTGATAAGTAAATGACGCTGAGAGACAAGTGCATCCCGAGATCCAGAGACCTCCCGCTG 210
Qy 121 CCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTCGAAATTTTATG 180
Db 211 CCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTCGAAATTTTATG 270
Qy 181 TTATATGTGCTGTAATGTGCTGAGAGAAAGCCCTGAAAAGTCTATCCCAATATGCA 240
Db 271 TTATATGTGCTGTAATGTGCTGAGAGAAAGCCCTGAAAAGTCTATCCCAATATGCA 330
Qy 241 CATCTATATATCCACAATTAAGCTAGATAGTGAACCTTAAGACGCTGTAATGATGCTG 300
Db 331 CATCTATATATCCACAATTAAGCTAGATAGTGAACCTTAAGACGCTGTAATGATGCTG 390
Qy 301 CACTTGGCACTCAGGGGGCGCTGCATTTTATGTAATGGGTCAATGATTCACCTTTTATG 360
Db 391 CACTTGGCACTCAGGGGGCGCTGCATTTTATGTAATGGGTCAATGATTCACCTTTTATG 450
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Qy 361 ATGCTTCCAAAGGCGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTGGAGAAAA 420
Db 451 ATGCTTCCAAAGGCGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTGGAGAAAA 510
Qy 421 TGATCATATATTTTATGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATAACTGAG 480
Db 511 TGATCATATATTTTATGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATAACTGAG 570
Qy 481 CACCTTCTTTTAAACAACAATATCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 540
Db 571 CACCTTCTTTTAAACAACAATATCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 630
Qy 541 GGTCCAGGAGGACCTTTCACCTTGACTATATGCG 576
Db 631 GGTCCAGGAGGACCTTTCACCTTGACTATATGCG 666
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RESULT 5

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US-10-860-790-74
; Sequence 74, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Panger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-860-790-74
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Query Match 100.0%; Score 576; DB 19; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;

Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TTCAAAGACATATTAGAAGTTGGAAAAATTAATTCATGTGAACCTAGACAAGTGTGTTAAGA 60
Db 91 TTCAAAGACATATTAGAAGTTGGAAAAATTAATTCATGTGAACCTAGACAAGTGTGTTAAGA 150
Qy 61 GTGATAAGTAAATGACGCTGAGAGACAAGTGCATCCCGAGATCCAGAGACCTCCCGCTG 120
Db 151 GTGATAAGTAAATGACGCTGAGAGACAAGTGCATCCCGAGATCCAGAGACCTCCCGCTG 210
Qy 121 CCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTCGAAATTTTATG 180
Db 211 CCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTCGAAATTTTATG 270
Qy 181 TTATATGTGCTGTAATGTGCTGAGAGAAAGCCCTGAAAAGTCTATCCCAATATGCA 240
Db 271 TTATATGTGCTGTAATGTGCTGAGAGAAAGCCCTGAAAAGTCTATCCCAATATGCA 330
Qy 241 CATCTATATATCCACAATTAAGCTAGATAGTGAACCTTAAGACGCTGTAATGATGCTG 300
Db 331 CATCTATATATCCACAATTAAGCTAGATAGTGAACCTTAAGACGCTGTAATGATGCTG 390
Qy 301 CACTTGGCACTCAGGGGGCGCTGCATTTTATGTAATGGGTCAATGATTCACCTTTTATG 360
Db 391 CACTTGGCACTCAGGGGGCGCTGCATTTTATGTAATGGGTCAATGATTCACCTTTTATG 450
Qy 361 ATGCTTCCAAAGGCGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTGGAGAAAA 420
Db 451 ATGCTTCCAAAGGCGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTGGAGAAAA 510
Qy 421 TGATCATATATTTTATGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATAACTGAG 480
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|||||
Db 511 TGATCATATATTTAGCATTAACAGACAGCGCGACACCGATTTTATTAATAAATGAG 570
Qy 481 CACCTCTCTTTTAAACAAATGCGGTTTATTTCTAGATGATGCTCATCCGGAAT 540
Db 571 CACCTCTCTTTTAAACAAATGCGGTTTATTTCTAGATGATGCTCATCCGGAAT 630
Qy 541 GGTCCAGGAGAGACCTTTCACCTTACTATATGCG 576
Db 631 GGTCCAGGAGAGACCTTTCACCTTACTATATGCG 666

RESULT 6
US-10-198-846-13583
; Sequence 13583, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for windows version 4.0
; SEQ ID NO 13583
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 1484, 1497,
; LOCATION: 1554, 1578, 1585, 1591, 1596
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13583

Query Match 100.0%; Score 576; DB 14; Length 1596;
Best Local Similarity 100.0%; Pred. No. 1.6e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAAGACATATTAAGTTGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGA 60
Db 267 TTCAAGACATATTAAGTTGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGA 326
Qy 61 GTGATAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 327 GTGATAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 386
Qy 121 CCTGTACCTGGGAGTGAAGAGAGAGATGATGATGTTCTTTGCTCTGAATTTTAA 180
Db 387 CCTGTACCTGGGAGTGAAGAGAGATGATGATGTTCTTTGCTCTGAATTTTAA 446
Qy 181 TTATATGCTGTGAATGTTGCTTGAAGAACCCCTCGAAAGTCTATCCCAATATCCA 240
Db 447 TTATATGCTGTGAATGTTGCTTGAAGAACCCCTCGAAAGTCTATCCCAATATCCA 506
Qy 241 CATCTATATTCACAAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 300
Db 507 CATCTATATTCACAAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 566
Qy 301 CACTTGCACCTCAGGAGGCGCTGATTTTAAATGATGATGATGATGATGATGATGATG 360
Db 567 CACTTGCACCTCAGGAGGCGCTGATTTTAAATGATGATGATGATGATGATGATGATG 626
Qy 361 ATGCTTCAAAAGTGTGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Db 627 ATGCTTCAAAAGTGTGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 686

Qy 421 TGATCATATATTTAGCATTAACAGACAGCGCGACACCGATTTTATTAATAAATGAG 480
Db 687 TGATCATATATTTAGCATTAACAGACAGCGCGACACCGATTTTATTAATAAATGAG 746
Qy 481 CACCTCTCTTTTAAACAAATGCGGTTTATTTCTAGATGATGCTCATCCGGAAT 540
Db 747 CACCTCTCTTTTAAACAAATGCGGTTTATTTCTAGATGATGCTCATCCGGAAT 806
Qy 541 GGTCCAGGAGAGACCTTTCACCTTACTATATGCG 576
Db 807 GGTCCAGGAGAGACCTTTCACCTTACTATATGCG 842

RESULT 7
US-09-814-353-19262
; Sequence 19262, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for windows version 4.0
; SEQ ID NO 19262
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 1965
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-19262

Query Match 100.0%; Score 576; DB 10; Length 1965;
Best Local Similarity 100.0%; Pred. No. 1.7e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAAGACATATTAAGTTGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGA 60
Db 1130 TTCAAGACATATTAAGTTGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGA 1189
Qy 61 GTGATAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 1190 GTGATAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1249
Qy 121 CCTGTACCTGGGAGTGAAGAGAGATGATGATGTTCTTTGCTCTGAATTTTAA 180
Db 1250 CCTGTACCTGGGAGTGAAGAGAGATGATGATGTTCTTTGCTCTGAATTTTAA 1309
Qy 181 TTATATGCTGTGAATGTTGCTTGAAGAACCCCTCGAAAGTCTATCCCAATATCCA 240
Db 1310 TTATATGCTGTGAATGTTGCTTGAAGAACCCCTCGAAAGTCTATCCCAATATCCA 1369
Qy 241 CATCTATATTCACAAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 300

Db 1370 CATCTTATATTCACCAATTAAGCTAGATGATACCTTAAGCGCTGATTTGATGCG 1429
Qy 301 CACTTGGCAACTCAGGGGCGGCTGCAATTTAGTATGGGTCAATGATTCACCTTTATG 360
Db 1430 CACTTCCCAACTCAGGGGCGGCTGCAATTTAGTATGGGTCAATGATTCACCTTTATG 1489
Qy 361 ATGCTTCCAAAGGCTGCTGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Db 1490 ATGCTTCCAAAGGCTGCTGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1549
Qy 421 TGATCATTAATTTTATGACATAAAGAGAGAGTGGCGACACCGATTTTAAATAAAGTACG 480
Db 1550 TGATCATTAATTTTATGACATAAAGAGAGAGTGGCGACACCGATTTTAAATAAAGTACG 1609
Qy 481 CACCTTCTTTTAAACAAACAATGCGGCTTATTTCTCAGATGATGTCATCCGTGAAT 540
Db 1610 CACCTTCTTTTAAACAAACAATGCGGCTTATTTCTCAGATGATGTCATCCGTGAAT 1669
Qy 541 GGTCCAGGGAAGACCTTTCACCTTGACTATATGGC 576
Db 1670 GGTCCAGGGAAGACCTTTCACCTTGACTATATGGC 1705

RESULT 8

US-09-850-178-23
Sequence 23, Application US/09850178
Patent No. US20020034749A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Billings-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colipite, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Russell, John C.
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klags, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Stroupe, Stephen D.
APPLICANT: Gordon, Julian
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
FILE REFERENCE: 6251 US.P1
CURRENT APPLICATION NUMBER: US/09/850,178
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 2591
TYPE: DNA
ORGANISM: Homo sapiens
US-09-850-178-23

Query Match 100.0%; Score 576; DB 9; Length 2591;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAAAGACATATTAGAAAGTTGGAAATAATTCATGTGAACATGAGTGTGTTAAGA 60
Db 1111 TTCAAAGACATATTAGAAAGTTGGAAATAATTCATGTGAACATGAGTGTGTTAAGA 1170
Qy 61 GTGATAAGTAAATGACAGTGGAGACAAGTGCATCCCGAGATCTCAGGAGACTCCCGCTG 120
Db 1171 GTGATAAGTAAATGACAGTGGAGACAAGTGCATCCCGAGATCTCAGGAGACTCCCGCTG 1230
Qy 121 CCTGTCACTGGGAGGTGAGAGACAGAGATATGATGTTCTTTGCTGAAATTTTAA 180
Db 1231 CCTGTCACTGGGAGGTGAGAGACAGAGATATGATGTTCTTTGCTGAAATTTTAA 1290

Qy 181 TTATATGTGCTGATATGTTGCTCTGAGAGAAAGCCCTGAAAGGTCTATCCCAATATCCA 240
Db 1291 TTATATGTGCTGATATGTTGCTCTGAGAGAAAGCCCTGAAAGGTCTATCCCAATATCCA 1350
Qy 241 CATCTTATATTCACCAATTAATTAAGCTGTATGATGATGATGATGATGATGATGATGATG 300
Db 1351 CATCTTATATTCACCAATTAATTAAGCTGTATGATGATGATGATGATGATGATGATGATG 1410
Qy 301 CACTTGGCAACTCAGGGGCGGCTGCAATTTAGTATGGGTCAATGATTCACCTTTATG 360
Db 1411 CACTTGGCAACTCAGGGGCGGCTGCAATTTAGTATGGGTCAATGATTCACCTTTATG 1470
Qy 361 ATGCTTCCAAAGGCTGCTGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Db 1471 ATGCTTCCAAAGGCTGCTGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1530
Qy 421 TGATCATTAATTTTATGACATAAAGAGAGAGTGGCGACACCGATTTTAAATAAAGTACG 480
Db 1531 TGATCATTAATTTTATGACATAAAGAGAGAGTGGCGACACCGATTTTAAATAAAGTACG 1590
Qy 481 CACCTTCTTTTAAACAAACAATGCGGCTTATTTCTCAGATGATGTCATCCGTGAAT 540
Db 1591 CACCTTCTTTTAAACAAACAATGCGGCTTATTTCTCAGATGATGTCATCCGTGAAT 1650
Qy 541 GGTCCAGGGAAGACCTTTCACCTTGACTATATGGC 576
Db 1651 GGTCCAGGGAAGACCTTTCACCTTGACTATATGGC 1686

RESULT 9

US-09-896-738-1
Sequence 1, Application US/09896738
Patent No. US20020165347A1
GENERAL INFORMATION:
APPLICANT: Fox, Michael
APPLICANT: Sullivan, John K.
APPLICANT: Pang, Mei
TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
FILE REFERENCE: 00-513-A
CURRENT APPLICATION NUMBER: US/09/896,738
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,645
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2603
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (53)..(901)
US-09-896-738-1

Query Match 100.0%; Score 576; DB 9; Length 2603;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAAAGACATATTAGAAAGTTGGAAATAATTCATGTGAACATGAGTGTGTTAAGA 60
Db 1103 TTCAAAGACATATTAGAAAGTTGGAAATAATTCATGTGAACATGAGTGTGTTAAGA 1162
Qy 61 GTGATAAGTAAATGACAGTGGAGACAAGTGCATCCCGAGATCTCAGGAGACTCCCGCTG 120
Db 1163 GTGATAAGTAAATGACAGTGGAGACAAGTGCATCCCGAGATCTCAGGAGACTCCCGCTG 1222
Qy 121 CCTGTCACTGGGAGGTGAGAGACAGATATGATGTTCTTTGCTGAAATTTTAA 180
Db 1223 CCTGTCACTGGGAGGTGAGAGACAGATATGATGTTCTTTGCTGAAATTTTAA 1282
Qy 181 TTATATGTGCTGATATGTTGCTCTGAGAGAAAGCCCTGAAAGGTCTATCCCAATATCCA 240
Db 1283 TTATATGTGCTGATATGTTGCTCTGAGAGAAAGCCCTGAAAGGTCTATCCCAATATCCA 1342

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QY 241 CATCTATATTCACAAATTAAGCTGTAGATGACCTTAAGACGCTGCTAAATGACTGC 300
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Db 1343 CATCTATATTCACAAATTAAGCTGTAGATGACCTTAAGACGCTGCTAAATGACTGC 1402
QY 301 CACTTGCAGCACTCAGGGGGGGCTGCATTTTAAATGGGTCAATGATTCACCTTTTATG 360
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Db 1403 CACTTGCAGCACTCAGGGGGGGCTGCATTTTAAATGGGTCAATGATTCACCTTTTATG 1462
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
    |||
Db 1463 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1522
QY 421 TGATCATATTTTAAAGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATTAATCTGAG 480
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Db 1523 TGATCATATTTTAAAGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATTAATCTGAG 1582
QY 481 CACCTTCTTTTAAACAAATGCGGGTTTATTTCTGAGATGATGTTCACTCGTGAAT 540
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Db 1583 CACCTTCTTTTAAACAAATGCGGGTTTATTTCTGAGATGATGTTCACTCGTGAAT 1642
QY 541 GGTCCAGGAGAGACCTTTCACTTGAATATGCG 576
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Db 1643 GGTCCAGGAGAGACCTTTCACTTGAATATGCG 1678
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RESULT 10

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US-09-778-320-207
; Sequence 207, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-320-207
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Query Match 100.0%; Score 576; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATATTAGAAGTTGGGAAATTAATTCATGTGACATGACCAAGTGTGTTAAGA 60
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Db 1133 TTCAAAGACATATTAGAAGTTGGGAAATTAATTCATGTGACATGACCAAGTGTGTTAAGA 1192
QY 61 GTGATTAAGTAAATGACAGTGGAGACAGATGCAATCCCAAGATTCAGGAGCCTCCCTCG 120
    |||
Db 1193 GTGATTAAGTAAATGACAGTGGAGACAGATGCAATCCCAAGATTCAGGAGCCTCCCTCG 1252
QY 121 CCTGTCACTGGGGAGTGAAGACAGATAGTGCATGTTCTTGTCTCTGAAATTTTATG 180
    |||
Db 1253 CCTGTCACTGGGGAGTGAAGACAGATAGTGCATGTTCTTGTCTCTGAAATTTTATG 1312
QY 181 TTATATGTGCTGAATGTTGCTCTGAGAGAACCCCTGAGAAAGTCTATCCCAATATCA 240
    |||
Db 1313 TTATATGTGCTGAATGTTGCTCTGAGAGAACCCCTGAGAAAGTCTATCCCAATATCA 1372
QY 241 CATCTTATATTCACAAATTAAGCTGTAGATGACCTTAAGACGCTGCTAAATGACTGC 300
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Db 1373 CATCTTATATTCACAAATTAAGCTGTAGATGACCTTAAGACGCTGCTAAATGACTGC 1432
QY 301 CACTTGCAGCACTCAGGGGGGGCTGCATTTTAAATGGGTCAATGATTCACCTTTTATG 360
    |||
Db 1433 CACTTGCAGCACTCAGGGGGGGCTGCATTTTAAATGGGTCAATGATTCACCTTTTATG 1492
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
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Db 1493 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
QY 421 TGATCATATTTTAAAGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATTAATCTGAG 480
    |||
Db 1553 TGATCATATTTTAAAGATTAAGACAGAGAGTGGCGACACCGATTTTATTAATTAATCTGAG 1612
QY 481 CACCTTCTTTTAAACAAATGCGGGTTTATTTCTGAGATGATGTTCACTCGTGAAT 540
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Db 1613 CACCTTCTTTTAAACAAATGCGGGTTTATTTCTGAGATGATGTTCACTCGTGAAT 1672
QY 541 GGTCCAGGAGAGACCTTTCACTTGAATATGCG 576
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Db 1673 GGTCCAGGAGAGACCTTTCACTTGAATATGCG 1708
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RESULT 11

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US-09-910-689-207
; Sequence 207, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-689-207
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Query Match 100.0%; Score 576; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATATTAGAAGTTGGGAAATTAATTCATGTGACATGACCAAGTGTGTTAAGA 60
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Db 1133 TTCAAAGACATATTAGAAGTTGGGAAATTAATTCATGTGACATGACCAAGTGTGTTAAGA 1192
QY 61 GTGATTAAGTAAATGACAGTGGAGACAGATGCAATCCCAAGATTCAGGAGCCTCCCTCG 120
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Db 1193 GTGATTAAGTAAATGACAGTGGAGACAGATGCAATCCCAAGATTCAGGAGCCTCCCTCG 1252
QY 121 CCTGTCACTGGGGAGTGAAGACAGATAGTGCATGTTCTTGTCTCTGAAATTTTATG 180
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Db 1253 CCTGTCACTGGGGAGTGAAGACAGATAGTGCATGTTCTTGTCTCTGAAATTTTATG 1312
QY 181 TTATATGTGCTGAATGTTGCTCTGAGAGAACCCCTGAGAAAGTCTATCCCAATATCA 240
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Db 1313 TTATATGTGCTGAATGTTGCTCTGAGAGAACCCCTGAGAAAGTCTATCCCAATATCA 1372
QY 241 CATCTTATATTCACAAATTAAGCTGTAGATGACCTTAAGACGCTGCTAAATGACTGC 300
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Db 1373 CATCTTATATTCACAAATTAAGCTGTAGATGACCTTAAGACGCTGCTAAATGACTGC 1432
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QY 301 CACTTGGCACTGAGGGGCGCTGCTATTTAGTAATGGGTCAAAATGATTCACCTTTATG 360
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Db 1433 CACTTGGCACTGAGGGGCGCTGCTATTTAGTAATGGGTCAAAATGATTCACCTTTATG 1492
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QY 361 ATGCTTCAAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
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Db 1493 ATGCTTCAAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
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QY 421 TGATCATTAATTTTAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
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Db 1553 TGATCATTAATTTTAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612
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|
|
QY 481 CACCTTCTTTTAAACAAACAAATGCGAGTTTATTTCTCAGATGATGATCCGTAAT 540
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|
|
Db 1613 CACCTTCTTTTAAACAAACAAATGCGAGTTTATTTCTCAGATGATGATCCGTAAT 1672
|
|
|
QY 541 GGTCCAGGAGGAGACCTTTGACCTTGACTATATGGC 576
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|
|
Db 1673 GGTCCAGGAGGAGACCTTTGACCTTGACTATATGGC 1708
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|
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```

RESULT 12

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US-09-884-441-391
; Sequence 391, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-441-391
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Query Match 100.0%; Score 576; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAGACATATTAGAGTTGGGAAAATTAATCATGTGAACCTAGACAGTGTGTTAAGA 60
|
|
|
Db 1133 TTCAAGACATATTAGAGTTGGGAAAATTAATCATGTGAACCTAGACAGTGTGTTAAGA 1192
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|
QY 61 GTGATTAAGTAAATGACGCTGAGAGACAGATGATCCCAATCTCAGGAGCTCCCTCG 120
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|
|
Db 1193 GTGATTAAGTAAATGACGCTGAGAGACAGATGATCCCAATCTCAGGAGCTCCCTCG 1252
|
|
|
QY 121 CCTGTCACTGGGAGTGAAGAGACAGATGATCCCAATCTCAGGAGCTCCCTCG 180
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|
|
Db 1253 CCTGTCACTGGGAGTGAAGAGACAGATGATCCCAATCTCAGGAGCTCCCTCG 1312
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QY 181 TTATATGTGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGTCTATCCCAACATATCA 240
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|
Db 1313 TTATATGTGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGTCTATCCCAACATATCA 1372
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|
QY 241 CATCTTATATTTCCAAATTAAGCTGTAGTATGATCCCTTAAGAGCTGCTGTAATGATGC 300
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|
Db 1373 CATCTTATATTTCCAAATTAAGCTGTAGTATGATCCCTTAAGAGCTGCTGTAATGATGC 1432
|
|
|
QY 301 CACTTGGCACTGAGGGGCGCTGCTATTTAGTAATGGGTCAAAATGATTCACCTTTATG 360
|
|
|
Db 1433 CACTTGGCACTGAGGGGCGCTGCTATTTAGTAATGGGTCAAAATGATTCACCTTTATG 1492
|
|
|
QY 361 ATGCTTCAAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
|
|
|
Db 1493 ATGCTTCAAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
|
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```

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QY 421 TGATCATTAATTTTAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
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|
|
Db 1553 TGATCATTAATTTTAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612
|
|
|
QY 481 CACCTTCTTTTAAACAAACAAATGCGAGTTTATTTCTCAGATGATGATCCGTAAT 540
|
|
|
Db 1613 CACCTTCTTTTAAACAAACAAATGCGAGTTTATTTCTCAGATGATGATCCGTAAT 1672
|
|
|
QY 541 GGTCCAGGAGGAGACCTTTGACCTTGACTATATGGC 576
|
|
|
Db 1673 GGTCCAGGAGGAGACCTTTGACCTTGACTATATGGC 1708
|
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|
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RESULT 13

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US-09-907-969-391
; Sequence 391, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Hall, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-969-391
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Query Match 100.0%; Score 576; DB 10; Length 2627;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAGACATATTAGAGTTGGGAAAATTAATCATGTGAACCTAGACAGTGTGTTAAGA 60
|
|
|
Db 1133 TTCAAGACATATTAGAGTTGGGAAAATTAATCATGTGAACCTAGACAGTGTGTTAAGA 1192
|
|
|
QY 61 GTGATTAAGTAAATGACGCTGAGAGACAGATGATCCCAATCTCAGGAGCTCCCTCG 120
|
|
|
Db 1193 GTGATTAAGTAAATGACGCTGAGAGACAGATGATCCCAATCTCAGGAGCTCCCTCG 1252
|
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|
QY 121 CCTGTCACTGGGAGTGAAGAGACAGATGATCCCAATCTCAGGAGCTCCCTCG 180
|
|
|
Db 1253 CCTGTCACTGGGAGTGAAGAGACAGATGATCCCAATCTCAGGAGCTCCCTCG 1312
|
|
|
QY 181 TTATATGTGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGTCTATCCCAACATATCA 240
|
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|
Db 1313 TTATATGTGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGTCTATCCCAACATATCA 1372
|
|
|
QY 241 CATCTTATATTTCCAAATTAAGCTGTAGTATGATCCCTTAAGAGCTGCTGTAATGATGC 300
|
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|
Db 1373 CATCTTATATTTCCAAATTAAGCTGTAGTATGATCCCTTAAGAGCTGCTGTAATGATGC 1432
|
|
|
QY 301 CACTTGGCACTGAGGGGCGCTGCTATTTAGTAATGGGTCAAAATGATTCACCTTTATG 360
|
|
|
Db 1433 CACTTGGCACTGAGGGGCGCTGCTATTTAGTAATGGGTCAAAATGATTCACCTTTATG 1492
|
|
|
QY 361 ATGCTTCAAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
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Db 1493 ATGCTTCAAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
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Db 1613 CACCTTCTTTTAAACAACAANGCGGTTTATTCTCAGATGATGTTCTATCCGTGAT 1672
Qy 541 GGTCCAGGGAAGACCTTTCACTTGACTATATGGC 576
Db 1673 GGTCCAGGGAAGACCTTTCACTTGACTATATGGC 1708

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Job time : 396.201 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
9786.800 Million cell updates/sec

Title: US-09-763-978B-10

Perfect score: 576

Sequence: 1 ttcaagacatattagaatg.....ttcacctgacatattgac 576

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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7: gb_est7:*
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9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 574.4 | 99.7 | 2431 | 7 | CR603772 full-length |
| 2 | 562.4 | 97.6 | 610 | 3 | CN259817 17006000 |
| 3 | 526.4 | 91.4 | 939 | 5 | BX371687 BX371687 |
| 4 | 523 | 90.8 | 622 | 7 | CN259814 17006001 |
| 5 | 440.6 | 76.5 | 455 | 2 | BE083024 RC2-BT064 |
| 6 | 433.4 | 75.2 | 624 | 7 | CN259815 17006000 |
| 7 | 421 | 73.1 | 779 | 6 | CA311913 UT-CF-FNO |
| 8 | 419.8 | 72.9 | 661 | 2 | BE741325 601594166 |
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| 11 | 281 | 48.8 | 698 | 7 | CN259812 17006001 |
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| 14 | 121.4 | 21.1 | 925 | 5 | AX369964 BX369964 |
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| 16 | 94.6 | 16.4 | 812 | 8 | BH280041 CH230-109 |
| 17 | 92 | 16.0 | 255 | 7 | CR903676 1663C03.Y |
| 18 | 90.4 | 15.7 | 351 | 1 | AI698956 w31h09.x |
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| 21 | 76 | 13.2 | 530 | 4 | BI963964 1663C03.Y |
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| 23 | 41.8 | 7.3 | 507 | 8 | AZ332474 1M061B01 |
| 24 | 40.8 | 7.1 | 658 | 9 | AG147829 Pan trogl |

| | | | | | | |
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| 25 | 40.4 | 7.0 | 501 | 8 | BH697243 | BH697243 BOMFOX6TR |
| 26 | 40.2 | 7.0 | 1031 | 9 | CNS00CF2 | AL059199 Drosophila |
| 27 | 40 | 6.9 | 1190 | 3 | CR719416 | CR719416 Terradon |
| 28 | 39 | 6.8 | 1101 | 9 | CNS0151S | AL105502 Drosophila |
| 29 | 38.8 | 6.7 | 302 | 5 | BP068460 | BP068460 BP068460 |
| 30 | 38.8 | 6.7 | 567 | 8 | B2205357 | B2205357 CH230-436 |
| 31 | 38.2 | 6.6 | 523 | 1 | AL601909 | AL601909 DKRP213P |
| 32 | 38 | 6.6 | 755 | 5 | BU258011 | BU258011 603747820 |
| 33 | 37.8 | 6.6 | 539 | 7 | CV401235 | CV401235 QV4-NN114 |
| 34 | 37.8 | 6.6 | 912 | 9 | CG191398 | CG191398 PUCAC65TD |
| 35 | 37.8 | 6.6 | 926 | 9 | CG191397 | CG191397 PUCAC65TB |
| 36 | 37.6 | 6.5 | 524 | 6 | CA667778 | CA667778 w1Leul.pko |
| 37 | 37.6 | 6.5 | 843 | 9 | CL426387 | CL426387 ZMMBB044 |
| 38 | 37.4 | 6.5 | 746 | 5 | BU258987 | BU258987 603743026 |
| 39 | 37.4 | 6.5 | 799 | 5 | BX137735 | BX137735 Dario rer |
| 40 | 37.4 | 6.5 | 839 | 5 | BU111185 | BU111185 603127240 |
| 41 | 37.4 | 6.5 | 894 | 5 | BU355366 | BU355366 603473992 |
| 42 | 37.2 | 6.5 | 576 | 9 | CL372745 | CL372745 RPI144.30 |
| 43 | 37.2 | 6.5 | 748 | 9 | CR339430 | CR339430 Medicago |
| 44 | 37.2 | 6.5 | 1016 | 8 | CC270576 | CC270576 CH261-119 |
| 45 | 37.2 | 6.5 | 1201 | 9 | CNS010CB | AL098789 Drosophila |

ALIGNMENTS

| | | | | | |
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| RESULT 1 | CR603772 | 2431 bp | mrna | linear | HTC 21-JUN-2004 |
| LOCUS | CR603772 | 2431 bp | mrna | linear | HTC 21-JUN-2004 |
| DEFINITION | full-length cDNA clone CS0D1039YG21 of Placenta Cot 25-normalized | | | | |
| ACCESSION | CR603772 | | | | |
| VERSION | CR603772.1 | GI:50484579 | | | |
| KEYWORDS | HTC; CNSUT_cDNA | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | 1 (bases 1 to 2431) | | | | |
| AUTHORS | Li, W.B., Gruber, C., Jesse, J., and Polyes, D. | | | | |
| TITLE | Full-length cDNA libraries and normalization | | | | |
| JOURNAL | Unpublished | | | | |
| REMARK | Contact: Peng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue | | | | |
| REFERENCE | 2 (bases 1 to 2431) | | | | |
| AUTHORS | Genoscope. | | | | |
| TITLE | Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage | | | | |
| JOURNAL | BP 191 91006 EXRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr) | | | | |
| COMMENT | Web: www.genoscope.cns.fr | | | | |
| | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1. 2431 | | | | |
| | /organism="Homo sapiens" | | | | |
| | /mol_type="mrna" | | | | |
| | /db_xref="taxon:9606" | | | | |
| | /clone="CS0D1039YG21" | | | | |
| | /cistype="Placenta Cot 25-normalized" | | | | |
| | /plasmid="pCMVSPORT_6" | | | | |
| ORIGIN | | | | | |
| Query Match | 99.7% | Score 574.4 | DB 3 | Length 2431 | |
| Best Local Similarity | 99.8% | Pred. No. 2e-154 | 1 | Indels 0 | Gaps 0 |
| Matches | 575 | Conservative | 0 | Mismatches | 1 |
| Qy | 1 | TTCAAGACATATTAGAGTTGGAAATATTCATGTAACATAGCAAGTGTGTTAAG | 60 | | |
| Db | 982 | TTCAAGACATATTAGAGTTGGAAATATTCATGTAACATAGCAAGTGTGTTAAG | 1041 | | |

| | | | | |
|------------|-------------------------------------------------------------------|--------|----------------------------------------------------------------|------------------------|
| Oy | | 61 | GMGATTAAGTAAATGACGTGGAGACAGTGCAATCCCGAATCTCAGGACCTCCCCCTG | 120 |
| Dd | | 1042 | GGATTAAATGAATAATGCACGTGGAGACAAGTCGATCCCAAGATCTCAGGACCTCCCCCTG | 1101 |
| Oy | | 121 | CCTGTCACTCTGGGGAGTGAGAGA CAGAGATAGTGATCTTTCTCTCTGAATTTTTAG | 180 |
| Dd | | 1102 | CCTGTCACTCTGGGGAGTGAGAGA CAGAGATAGTGATCTTTCTCTCTGAATTTTTAG | 1161 |
| Oy | | 181 | TTATATATGCTGTATATGTTGCTCTGAGGAAGCCCTGGAAAAGTCTATCCCAACTATCCA | 240 |
| Dd | | 1162 | TTATATATGCTGTATATGTTGCTCTGAGGAAGCCCTGGAAAAGTCTATCCCAACTATCCA | 1221 |
| Oy | | 241 | CATCTTATATTTCCACAATTAAGCTGTATGTAATGACCCTAAGACGCTCTAATTTGACTGC | 300 |
| Dd | | 1222 | CATCTTATATTTCCACAATTAAGCTGTATGTAATGACCCTAAGACGCTCTAATTTGACTGC | 1281 |
| Oy | | 301 | CAC TTCGCAACTCAGGGCGGCTGCA TTTTAGTAATGAGGTCMAATGATTCAC TTTTATG | 360 |
| Dd | | 1282 | CAC TTCGCAACTCAGGGCGGCTGCA TTTTAGTAATGAGGTCMAATGATTCAC TTTTATG | 1341 |
| Oy | | 361 | ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCAC TGCAAAATGCCAAATGTTGAGAAAA | 420 |
| Dd | | 1342 | ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCAC TGCAAAATGCCAAATGTTGAGAAAA | 1401 |
| Oy | | 421 | TGATCATATATTTTAGCATTAACAGACAGTGGCGCACACCGATTTTAAATTAATAACTGAG | 480 |
| Dd | | 1402 | TGATCATATATTTTAGCATTAACAGACAGTGGCGCACACCGATTTTAAATTAATAACTGAG | 1461 |
| Oy | | 481 | CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAT | 540 |
| Dd | | 1462 | CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAT | 1521 |
| Oy | | 541 | GCTCAGGAGAGACCTTTCACCTTGACATATATGSC | 576 |
| Dd | | 1522 | GCTCAGGAGAGACCTTTCACCTTGACATATATGSC | 1557 |
| RESULT 2 | | | | |
| LOCUS | CN259817 | 610 bp | mRNA | linear EST 16-MAY-2004 |
| DEFINITION | 17000600024783 GRN_FREHP Homo sapiens cDNA 5', mRNA sequence. | | | |
| ACCESSION | CN259817 | | | |
| VERSION | CN259817.1 GI:47276231 | | | |
| KEYWORDS | EST. | | | |
| SOURCE | Homo sapiens (human) | | | |
| ORGANISM | Homo sapiens | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| | 1 (bases 1 to 610) | | | |
| | Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., | | | |
| | Li,Y., Xu,C., Fang,R., Guelter,K., Rao,M.S., Mandlam,R., | | | |
| | Lebkowski,J and Stanton,L.W. | | | |
| | transcriptome characterization elucidates signaling networks that | | | |
| | control human ES cell growth and differentiation | | | |
| | Nat. Biotechnol. 22 (6), 707-716 (2004) | | | |
| JOURNAL | Contact: Brandenberger R | | | |
| COMMENT | Regenerative Medicine | | | |
| | Genon Corporation | | | |
| | 230 Constitution Drive, Menlo Park, CA 94025, USA | | | |
| | Tel: 650 473 8658 | | | |
| | Fax: 650 473 7760 | | | |
| | Email: rbrandenberger@genon.com | | | |
| | Insert Length: 610 Std Error: 0.00. | | | |
| FEATURES | location/Qualifiers | | | |
| source | 1..610 | | | |
| | /organism="Homo sapiens" | | | |
| | /mol_type="mRNA" | | | |
| | /db_xref="taxon:9606" | | | |
| | /tissue_type="embryonic stem cells, | | | |
| | line" | | | |
| | /clone_lib="GRN_FREHP" | | | |
| | /note="Oligo dt primed, full-length enriched cDNA library | | | |

ORIGIN

from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

| | | | | |
|-----------------------|----------------|--------------------|----------|------------|
| Query Match | 97.6% | Score 562 | DB 7 | Length 610 |
| Best Local Similarity | 100.0% | Pred. NO. 5.4e-151 | | |
| Matches 562 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

| QY | 15 | AGAAGTTGGGAAAAATTAATTCATGTGAACTGACAAAGTGTGTAAGAGTAACTAAAT | 74 |
|------------|-------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|-----|
| Db | 6 | AGAAATTGGGAAAAATTAATTCATGTGAACTGACAAAGTGTGTAAGAGTAACTAAAT | 65 |
| QY | 75 | GCACGTGAGACAAAGTGCATCCCAAGATCTTCAGGAACTCCCTGCCTGTCACTTGAGG | 134 |
| Db | 66 | GCACTGTGAGACAAAGTGCATCCCAAGATCTTCAGGAACTCCCTGCCTGTCACTTGAGG | 125 |
| QY | 135 | AGTAGAGAGACAGAGATAGTGCATGTTCTTTGTCTCTGAAATTTTAAGTAAATGAGCTGTA | 194 |
| Db | 126 | AGTAGAGAGACAGAGATAGTGCATGTTCTTTGTCTCTGAAATTTTAAGTAAATGAGCTGTA | 185 |
| QY | 195 | ATGTTGCTCTGAGGAAGGCCCTGGAAAGTCTATCCCAACATATCCACATCTTAATTTCCA | 254 |
| Db | 186 | ATGTTGCTCTGAGGAAGGCCCTGGAAAGTCTATCCCAACATATCCACATCTTAATTTCCA | 245 |
| QY | 255 | CAAAATTAAAGCTGTAGTATGTATACCCCTAAGACGCTGCTAATTAAGACCTTGCGAACTCA | 314 |
| Db | 246 | CAAAATTAAAGCTGTAGTATGTATACCCCTAAGACGCTGCTAATTAAGACCTTGCGAACTCA | 305 |
| QY | 315 | GGGGCGGCTGATTTTATGTAATGGGTCAAAATGATTCATTTTATGATGCTTCCAAAGGT | 374 |
| Db | 306 | GGGGCGGCTGATTTTATGTAATGGGTCAAAATGATTCATTTTATGATGCTTCCAAAGGT | 365 |
| QY | 375 | GCCTTGGCTTCTCTCCCAACTGACAAATGCGCAAGTGGAGAAAAATGATCATTAATTTTA | 434 |
| Db | 366 | GCCTTGGCTTCTCTCCCAACTGACAAATGCGCAAGTGGAGAAAAATGATCATTAATTTTA | 425 |
| QY | 435 | GCATTAACACAGACAGTGGCGACACCCGATTTTAATTAATTAACATGACACCTTCTTTTAA | 494 |
| Db | 426 | GCATTAACACAGACAGTGGCGACACCCGATTTTAATTAATTAACATGACACCTTCTTTTAA | 485 |
| QY | 495 | ACAAACAAATCCGGGGTTTATTTCTCAGATGATGTTCAATCCGTGAATGGTCCAGGGAAGGA | 554 |
| Db | 486 | ACAAACAAATCCGGGGTTTATTTCTCAGATGATGTTCAATCCGTGAATGGTCCAGGGAAGGA | 545 |
| QY | 555 | CCTTTCACTTGCATTAATGCG 576 | |
| Db | 546 | CCTTTCACTTGCATTAATGCG 567 | |
| RESULT 3 | | | |
| LOCUS | EX371687/c | | |
| DEFINITION | EX371687 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA | | |
| ACCESSION | EX371687 | | |
| VERSION | EX371687.2 | | |
| KEYWORDS | EST. | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | |
| AUTHORS | Li, W.B., Gruber, C., Jesssee, J. and Polayes, D. | | |
| TITLE | Full-length cDNA libraries and normalization | | |
| JOURNAL | Unpublished (2001) | | |
| COMMENT | On May 8, 2003 this sequence version replaced gi:30459784. | | |
| | Contact: Genoscope | | |
| | Genoscope - Centre National de Sequencage | | |
| | 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE | | |
| | Email: sefre@genoscope.cns.fr, Web : www.genoscope.cns.fr | | |
| | 1st strand cDNA was primed with a NotI-cis(dAT) primer. Five primers | | |
| | end enriched, double-strand cDNA was digested with Not I and cloned | | |
| | into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library | | |

was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 742.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS08A1021B08_CS01978_1ec=742.r.

FEATURES

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1. .939
/organism="Homo sapiens"
/mol_type="mRNA"
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/notes="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

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Query Match          91.4%; Score 526.4; DB 5; Length 939;
Best Local Similarity 98.4%; Pred. No. 1.2e-140;
Matches 571; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

QY      1  TTCAAAGACATA-TTGAAGTTGGGAAATTA-TTCATGTGAAGTACAGAG-TGTGTTA 57
DB      930  TTCAAAGACATATTGAAGTTGGGAAATTA-TTCATGTGAAGTACAGAG-TGTGTTA 871
QY      58  AGAGTGTAAATGAATGACGCTGGAGACAGATGATCCCAAGATCTCAGGA-CTTCC 116
DB      870  AGAGTGTAAATGAATGACGCTGGAGACAGATGATCCCAAGATCTCAGGAAGCCCTCC 811
QY      117  CCGCCGTGACCTGGGAGTGAAGAGCAGATGATGATGCTTGTCTGTGAATTT 176
DB      810  CCGCCGTGACCTGGGAGTGAAGAGCAGATGATGATGCTTGTCTGTGAATTT 751
QY      177  TTAGTTATATGCTGTATGTTGCTCTGAGGAAGCCCTGGAAGTCTATCCACATA 236
DB      750  TTAGTTATATGCTGTATGTTGCTCTGAGGAAGCCCTGGAAGTCTATCCACATA 691
QY      237  TTCACATCTTATATTCACAATTAAGCTGTATGATGATCCCTAAGCGTCTAATGA 296
DB      690  TTCACATCTTATATTCACAATTAAGCTGTATGATGATCCCTAAGCGTCTAATGA 631
QY      297  CTGCACTTGGCACTCAGGGGCGGCTGATTTAGTAAGGTCGAATGATTCACCTTT 356
DB      630  CTGCACTTGGCACTCAGGGGCGGCTGATTTAGTAAGGTCGAATGATTCACCTTT 571
QY      357  TATGATGCTTCCAAAGGTCCTGCTTCTCCCACTGACAAATGCCAAAGTTGAGA 416
DB      570  TATGATGCTTCCAAAGGTCCTGCTTCTCCCACTGACAAATGCCAAAGTTGAGA 511
QY      417  AAAATGATCAATATTTAGCATTAACAGAGCAGTGGCGGACACCGATTTATTAATAC 476
DB      510  AAAATGATCAATATTTAGCATTAACAGAGCAGTGGCGGACACCGATTTATTAATAC 451
QY      477  TGAGCACTCTTTTAAACAATTTGGGGTTATTTCTGATGATGATGATTCACCTT 536
DB      450  TGAGCACTCTTTTAAACAATTTGGGGTTATTTCTGATGATGATGATTCACCTT 391
QY      537  GAATGTCAGGAGACCTTTCACCTTACTATATGCG 576
DB      390  GAATGTCAGGAGACCTTTCACCTTACTATATGCG 351
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RESULT 4
CN259814      622 bp      mRNA      linear      EST 16-MAY-2004
LOCUS        17006000107256 GRN_PREHER Homo sapiens cDNA 5', mRNA sequence.
DEFINITION   CN259814
ACCESSION    CN259814
VERSION      CN259814.1 GI:47276228
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
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REFERENCE

1 (bases 1 to 622)
Brandenberger R., Wei H., Zhang S., Lei S., Muraige J., Fisk G.J., Li Y., Xu C., Fang R., Guegler K., Rao M.S., Mandalam R., Lebkowski J and Stanton L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)

TITLE

JOURNAL

COMMENT

Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 7658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 622 Std Error: 0.00.
Location/Qualifiers

FEATURES

source

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1. .622
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/mol_type="mRNA"
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/issue_type="embryonic stem cells, DMSO-treated H9 cell line"
/notes="oligo dt primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"
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ORIGIN

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Query Match          90.8%; Score 523; DB 7; Length 622;
Best Local Similarity 100.0%; Pred. No. 1e-119;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTCAAAGACATATTAGAAGTTGGGAAATTAATTCATGTGAAGTACAGCAAGTGTTAAGA 60
DB      100  TTCAAAGACATATTAGAAGTTGGGAAATTAATTCATGTGAAGTACAGCAAGTGTTAAGA 159
QY      61  GTGATTAATTAATGACAGCTGGAGACAGATGATCCCAAGATCTCAGGAGCTCCCTG 120
DB      160  GTGATTAATTAATGACAGCTGGAGACAGATGATCCCAAGATCTCAGGAGCTCCCTG 219
QY      121  CCTGCACTGGGAGTGAAGAGCAGATGATGATGCTTGTCTGTGAATTTTAA 180
DB      220  CCTGCACTGGGAGTGAAGAGCAGATGATGATGCTTGTCTGTGAATTTTAA 279
QY      181  TTATATGCTGTATGATGCTCTGAGGAAGCCCTGGAAGTCTATCCACATATCCA 240
DB      280  TTATATGCTGTATGATGCTCTGAGGAAGCCCTGGAAGTCTATCCACATATCCA 339
QY      241  CATCTTATATTCACAATTAAGCTGTATGATGATCCCTAAGCGTCTAATGACTGC 300
DB      340  CATCTTATATTCACAATTAAGCTGTATGATGATCCCTAAGCGTCTAATGACTGC 399
QY      301  CACTTGGCACTCAGGGGCGGCTGATTTAGTAAGGTCGAATGATTCACCTTTTATG 360
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QY      361  ATGCTTCCAAAGGTCCTTGCTTCTCCCACTGACCAATGCCAAAGTTGAGAAAA 420
DB      460  ATGCTTCCAAAGGTCCTTGCTTCTCCCACTGACCAATGCCAAAGTTGAGAAAA 519
QY      421  TGATCATATTTTGAATTAACAGAGCAGTGGCGGACACCGATTTTATTAATTAAGTAG 480
DB      520  TGATCATATTTTGAATTAACAGAGCAGTGGCGGACACCGATTTTATTAATTAAGTAG 579
QY      481  CACCTTCTTTTAAACAATGCGGGTTATTTCTCAGAT 523
DB      580  CACCTTCTTTTAAACAATGCGGGTTATTTCTCAGAT 622
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RESULT 5

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BE083024
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LOCUS BE083024 455 bp mRNA linear EST 12-JUN-2000
DEFINITION RC2-BT0642-240300-018-a02 BT0642 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE083024
VERSION BE083024.1 GI:8473332
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
Dias, Neco, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FADESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC2-BT0642-240
300-018-a02&ct=2000-03-24&ct=1)
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High quality sequence start: 10
High quality sequence stop: 455.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0642"
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match 76.5%; Score 440.6; DB 2; Length 455;
Best Local Similarity 99.1%; Pred. No. 5.9e-116;
Matches 443; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

10 AATATGAGAGTGGGAAATTAATTCATGTAAGTGAAGAGTGTGTAAGAGGATTAAGT 69
9 AATATGAGAGTGGGAAATTAATTCATGTAAGTGAAGAGTGTGTAAGAGGATTAAGT 68
70 AAAATGCACTGGAGAGCAAGATGATCCAGATCTTCAGGAGACTCCCTGCTGTCAAC 129
69 AAAATGCACTGGAGAGCAAGATGATCCAGATCTTCAGGAGACTCCCTGCTGTCAAC 128
130 TGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGTCTCTGAAATTTTAAATTATG 189
129 TGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGTCTCTGAAATTTTAAATTATG 188
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189 CTGTATGTTGCTCTGAGAGAGCCCTGAAAGTCAATCCCAATATCCACATCTTATA 248
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Db 309 ACTCAGGGGCGGCTGCATTTTATGTAATGGGCAATGATTAATCACTTTATATGCTTCCA 368
Qy 370 AAGTGCTGTGGCTTCTCTCCCACTGACCAATGCAAAAGTTGAGAAAAATGATCATTA 429
Db 369 AAGTGCTGTGGCTTCTCTCCCACTGACCAATGCAAAAGTTGAGAAAAATGATCATTA 428
Qy 430 TTTTGCATTAACAGACAGCTGGCGCA 456
Db 429 TTTTGCATTAACAGACAGCTGGCGCA 455

RESULT 6
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LOCUS CN259815 624 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700600019460 GRN_PRENBU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259815
VERSION CN259815.1 GI:47276229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 624)
Brandenberger, R., Mei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M. S., Mandilam, R.,
Lebkowski, J. and Stanton, L. W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 624 Std Error: 0.00.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN PRENBU"
/note="Oligo dT primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

ORIGIN
Query Match 75.2%; Score 433.4; DB 7; Length 624;
Best Local Similarity 99.8%; Pred. No. 7.6e-114;
Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

142 GGACAGATAGTGCATGTTCTTGTCTGTAATTTTAAATTAATGATGCTGTAATGTTGC 201
1 GGACAGATAGTGCATGTTCTTGTCTGTAATTTTAAATTAATGATGCTGTAATGTTGC 60
202 TTTGAGGAAGCCCTGGAAGAGTCTATCCCAATATCCCAATCTTAATTCACAAATTA 261
61 TTTGAGGAAGCCCTGGAAGAGTCTATCCCAATATCCCAATCTTAATTCACAAATTA 120
262 AGCTGATGATGATCCCTTAAGAGAGCTGCTAATTTGACTGCCACTTGCAACTGAGGGGCG 321
121 AGCTGATGATGATCCCTTAAGAGAGCTGCTAATTTGACTGCCACTTGCAACTGAGGGGCG 180
322 CTGCATTTTATGATGAGGTCAAAATGATTCACCTTTTATGATGCTTCCAAAGGTGCTTGG 381

/clone="IMAGE:3947872"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NH_MGC_9"
 /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 72.9%; Score 419.8; DB 2; Length 681;
 Best Local Similarity 99.3%; Pred. No. 6,6e-110;
 Matches 432; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 TTCAAAGACATATTAGAGTTGGGAAATATTATTCATGTAGCAAGAGTGTAAAGA 60
 DB 247 TTCAAAGACATATTAGAGTTGGGAAATATTATTCATGTAGCAAGAGTGTAAAGA 306
 QY 61 GGTATTAAGTAAATGACGCTGGAGAGCAATGCAATCCGACATCTGAGGAGCTCCGCCG 120
 DB 307 GGTATTAAGTAAATGACGCTGGAGAGCAATGCAATCCGACATCTGAGGAGCTCCGCCG 366
 QY 121 CCTGTACCTGGGAGGTGAGAGACAGATAGTCATGTTCTTCTTCTGTAATTTTAG 180
 DB 367 CCTGTACCTGGGAGGTGAGAGACAGATAGTCATGTTCTTCTTCTGTAATTTTAG 426
 QY 181 TTATATGTCTGTATGTGCTCTGAGAGAGCCCTGAGAAAGTCTATCCCAATATGCA 240
 DB 427 TTATATGTCTGTATGTGCTCTGAGAGAGCCCTGAGAAAGTCTATCCCAATATGCA 486
 QY 241 CATCTTATTTCCCAAAATTAGAGTGTATGTAATGTAACCTTAAGCGGTGTAATTAATGAC 300
 DB 487 CATCTTATTTCCCAAAATTAGAGTGTATGTAATGTAACCTTAAGCGGTGTAATTAATGAC 546
 QY 301 CACTTGCAGCACTCAGGGGCGGCTGATTTTGAATGGTCAAAATGATTCACCTTTTATG 360
 DB 547 CACTTGCAGCACTCAGGGGCGGCTGATTTTGAATGGTCAAAATGATTCACCTTTTATG 606
 QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGA-AAA 419
 DB 607 ATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGACCAA 666
 QY 420 ATGATCATATTTTA 434
 DB 667 CTGATCATATTTTA 681

RESULT 9
 CN259816 427 bp mRNA linear EST 16-MAY-2004
 LOCUS CN259816
 DEFINITION 17000600060609 GRN_PRENED Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN259816
 VERSION CN259816.1 GI:47276230
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 427)
 AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.
 TITLE Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
 Insert Length: 427 Std Error: 0.00.
 Location/Qualifiers

FEATURES

source

1. 427
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
 /clone_lib="GRN_PRENED"
 /note="Oligo dt primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."

ORIGIN

Query Match 68.9%; Score 397; DB 7; Length 427;
 Best Local Similarity 100.0%; Pred. No. 2,3e-103;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 GTTATATGCTGTATGTTGCTCTGAGAGAGCCCTGAGAAAGTCTATCCCAATATCC 239
 DB 1 GTTATATGCTGTATGTTGCTCTGAGAGAGCCCTGAGAAAGTCTATCCCAATATCC 60
 QY 240 ACATCTTATTTCCCAAAATTAGCTGTATGTAATGTAACCTTAAGCGGTGTAATGACTG 299
 DB 61 ACATCTTATTTCCCAAAATTAGCTGTATGTAATGTAACCTTAAGCGGTGTAATGACTG 120
 QY 300 CCACTTCCGCACTCAGGGGCGGCTGATTTTGAATGGTCAAAATGATTCACCTTTTAT 359
 DB 121 CCACTTCCGCACTCAGGGGCGGCTGATTTTGAATGGTCAAAATGATTCACCTTTTAT 180
 QY 360 GATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 419
 DB 181 GATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 240
 QY 420 ATGATCATATTTTGAATTAAGAGAGAGTGGGAGACCGGATTTTAAATTAATGAGA 479
 DB 241 ATGATCATATTTTGAATTAAGAGAGAGTGGGAGACCGGATTTTAAATTAATGAGA 300
 QY 480 GCACCTTCTTTTAAACAAATGCGGTTATTTCTCAGATGATGTTCTCCGTGAA 539
 DB 301 GCACCTTCTTTTAAACAAATGCGGTTATTTCTCAGATGATGTTCTCCGTGAA 360
 QY 540 TGGTCAGGAGAGACCTTTGACCTTGAATATGAGC 576
 DB 361 TGGTCAGGAGAGACCTTTGACCTTGAATATGAGC 397

RESULT 10
 CN259810 737 bp mRNA linear EST 16-MAY-2004
 LOCUS CN259810
 DEFINITION 17000600184202 GRN_PRENED Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN259810
 VERSION CN259810.1 GI:47276224
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 737)
 AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.
 TITLE Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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 Location/Qualifiers

FEATURES

source

1. 737
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_1ib="GRN PRENEU"
 /note="Toligo dt primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic and mitogens."

ORIGIN

Query Match 54.5%; Score 314; DB 7; Length 737;
 Best Local Similarity 100.0%; Pred. No. 2.4e-79;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCTGTAGTATGACCTTAAAGCGTGTAAATGACCTTGCACCTTGCACCTCAGGGGCGC 322
 DB 1 GCTGTAGTATGACCTTAAAGCGTGTAAATGACCTTGCACCTTGCACCTCAGGGGCGC 60
 QY 323 TGCATTTTAAATGAGGTCATTAATGATGCTTTCCTCAAGGCTTGGC 382
 DB 61 TGCATTTTAAATGAGGTCATTAATGATGCTTTCCTCAAGGCTTGGC 120
 QY 383 TTCTCTTCCCACTGACCAATGCGCAATGAGAAAATGATCAATTTTAAAGATTAAC 442
 DB 121 TTCTCTTCCCACTGACCAATGCGCAATGAGAAAATGATCAATTTTAAAGATTAAC 180
 QY 443 AGAGCACTCGGCGCACCGATTTTAAATGAGCACTTCTTTTAAACAAACAA 502
 DB 181 AGAGCACTCGGCGCACCGATTTTAAATGAGCACTTCTTTTAAACAAACAA 240
 QY 503 ATCGGGTTTATTTCTCAATGATGTTTATTCCTGATGCTTCCAGGAGACCTTTTAC 562
 DB 241 ATCGGGTTTATTTCTCAATGATGTTTATTCCTGATGCTTCCAGGAGACCTTTTAC 300
 QY 563 CTGACTATATGCG 576
 DB 301 CTGACTATATGCG 314

RESULT 11

CN259812 698 bp mRNA linear EST 16-MAY-2004
 LOCUS 170006001.77307 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
 DEFINITION CN259812
 ACCESSION CN259812
 VERSION CN259812.1 GI:47276226
 KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 698)

REFERENCE

AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
 Lebkowski, J. and Stanton, L. W.
 Transcriptional characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)

JOURNAL

COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 698 Std Error: 0.00.

FEATURES

source

Location/Qualifiers
 1. 698
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, DMSO-treated H9 cell
 line"
 /clone_1ib="GRN PREHEP"
 /note="Toligo dt primed, full-length enriched cDNA library
 from DMSO-treated hES cell line H9 (p22) maintained in
 feeder-free conditions"

ORIGIN

Query Match 48.8%; Score 281; DB 7; Length 698;
 Best Local Similarity 99.7%; Pred. No. 8.2e-70;
 Matches 292; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCAAAGACATATTAGAAAGTTGGAAATTAATCATGTGAACAGTGAAGTGTATAGA 60
 DB 406 TTCAAAGACATATTAGAAAGTTGGAAATTAATCATGTGAACAGTGAAGTGTATAGA 465
 QY 61 GTGATTAAGTAAATGACCGTGAGACAGTGCATCCCAAGATTCAGGAGCTCCCTTG 120
 DB 466 GTGATTAAGTAAATGACCGTGAGACAGTGCATCCCAAGATTCAGGAGCTCCCTTG 525
 QY 121 CCTGTACCTGGGAGTGAAGAGACAGATAGCATGTTCTTGTCTGAAATTTTAA 180
 DB 526 CCTGTACCTGGGAGTGAAGAGACAGATAGCATGTTCTTGTCTGAAATTTTAA 565
 QY 181 TTATATGCTGTAAATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCCAATATCCA 240
 DB 586 TTATATGCTGTAAATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCCAATATCCA 645
 QY 241 CATCTTATATTCACAAATTAAGCTGTATATGA-CCCTAAGCGCTGCTAA 292
 DB 646 CATCTTATATTCACAAATTAAGCTGTATATGA-CCCTAAGCGCTGCTAA 698

RESULT 12

Bu679990 481 bp mRNA linear EST 07-OCT-2002
 LOCUS UI-CF-DUI-aba-c-02-0-UI-.s1 UI-CF-DUI Homo sapiens cDNA clone
 DEFINITION UI-CF-DUI-aba-c-02-0-UI 3', mRNA sequence.
 ACCESSION Bu679990
 VERSION Bu679990.1 GI:23528471
 KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 481)

REFERENCE

AUTHORS Bonaldo, M. F., Lennon, G. and Soares, M. B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)

JOURNAL

COMMENT MEDLINE
 PUBMED
 97044477
 8889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.reagen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=yes

FEATURES

Location/Qualifiers
1..481
/organism="Homo sapiens"
/mol_type="cDNA"
/db_xref="taxon:9606"
/clone="UI-CF-DUI-aba-c-02-0-UI"
/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone.lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; UI-CF-DUI is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCGCTAGGC.
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG LIB=UI-CF-DUI
TAG_SEQ=GCGCTAGGC"

ORIGIN

Query Match 45.3%; Score 260.8; DB 5; Length 481;
Best Local Similarity 96.9%; Pred. No. 5.1e-64;
Matches 277; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

1 TTCAAGACATTTAGAGTGGGAAATTAATTCATGTAACAGACAGTGTAAAGA 60
196 TTCAAGACATTTAGAGTGGGAAATTAATTCATGTAACAGAGTGTAAAGA 255
61 GTGATTAAGTAATGACGCTGAGACAGATGCCAGATCTCAGGAGCTCCCTG 120
256 GTGATTAAGTAATGACGCTGAGACAGATGCCAGATCTCAGGAGCTCCCTG 315
121 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTGTCTCTGAATTTAG 180
316 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTGTCTCTGAATTTAG 375
181 TTAATGCTGTAATGTTGCTCTGAGAAAGCCCTGGAAGCTATCCCAATATCA 240
376 TTAATGCTGTAATGTTGCTCTGAGAAAGCCCTGGAAGCTATCCCAATATCA 435
241 CATCTTA--TATTCACAATTAAGCTGATGATGATACCTTAAGAC 284
436 CATCTTAAGATTCACAAATTAACCTGATGATGATACCTTAAGAC 481

RESULT 13

AO214963 510 bp DNA linear GSS 18-SEP-1998
LOCUS AO214963
DEFINITION HS.3062.B2.E01.MR.CIT.Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 COL=2 Row=J, genomic survey sequence.

ACCESSION AO214963
VERSION AO214963
KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 510)
Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T., Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and Hood L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PubMed 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3062 Row: J Column: 2
Class: BAC ends
High quality sequence stop: 510.

FEATURES

source

1..510
Location/Qualifiers
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/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 33.2%; Score 191; DB 8; Length 510;
Best Local Similarity 78.6%; Pred. No. 7.6e-44;
Matches 257; Conservative 0; Mismatches 60; Indels 10; Gaps 2;

1 TTCAAGACATTTAGAGTGGGAAATTAATTCATGTAACAGACAGTGTAAAGA 60
191 TTCCCGGAGTATTTAAATGCGGAGCTGTTATTCATGTAACAGTGTAAAGA 247
61 GTGATTAAGTAATGACGCTGAGACAGATGCCAGATCTCAGGAGCTCCCTG 120
248 -----TCTTATCTATCAAGAGACAGATGTCATCCAGATCTCAGGAGCTCCCTG 302
121 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTGTCTCTGAATTTAG 180
303 CCTATCACTGGGAGTGAAGACAGATGTCATGTTCTTGTCTCTGAATTTAG 362
181 TTAATGCTGTAATGTTGCTCTGAGAAAGCCCTGGAAG--TCTATCCCAATATC 238
363 TTAATGCTGTAATGTTGCTCTGAGAAAGCCCTGGAAGTCTCTATCCCAATATCA 422
239 CACATCTATATTCACAATTAAGCTGATGATGATACCTTAAGACGCTGATTTGACT 298
423 CACATCTATATTCACAATTAAGCTGATGATGATGATGATGATGATGATGATGACT 482
299 GCCACTTGCACACTGAGGAGCGGCTGC 325
483 GCCCTACAGCACTCGGAGAGCATTTGC 509

RESULT 14

BX369964 925 bp mRNA linear EST 26-APR-2004
LOCUS BX369964
DEFINITION BX369964 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA clone CS0D103Y621 5-PRIME, mRNA sequence.

ACCESSION BX369964
VERSION BX369964
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 925)
Li W.B., Gruber C., Jessee J. and Polayes D.

Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: segrete@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
742.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0BAG0302A11_CS02865_1sc=742.r.
Location/Qualifiers

source
1. .925
/organism="Homo sapiens"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 21.1%; Score 121.4; DB 5; Length 925;
Best Local Similarity 98.5%; Pred. No. 1.1e-23;
Matches 133; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 TTCAAGACATATTAGAGTTGGGAAATATTCATGTGACTGACAGAGTGTG-TTAA 59
Db 728 TTCAAGACATATTAGAGTTGGGAAATATTCATGTGACTGACAGAGTGTG 787
Qy 60 AGTATTAAGTAAATGACGCGGAGACAGTGCATCCCGATCTCGGGACCTCCCT 119
Db 788 AGTATTAAGTAAATGACGCGGAGACAGTGCATCCCGATCTCGGGACCTCCCT 847
Qy 120 GCGTGTACCTGGGG 134
Db 848 GCGTGTACCTGGGG 862

RESULT 15
CR844392/c 611 bp DNA linear GSS 27-SEP-2004
LOCUS GR0AAA79CH04FM1 INRA BAC Bos taurus genomic clone INRAD_713D08, DNA
DEFINITION sequence, genomic survey sequence.
ACCESSION CR844392
VERSION CR844392.1 GI:52780480
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE 1 (bases 1 to 611)
AUTHORS Eggen, A., Schibler, L. and Roy, A.
TITLE Bovine BAC End Sequences from the INRA bovine BAC library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 611)
AUTHORS
TITLE Genoscope.
JOURNAL Direct Submission
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrete@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Department of Animal Genetics - LGBC
INRA
78350 Jouy-en-Josas, France
Tel: 33 1 34 65 24 24
Fax: 33 1 34 65 24 78
Email: eggen@jouy.inra.fr
Clones are derived from the INRA bovine BAC library
(http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library

availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBMC) by INRA (Jouy-en-Josas) and Genoscope
(Evry) Plate: 713 row: D column: 08
Seq primer: M13 Forward
Class: BAC ends.

FEATURES
source
Location/Qualifiers

1. .611
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/db_xref="taxon:9913"
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/sex="male"
/cell_type="fibroblast"
/clone_lib="INRA bovine BAC"
/note="Vector: pBelobAC11; Site 1: HindIII; Holstein bull;
INRA Bovine BAC library (Male) produced by Andre
Eggen-Genoscope sequence ID : GR0AAA79CH04FM1"

ORIGIN

Query Match 18.1%; Score 104.2; DB 9; Length 611;
Best Local Similarity 75.7%; Pred. No. 9.3e-19;
Matches 196; Conservative 0; Mismatches 53; Indels 10; Gaps 5;

Qy 325 CATTTTAAATAGGCTCAATGATTCACCTTTTATGATGCTTCCAAAGGCTGCTT 384
Db 280 CATTTTAAATAGGCTCAATGATTCACCTTTTATGATGCTTCCAAAGGCTGCTT 222
Qy 385 CTCTCCCACTGACCAATGSC-----AAAGTGAGAAAATGATCATATTTAGCAT 439
Db 221 CTCTCCCACTGACCAATGSCCAAGAAAATGATGATCATATTTTAAACATA 162
Qy 440 AACAGACACTGCGGACAC--GATTTTAAATAAATGACACCTCTTTT-AAAC 496
Db 161 AAAATGTAAGTGAAGACACTGATTTTCTAAACTATGACACATCTTATTTAAAC 102
Qy 497 AAACAAATGGGTTTATTTCTGAGATGATTCATCCGATGATGTCGAGG-AAAGAC 555
Db 101 AAACAAATGGTATTTACTTCTGAGATGATTCATCCGATGATGTCGAGG-AAAGAC 42
Qy 556 CTTTCACTTGACATATG 574
Db 41 CTCTCATCTTGACATATG 23

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Job time : 2243.26 secs

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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 07:16:54 ; Search time 4106.01 Seconds

(Without alignments)
10502.938 Million cell updates/sec

Title: US-09-763-978B-11

Perfect score: 890
Sequence: 1 caagctctggagctctctctctctctctctctctctctctctctctct 890

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank1:*
1: gb_ba:*
2: gb_ptg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 45 | 433.8 | 48.7 | 635 | 6 AR255400 | AR255400 Sequence |

ALIGNMENTS

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| LOCUS | BD235840 | 890 bp | DNA | linear | PAT 17-JUL-2003 | | | | | | | | | | | |
| DEFINITION | A novel method of diagnosing, monitoring, staging, imaging and treating various cancers. | | | | | | | | | | | | | | | |
| ACCESSION | BD235840 | | | | | | | | | | | | | | | |
| VERSION | BD235840.1 | GI:33045610 | | | | | | | | | | | | | | |
| KEYWORDS | JP 2002523760-A/11. | | | | | | | | | | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | | | | | | | | | | | |
| ORGANISM | Homo sapiens | | | | | | | | | | | | | | | |
| REFERENCE | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | | | | | | | | | | | | |
| AUTHORS | 1 (bases 1 to 890) | | | | | | | | | | | | | | | |
| TITLE | Salceda,S., Sun,Y., Recipon,H. and Cafferey,R. | | | | | | | | | | | | | | | |
| JOURNAL | A novel method of diagnosing, monitoring, staging, imaging and treating various cancers | | | | | | | | | | | | | | | |
| COMMENT | Patent: JP 2002523760-A 11 30-JUL-2002; | | | | | | | | | | | | | | | |
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| PI | SUSANA SALCEDA, YONGMING SUN, HERVE RECIPON, ROBERT CAFFEREY PC | | | | | | | | | | | | | | | |
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| | ,A61K49/00,A61K49/00, PC | | | | | | | | | | | | | | | |
| | A61K51/00,C07K16/32,C12N15/09,C12Q1/68,C12N15/00,A61K49/02 CC | | | | | | | | | | | | | | | |
| | A novel method of diagnosing, monitoring, staging, imaging and treating | | | | | | | | | | | | | | | |
| CC | treating | | | | | | | | | | | | | | | |
| CC | various cancers | | | | | | | | | | | | | | | |
| FT | Key | | | | | | | | | | | | | | | |
| FT | Source | | | | | | | | | | | | | | | |
| FT | Location/Qualifiers | | | | | | | | | | | | | | | |
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| Query Match | 100.0%; Score 890; DB 6; Length 890; | | | | | | | | | | | | | | | |

Best Local Similarity 100.0%; Pred. No. 3.7e-262;
Matches 890; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS BD265002 2627 bp DNA linear PAT 17-JUL-2003
DEFINITION BD265002 Compositions and methods for the therapy and diagnosis of ovarian cancer.
ACCESSION BD265002
VERSION BD265002.1 GI:33074770
KEYWORDS JP 2002532093-A/387.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham, J. L., King, G. E., Algate, P. A. and Frudakis, T. N.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer.
JOURNAL JOURNAL
CORIXA CORP
PATENT: JP 2002532093-A 387 02-OCT-2002;

COMMENT OS Homo sapiens (human)
PN JP 2002532093-A/387

PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588356
PR 17-DEC-1998 US 09/215681, 17-DEC-1998 US 09/216003 PR
23-JUN-1999 US 09/338933, 24-SEP-1999 US 09/404879 PI
JENNIFER L MITCHAM, GORDON E KING, PAUL A ALGATE, TONY N FRUDAKIS PC
C12N15/09, A61K31/7115, A61K35/14, A61K35/76, A61K39/00, A61K39/395, PC
A61K39/395, PC
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PC G01N33/574, G01N33/577, C12N15/00, C12N5/00, C12N5/00 CC
Compositions and methods for the therapy and diagnosis of CC

ovarian cancer

FT Key Location/Qualifiers

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FEATURES location/Qualifiers

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Query Match 98.7%; Score 878; DB 6; Length 2627;

Best Local Similarity 99.9%; Pred. No. 2e-258;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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RESULT 3
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DEFINITION Sequence 391 from patent US 6468546.
ACCESSION AR238405
VERSION AR238405.1 GI:27283369
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham,J.L., King,G.E. and Algate,P.A.
TITLES Compositions and methods for therapy and diagnosis of ovarian cancer.
JOURNAL Patent: US 6468546-A 391 22-OCT-2002;
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Query Match 98.7%; Score 878; DB 6; Length 2627;
Best Local Similarity 99.9%; Pred. No. 2e-258;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAAAGCTGAGGCTTCTCTTCCATCTGCGAGCAAGCTTAAGACCTCAGTTTCAATA 60
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DEFINITION Sequence 391 from patent US 6699664.
ACCESSION AR478744
VERSION AR478744.1 GI:47237396
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Reter,M.W.,
Fanger,G.R., Reed,S.G., Vedrick,T.S. and Carter,D.
TITLES Compositions and methods for the therapy and diagnosis of ovarian cancer.
JOURNAL Patent: US 6699664-A 391 02-MAR-2004;
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Best Local Similarity 99.9%; Pred. No. 2e-258;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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RESULT 5
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LOCUS
DEFINITION Sequence 207 from Patent WO0140269.
ACCESSION AX156350
VERSION AX156350.1 GI:14537350
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dillon,D.C., Day,C.H., Jiang,Y., Houghton,R.L., Mitcham,J.L. and
Wang,A.
TITLE Compositions and methods for therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0140269-A 207 07-JUN-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..2627

ORIGIN
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/mol_type="unassigned DNA"
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Query Match 98.7%; Score 878; DB 6; Length 2627;
Best Local Similarity 99.9%; Pred. No. 2e-258;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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AX366624 2627 bp DNA linear PAT 15-FEB-2002
LOCUS
AX366624

DEFINITION Sequence 391 from Patent WO0206317.
ACCESSION AX366624
VERSION AX366624.1 GI:18698046
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W., Fanger,G.R., Reed,S.G., Vedvick,T.S., Carter,D., Hill,P. and Albane,E.
TITL Composition and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: WO 0206317-A 391 24-JAN-2002;
CORIXA CORPORATION (US)
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Best Local Similarity 99.9%; Pred. No. 2e-258;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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DB 2320 TCTCCGAGACCTCTCGGCAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2379
QY 661 GCACACAGACCTTTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

DB 2380 GCACACAGACCTTTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2439
QY 721 AACCTTGAAGAAAGAAATTAATCTTGTTCACGCCCCCTTCCACACTCTGATGTGA 780
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LOCUS
DEFINITION Sequence 1 from Patent WO020624.
ACCESSION AX403048
VERSION AX403048.1 GI:21388028
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Fox,G., Sullivan,J.K. and Fang,M.
TITL B7-like molecules and uses thereof
JOURNAL Patent: WO 020624-A 1 10-JAN-2002;
Amgen, Inc. (US)
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PYLMLK"
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Query Match 98.6%; Score 877.6; DB 6; Length 2603;
Best Local Similarity 99.8%; Pred. No. 2.6e-258;
Matches 888; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
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 AX375860 2626 bp DNA linear PAT 01-MAR-2002
 LOCUS Sequence 7 from Patent WO0194641.
 DEFINITION AX375860
 ACCESSION AX375860
 VERSION AX375860.1 GI:19170332
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 O'Le, E., McLachlan, K. and Heard, C.
 Gene targets and ligands that bind thereto for treatment and
 diagnosis of ovarian carcinomas
 Patent: WO 0194641-A 7 13-DEC-2001;
 Idex Pharmaceuticals Corporation (US)
 JOURNAL Location/Qualifiers
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 Best Local Similarity 99.8%; Pred. No. 6; Le-258;
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 LOCUS Human DNA sequence from clone RPL1-229A19 on chromosome 1, complete
 DEFINITION sequence.
 ACCESSION AL391476
 VERSION AL391476.20 GI:15131484
 KEYWORDS
 HTG. Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 Wallis, J.
 Direct Submission
 Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,

COMMENT

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:14970375.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
RP11-229A19 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see
<http://www.choi1.org/bacpac/home.htm>
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-229A19 The true left end of clone RP11-287H7 is at 67254 in this sequence. The true right end of clone RP4-570D9 is at 57439 in this sequence.

FEATURES

source

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745. .1182
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Best Local Similarity 99.6%; Pred. No. 8.1e-257;
Matches 886; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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LOCUS      HSR808167
DEFINITION      Homo sapiens mRNA; cDNA DKFZp779B1717 (from clone DKFZp779B1717).
ACCESSION      BX648021
VERSION      BX648021.1 GI:34367180
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2671)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Well,B., Amlid,C., Ossanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German Human cDNA Consortium
CONSTRM
Direct Submission
Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuberberg, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp779B1717) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
FEATURES
Location/Qualifiers
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RESULT 12
AR238092 1567 bp DNA linear PAT 20-DEC-2002
LOCUS AR238092
DEFINITION Sequence 74 from patent US 6468546.
ACCESSION AR238092 GI:27283056
VERSION AR238092.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., King,G.E. and Aljate,P.A.
TITLE Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6468546-A 74 22-OCT-2002;
FEATURES
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/organism="unknown"
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ORIGIN

Query Match 97.3%; Score 866; DB 6; Length 1567;
Best Local Similarity 99.8%; Pred. No. 9.3e-255;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 1 CAAAGCTGAGGCTTCTGCTTCCATCTGCGAGACAGCTAAGACCTCAGTTTCAATA 60
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Qy 121 TGAAGCAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGTGTACTATCAAC 180
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Db 1457 ACCACTGCTTCTGAGACCTTGAAGCAGGTGACTGTATTAATGTTGTTAAGAAAC 1516
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Db 1517 TGAATTTAGATTTCTGATGTTCAAGAGATGATTAATATACATTTCT 1566

RESULT 13
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LOCUS AR257633
DEFINITION Sequence 74 from patent US 6488931.
ACCESSION AR257633
VERSION AR257633.1 GI:27307708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLE Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6488931-A 74 03-DEC-2002;
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Query Match 97.3%; Score 866; DB 6; Length 1567;
Best Local Similarity 99.8%; Pred. No. 9.3e-255;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
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Db 679 CAAAGCTGAGGCTTCTGCTTCCATCTGCGAGACAGCTAAGACCTCAGTTTCAATA 738

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LOCUS AR283679
DEFINITION Sequence 74 from patent US 6528253.
ACCESSION AR283679
VERSION AR283679.1 GI:29720576
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Fridakis,T.N. and King,G.B.
TITLES Compositions and methods for diagnosis of ovarian cancer
JOURNAL Patent: US 6528253-A 74 04-MAR-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 9.3e-255;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 CAAGCTCTAGAGGCTTCTCTTTCATCTGCTGAGCAGTGAAGACTCAGTTTCAATA 60
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LOCUS AR443353
DEFINITION Sequence 74 from patent US 6670463.

ACCESSION AR443353
VERSION AR443353.1 GI:42671132
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Micham,J.L., Frudakis,T.N. and King,G.E.
TITLE Compositions and methods for therapy of ovarian cancer
JOURNAL Patent: US 6670463-A 74 30-DEC-2003;
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Location/Qualifiers
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ORIGIN

Query Match 97.3%; Score 866; DB 6; Length 1567;
Best Local Similarity 99.8%; Pred. No. 9.3e-255;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 CAAGCTTGAGGCTTCTCTTCATCTGCGTGAAGCTTAAGCTCAGTTTCAATA 60
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QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCATCTCCGGGGAAATGTC 120
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 05:15:03 ; Search time 545.854 Seconds

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Title: US-09-763-978b-11

Perfect score: 890

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 11 | 878 | 98.7 | 2627 | 9 | ADA08544 | Ada08544 Human ova |
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| 13 | 878 | 98.7 | 2627 | 10 | ADG46174 | Adg46174 Human ov |
| 14 | 878 | 98.7 | 2627 | 12 | ADN40452 | Adn40452 Human br |
| 15 | 878 | 98.7 | 2690 | 12 | ADP81075 | Adp81075 Human ov |
| 16 | 878 | 98.7 | 3357 | 6 | AAAD2519 | Aad22519 Human B7- |
| 17 | 877.6 | 98.6 | 2603 | 6 | AAAD29253 | Aad29253 Human B7- |
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| 19 | 867 | 97.4 | 2591 | 6 | ABLS7354 | Ab157354 Breast BS |
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| 25 | 866 | 97.3 | 2587 | 3 | AAZ90470 | AAZ90470 Cancer sp |
| 26 | 856.6 | 96.2 | 2626 | 4 | AAZ65593 | AAZ65593 DNA enco |
| 27 | 856.6 | 96.2 | 2626 | 6 | AAAD3256 | AAAD3256 Human B7- |
| 28 | 807 | 90.7 | 846 | 5 | ADL63234 | ADL63234 Human ova |
| 29 | 804.4 | 90.4 | 836 | 4 | AAFP4856 | AAFP4856 Human bre |
| 30 | 711 | 79.9 | 725 | 6 | ABLS7361 | ABLS7361 Breast BS |
| 31 | 629.2 | 70.7 | 1808 | 12 | ADH50892 | ADH50892 Breast an |
| 32 | 629.2 | 70.7 | 1898 | 12 | ADH50893 | ADH50893 Breast an |
| 33 | 626.2 | 70.4 | 1811 | 6 | ABST6536 | ABST6536 cDNA enco |
| 34 | 626.2 | 70.4 | 1811 | 6 | ABST6420 | ABST6420 cDNA enco |
| 35 | 626.2 | 70.4 | 1811 | 8 | ACCS0158 | ACCS0158 Breast ca |
| 36 | 626.2 | 70.4 | 1811 | 10 | ADH80507 | ADH80507 Ovarian c |
| 37 | 626.2 | 70.4 | 1811 | 12 | ADP81074 | ADP81074 Human ova |
| 38 | 552 | 62.0 | 563 | 6 | ABLS0970 | ABLS0970 Human ova |
| 39 | 544 | 61.1 | 555 | 6 | AAAS61836 | AAAS61836 Lung smal |
| 40 | 517 | 58.1 | 1596 | 11 | ACN92433 | ACN92433 Breast ca |
| 41 | 494.6 | 55.6 | 1598 | 6 | ABT09900 | ABT09900 Human bre |
| 42 | 494.6 | 55.6 | 1598 | 6 | ABLT78520 | ABLT78520 Human ova |
| 43 | 494.6 | 55.5 | 524 | 6 | ABLT79323 | ABLT79323 Human ova |
| 44 | 487.8 | 54.8 | 578 | 5 | ADL43792 | ADL43792 Human ova |
| 45 | 480 | 53.9 | 491 | 2 | AAAS9818 | AAAS9818 DNA seq |

ALIGNMENTS

| | |
|----------|---------------------------------------------------------------------------|
| RESULT 1 | AAZ90480 |
| ID | AAZ90480 standard; cDNA; 890 BP. |
| AC | AAZ90480; |
| DT | 06-JUN-2000 (first entry) |
| DE | Cancer specific gene (clone ID 16656542) fragment #11. |
| XX | CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast; |
| KW | endometrial; uterine; lung; cytotoxic; ss. |
| OS | Homo sapiens. |
| XX | XX |
| PN | WO200012758-A1. |
| PD | 09-MAR-2000. |
| PF | 01-SEP-1999; 99WO-US019655. |
| PR | 02-SEP-1998; 98US-0098880P. |
| PA | (DIAD-) DIADEXUS LLC. |
| PI | Salceda S, Sun Y, Recipon H, Cafterkey R; |
| DR | WPI; 2000-256657/22. |
| XX | XX |
| PT | Diagnosing, staging, monitoring, imaging and treating cancer especially |
| PT | gynecological cancers e.g. breast, ovarian cancer and lung cancer. |
| PT | involves measuring cancer specific gene levels in cells and body fluids. |
| XX | Claim 9; Page 51; 58pp; English. |
| PS | The invention relates to detecting, diagnosing metastasis and staging |
| CC | cancer by measuring levels of cancer specific genes (CSG) in cells, |
| CC | tissues or body fluids. Their remission and progression, decreases and |
| CC | increases in CSG levels, is also monitored, by periodic sample analysis. |
| CC | The methods are useful for detecting cancers, especially gynecologic |
| CC | cancers which include ovarian, breast, endometrial and uterine cancer and |
| CC | lung cancer. Antibodies against the CSGs labeled with paramagnetic ions |
| CC | or a radioisotope is useful for imaging cancer and when conjugated with a |

CC cytotoxic agent are useful for treating cancer. The present sequence
 XX represents a CSG (clone ID: 16656542 and gene ID: 234617) fragment
 SQ Sequence 890 BP; 242 A; 213 C; 194 G; 241 T; 0 U; 0 Other;

Query Match 100.0%; Score 890; DB 3; Length 890;
 Best Local Similarity 100.0%; Pred. No. 1.5e-288;
 Matches 890; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTCCGCGACCTAAGACCTCAGTTTCAATA 60
 DB 1 CAAGCTCTGAGGCTTCTCTTCCATCTCCGCGACCTAAGACCTCAGTTTCAATA 60
 QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGATTTGCCCCCATCTCCGGGGAAATGTC 120
 DB 61 GCATCTAGAGCAGTGGGACTCAGCTGGGATTTGCCCCCATCTCCGGGGAAATGTC 120
 QY 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAGAGATACAGTCTACTACCAAC 180
 DB 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAGAGATACAGTCTACTACCAAC 180
 QY 181 TGTGTGATTAAGGCCAGGATGCTGCTCAACCTCCATCATGATACAGGAGCTCCCA 240
 DB 181 TGTGTGATTAAGGCCAGGATGCTGCTCAACCTCCATCATGATACAGGAGCTCCCA 240
 QY 241 TTAACAATACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTTTGAAT 300
 DB 241 TTAACAATACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTTTGAAT 300
 QY 301 AGAAAAAGGCTTGAAGAGAGGAGCCAAACAATCTGTCTCTCTCTCAATTAATGTCATT 360
 DB 301 AGAAAAAGGCTTGAAGAGAGGAGCCAAACAATCTGTCTCTCTCTCAATTAATGTCATT 360
 QY 361 GGAATTAAGCAATCTGTCTTGTGCTGTGCTGCTGAGACAGAGCCAGAACTCTATC 420
 DB 361 GGAATTAAGCAATCTGTCTTGTGCTGTGCTGCTGAGACAGAGCCAGAACTCTATC 420
 QY 421 GGGACACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTGGAAATGCTGTA 480
 DB 421 GGGACACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTGGAAATGCTGTA 480
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTCAATCTACCTGCAAG 540
 DB 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTCAATCTACCTGCAAG 540
 QY 541 CGAAGTCTGTAGAAGAAATGCTGAGTCTGCTGAGGTTTCTTACTCTGAATTAGA 600
 DB 541 CGAAGTCTGTAGAAGAAATGCTGAGTCTGCTGAGGTTTCTTACTCTGAATTAGA 600
 QY 601 TCTCCAGACCCCTTCTGCGCACAAATTAAGGCAACAAACATATACCTTCCATGAA 660
 DB 601 TCTCCAGACCCCTTCTGCGCACAAATTAAGGCAACAAACATATACCTTCCATGAA 660
 QY 661 GCACACACAGACTTTGAAAGCAAGCAATGACTCTGTAATTGAGGCTTGAAGGAATG 720
 DB 661 GCACACACAGACTTTGAAAGCAAGCAATGACTCTGTAATTGAGGCTTGAAGGAATG 720
 QY 721 AAGCTTGAAGAAAGAAATACTTGTTCACGCCCTTCCACACTCTCATGTGTTA 780
 DB 721 AAGCTTGAAGAAAGAAATACTTGTTCACGCCCTTCCACACTCTCATGTGTTA 780
 QY 781 ACCACTGCTTCTCTGAGCCTTGGAGCAGGTAAGTATTAATGTTTATAGAAAC 840
 DB 781 ACCACTGCTTCTCTGAGCCTTGGAGCAGGTAAGTATTAATGTTTATAGAAAC 840
 QY 841 TGAATTTAAGATTCTGATGTTCAAGAGAAATGATTAATATACATTTCT 890
 DB 841 TGAATTTAAGATTCTGATGTTCAAGAGAAATGATTAATATACATTTCT 890

RESULT 2
 AAAS4133
 ID AAAS4133 standard; DNA; 1020 BP.

XX AC AAAS4133;
 XX
 DT 08-FEB-2001 (first entry)
 DE Breast cancer protein BCU7 coding sequence.
 KW Breast cancer; diagnosis; prognosis; detection; screening; antibody;
 KW oestrogen receptor; anti-oestrogen; immune response; lymph node;
 KW metastases; tumour; BCR3; BCO8; BCI1; BCN1; BCN2; BCO2; BCX2;
 KW BCX3; BCA2; BCR2; BCU7; BCI3; human; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO20055629-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US006952.
 XX
 PR 15-MAR-1999; 99US-0026865.
 PR 12-NOV-1999; 99US-00439878.
 PR 12-NOV-1999; 98US-00440370.
 PR 15-NOV-1999; 99US-00440493.
 PR 16-NOV-1999; 99US-00440676.
 PR 16-NOV-1999; 99US-00440677.
 PR 29-NOV-1999; 99US-00450810.
 PR 02-DEC-1999; 99US-00453137.
 PR 08-MAR-2000; 2000US-00453137.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Mack D, Gish KC;
 XX
 DR WPI; 2000-638216/61.
 XX
 PT Screening drug candidates for their ability to modulate breast cancer by
 PT contacting the drug to a cell expressing an expression profile gene and
 PT determining modulation of expression of the gene.
 XX
 PS Disclosure; Fig 72; 258pp; English.
 XX
 PS New methods for screening drug candidates are described which comprise
 CC adding a drug candidate to a cell that expresses a protein selected from
 CC BCI1, BCA2, BCU7, BCN1, BCN5, BCO2, BCO5, BCR2, BCX2 and BCY3 or their
 CC fragments and determining the effect of the drug on the expression of
 CC those proteins. Antibodies to breast cancer genes (specifically BCI1 or
 CC its fragment (BCHI1 or BCHI2)) are useful for inhibiting and treating
 CC breast cancer in individuals who are non-responsive to anti-oestrogen and
 CC positive for oestrogen receptor. Compositions comprising BCI1 or a
 CC nucleic acid encoding BCI1 are useful for eliciting an immune response in
 CC an individual. The antibodies are also useful for the diagnosis and
 CC prognosis of breast cancer and for screening compositions which modulate
 CC the breast cancer phenotype. The method allows rapid and simple detection
 CC of lymph node metastases
 XX
 SQ Sequence 1020 BP; 287 A; 237 C; 215 G; 280 T; 0 U; 1 Other;
 Query Match 99.6%; Score 886.8; DB 3; Length 1020;
 Best Local Similarity 99.8%; Pred. No. 1.9e-287;
 Matches 888; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTCCGCGACCTAAGACCTCAGTTTCAATA 60
 DB 1 CAAGCTCTGAGGCTTCTCTTCCATCTCCGCGACCTAAGACCTCAGTTTCAATA 60
 QY 106 CAAGCTCTGAGGCTTCTCTTCCATCTCCGCGACCTAAGACCTCAGTTTCAATA 165
 DB 106 CAAGCTCTGAGGCTTCTCTTCCATCTCCGCGACCTAAGACCTCAGTTTCAATA 165
 QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGATTTGCCCCCATCTCCGGGGAAATGTC 120
 DB 61 GCATCTAGAGCAGTGGGACTCAGCTGGGATTTGCCCCCATCTCCGGGGAAATGTC 120
 QY 166 GCATCTAGAGCAGTGGGACTCAGCTGGGATTTGCCCCCATCTCCGGGGAAATGTC 225
 DB 166 GCATCTAGAGCAGTGGGACTCAGCTGGGATTTGCCCCCATCTCCGGGGAAATGTC 225
 QY 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAGAGATTAAGGCTACTACCAAC 180
 DB 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAGAGATTAAGGCTACTACCAAC 180
 QY 226 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAGAGATTAAGGCTACTACCAAC 285
 DB 226 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAGAGATTAAGGCTACTACCAAC 285

| | | | |
|----|-----|------------------------------------------------------------------|-----|
| OY | 181 | TAGTGAATAAAGCCAGGGATGCTGCTCAACCTCTACATGTACAGGGAGCTGCCCA | 240 |
| Db | 286 | TAGTGAATAAAGCCAGGGATGCTGCTCAACCTCTACATGTACAGGGAGCTGCCCA | 345 |
| OY | 241 | TTACAACCTAACCCGAAAGTGTCAACTGTGTCAGGACTTAAGAAACCTGGTTTGTAGT | 300 |
| Db | 346 | TTACAACCTAACCCGAAAGTGTCAACTGTGTCAGGACTTAAGAAACCTGGTTTGTAGT | 405 |
| OY | 301 | AGAAAAAGGCGCTGGAAAGAGGGGAGGCAACAAATCTGTCTGTCTTCCCACTTAGTCAAT | 360 |
| Db | 406 | AGAAAAAGGCGCTGGAAAGAGGGGAGGCAACAAATCTGTCTGTCTTCCCACTTAGTCAAT | 465 |
| OY | 351 | GGCAATAAAGCAATTCGTCTCTTTTGGCTGTGCTCAGCAAGAGAGCCGAACCTCTATC | 420 |
| Db | 466 | GGCAATAAAGCAATTCGTCTCTTTTGGCTGTGCTCAGCAAGAGAGCCGAACCTCTATC | 525 |
| OY | 421 | GGGCAACCCAGGATPAACATCTCTCAGTAAACAAGATTTGACAAAGGCTATAGGAAATGCTTGA | 480 |
| Db | 526 | GGGCAACCCAGGATPAACATCTCTCAGTAAACAAGATTTGACAAAGGCTATAGGAAATGCTTGA | 585 |
| OY | 481 | TGGGATTTATCTTCAGCTTGTGAGCTTCTTAAGTTTCTTCCCTTCATTTACCCGTGCAAG | 540 |
| Db | 586 | TGGGATTTATCTTCAGCTTGTGAGCTTCTTAAGTTTCTTCCCTTCATTTACCCGTGCAAG | 645 |
| OY | 541 | CCAAAGTTCTGTAAAGAGAAATGCTCTGAGTTCTAGCTCAAGTTTCTTACTGTGAATTTAGA | 600 |
| Db | 646 | CCAAAGTTCTGTAAAGAGAAATGCTCTGAGTTCTAGCTCAAGTTTCTTACTGTGAATTTAGA | 705 |
| OY | 601 | TCTCCAGAGCCCTTCCCTGGGCACAATTCAAATTAAGGCAACAAACATATATACCTTCAGTAA | 660 |
| Db | 706 | TCTCCAGAGCCCTTCCCTGGGCACAATTCAAATTAAGGCAACAAACATATATACCTTCAGTAA | 765 |
| OY | 661 | GCACAACACGACTTTTGAAGCAAGGCAATGACTGTGAATTAAGGAGCCCTTGAGAGATG | 720 |
| Db | 766 | GCACAACACGACTTTTGAAGCAAGGCAATGACTGTGAATTAAGGAGCCCTTGAGAGATG | 825 |
| OY | 721 | AAGCTTTGAAGGAAGAATACTTTTTCACAGCCCCCTCCCACTCTTCAGTGTGA | 780 |
| Db | 826 | AAGCTTTGAAGGAAGAATACTTTTTCACAGCCCCCTCCCACTCTTCAGTGTGA | 885 |
| OY | 781 | ACCACTGCGCTTCTGTGACCTTGGAGCCACGGTGACTGTATACATGTTGTTATAGAAAC | 840 |
| Db | 886 | ACCACTGCGCTTCTGTGACCTTGGAGCCACGGTGACTGTATACATGTTGTTATAGAAAC | 945 |
| OY | 841 | TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTCTT | 890 |
| Db | 946 | TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTCTT | 995 |

| | |
|----------|-------------------------------------------------------------------------|
| RESULT 3 | |
| AAK59821 | |
| ID | AAK59821 standard; DNA; 893 BP. |
| XX | |
| XX | AAK59821; |
| AC | |
| XX | |
| DT | 28-JUL-1999 (first entry) |
| XX | |
| DE | Consensus DNA sequence of BS265 nucleic acid. |
| XX | |
| XX | BS265: marker; breast disease; cancer; metastasis; atypical hyperplasia |
| KW | fibroadenoma; cyst; therapeutic antagonist; antibody; |
| KM | chromosomal anomaly; genetic immunization; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WC0925877-A1. |
| XX | |
| PD | 27-MAY-1999. |
| XX | |
| PF | 18-NOV-1998; |
| XX | |
| PR | 18-NOV-1997; 97US-00972376. |

| | |
|----|--------------------------------------------------------------------------|
| XX | (ABBO) ABBOTT LAB. |
| PA | |
| XX | |
| Pt | Billing-Medel PA, Cohen M, Colpites TL, Friedman PN, Gordon J, |
| Pt | Grenados EN, Hodges SC, Klaes MR, Kratochvil JD, Roberts-Rapp U, |
| Pt | Russell JC, Stroupe SD; |
| XX | |
| DR | WPI, 1999-347495/29. |
| XX | |
| PT | BS265 nucleic acid, marker for breast disease. |
| PS | Claim 1; Page 95; 102pd; English. |
| CC | The present sequence represents the consensus sequence of BS265 nucleic |
| CC | acid, derived from clones AAX59816-20. BS265 is a marker of breast |
| CC | disease, particularly cancer and its metastases, but also atypical |
| CC | hyperplasia, fibroadenoma and cysts, so detection/quantification of |
| CC | BS265, encoded polypeptides and antibodies is used for diagnosis, |
| CC | staging, monitoring, prognosis, in vivo imaging of, and determining |
| CC | predisposition to these diseases. The antibodies are useful as |
| CC | therapeutic antagonists (optionally coupled to a cytotoxicin), as |
| CC | immunoassay reagents and in competitive drug screens. The polynucleotide |
| CC | and its fragments, are used as probes and primers (in diagnostic assays, |
| CC | for quantifying gene expression, for detecting chromosomal anomalies and |
| CC | to isolate related sequences), for genetic immunization, as a source of |
| CC | therapeutic antisense, triplex-forming and ribozyme sequences, and for |
| CC | recombinant production of the protein |
| XX | |
| SQ | Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other; |
| | |
| | Query Match 98.7%; Score 878; DB 2; Length 893; |
| | Best Local Similarity 99.9%; Pred. No. 1.7e-284; |
| | Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1; |
| OY | 1 CAAGCTCTGAGAGCTTCTCTTCATCCTCGGTGAAGACTAAGACCTCAATTTCATA 60 |
| Dd | 1 CAAGCTCTGAGAGCTTCTCTTCATCCTCGGTGAAGACTAAGACCTCAATTTCATA 60 |
| OY | 61 GCATCTNAGACAGTGAGCATCTACGCTGGGTGATTTGCCCCCCCATCTCCGGGGAAATGTC 120 |
| Dd | 61 GCATCTNAGACAGTGAGCATCTACGCTGGGTGATTTGCCCCCCCATCTCCGGGGAAATGTC 120 |
| OY | 121 TGAAGAACAATTTTGTTGTAACCTCATATGAGGAGTGAAGAGAGATCAAGTGCATCAACAAC 180 |
| Dd | 121 TGAAGAACAATTTTGTTGTAACCTCATATGAGGAGTGAAGAGAGATCAAGTGCATCAACAAC 180 |
| OY | 181 TAGTGAGTAAAGGCGCAAGAGTGCCTCAACCTTCTCAATGTACAGGAGCGTCTCCCA 240 |
| Dd | 181 TAGTGAGTAAAGGCGCAAGAGTGCCTCAACCTTCTCAATGTACAGGAGCGTCTCCCA 240 |
| OY | 241 TTACACTAACCCATCCGAAGTGTCACTGTGTGAGACATPAGAAACCCTGTTTTGAGT 300 |
| Dd | 240 TTACACTAACCCATCCGAAGTGTCACTGTGTGAGACATPAGAAACCCTGTTTTGAGT 299 |
| OY | 301 AGAAAAAGGCGCTGGAAAGAGGGGAGCAAAATCTGTCTGCTCTCACTTAGTCATT 360 |
| Dd | 300 AGAAAAAGGCGCTGGAAAGAGGGGAGCAAAATCTGTCTGCTCTCACTTAGTCATT 359 |
| OY | 421 GGAGCACAGAGTAA CATCTCTCAGTGAACAGAGTGAACAAGGCGCTAAGGGAAAAGCGCTGA 480 |
| Dd | 420 GGAGCACAGAGTAA CATCTCTCAGTGAACAGAGTGAACAAGGCGCTAAGGGAAAAGCGCTGA 479 |
| OY | 481 TGGAATATATCTGAGCTGTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTACCTGCAAG 540 |
| Dd | 480 TGGAATATATCTGAGCTGTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTACCTGCAAG 539 |
| OY | 541 CCAGGTTCTGTAAGAGAAATGCGTGAAGTTCTAGCTCAGGTTTTCTTACTGTGAATTTAGA 600 |
| Dd | 540 CCAGGTTCTGTAAGAGAAATGCGTGAAGTTCTAGCTCAGGTTTTCTTACTGTGAATTTAGA 599 |

DT 12-AUG-2002 (first entry)
XX
XX Breast BS265 gene EST clone 3090742H1.
XX
XX BS265; human; breast; cancer; tumour; metastasis; diagnosis;
KW gene therapy; expressed sequence tag; EST; ss.
XX
XX Homo sapiens.
OS
PN US2002034749-A1.
XX
XX 21-MAR-2002.
XX
XX 07-MAY-2001; 2001US-00850178.
XX
XX 18-NOV-1997; 97US-00972376.
PR 18-NOV-1998; 98US-00193944.
XX
XX (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L A.
PA (RUSSE/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
P1 Granados EC, Hodges SC, KLAS MR, Kratochvil JD, Roberts-Rapp LA;
P1 Russell JC, Stroupe SD;
XX
XX WPI, 2002-403712/43.
DR
XX
XX New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
PT staging, monitoring, prognosticating, in vivo imaging, preventing,
PT treating, or determining the predisposition of an individual to breast
PT cancer.
XX
XX
XX Claim 1; Page 37; 52pp; English.
XX
XX
XX The present sequence is of BS265 gene expressed sequence tag (EST) full-
CC length sequence clone 3090742H1 (ATCC 98683). ESTs were derived from cDNA
CC libraries made from breast tumour tissues, breast non-tumour tissues and
CC numerous other tissues, and entered into a database as gene transcript
CC images. They were then evaluated to identify EST sequences that were
CC representative primarily of the breast tissue libraries, and were ranked
CC according to their abundance in target libraries and absence from
CC background libraries. Partial clones 3090742H1, 9991752, 92058967 and
CC g1615448 (see AB157345-48) represent the minimum number of clones that,
CC together with the present full-length sequence of clone 3090752H1, were
CC needed to form a contig and from which a consensus sequence (see
CC AB157330) was derived. ESTs corresponding to the consensus sequence of
CC BS265 were found in 33.3% (9/27) of breast tissue libraries, and in 0.6%
CC (3/476) of non-breast libraries. This set of contiguous and partially
CC overlapping cDNA sequences, designated as BS265 and transcribed from
CC breast tissue, and the polypeptides encoded by them, are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, in vivo
CC imaging, preventing, treating, or determining the predisposition of an
CC individual to diseases and conditions of the breast, such as breast
CC cancer. Also provided are antibodies which specifically bind to BS265
CC proteins, and agonists or inhibitors which prevent action of the
CC proteins, and which are useful for treatment of breast disease,
CC especially tumours and metastases
XX
XX Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other;
XX
XX Query Match 98.7%; Score 878; DB 6; Length 893;
XX Best Local Similarity 99.9%; Pred. No. 1.7e-284;
XX Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1

| | | |
|----------------------------------|-------------------------------------------------------------------|-----|
| QY | CAAGCTCTGAGGCTTCTCCCTTTCATACCTCGGTGAGACAGCTAAGACCTCACTTTTCAATA | 60 |
| Db | 1 CAAAGCTCTGAGGCTTCTCCCTTTCATCTCGGTGAGACAGCTAAGACCTCACTTTTCAATA | 60 |
| QY | 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGGCCCCCATCTCCGGGGAAATGTC | 120 |
| Db | 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGGCCCCCATCTCCGGGGAAATGTC | 120 |
| QY | 121 TGAAGACAATTTTGGTTTACCTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC | 180 |
| Db | 121 TGAAGACAATTTTGGTTTACCTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC | 180 |
| QY | 181 TAGTGTGATTAAGGCGCAGGGATGCTGTCAACCTCTTACATGTACAAGGAGCGTCTCCCA | 240 |
| Db | 181 TAGTGTGATTAAGGCGCAGGGATGCTGTCAACCTCTTACATGTACA -GAGCGTCTCCCA | 233 |
| QY | 241 TTACAACTACCCAACTCCGAAGTGTCAACTGTGTCCAGACTAAGAAACCTGTGTTTGAAGT | 300 |
| Db | 240 TTACAACTACCCAACTCCGAAGTGTCAACTGTGTCCAGACTAAGAAACCTGTGTTTGAAGT | 299 |
| QY | 301 AGAAAGGGCTCTGGAAAGAGGGGACCCAAATATGTGTCTCTTCTCACTTAAGTCAAT | 360 |
| Db | 300 AGAAAGGGCTCTGGAAAGAGGGGACCCAAATATGTGTCTCTTCTCACTTAAGTCAAT | 359 |
| QY | 361 GGGCAATTAAGCAATTTCTCTTTTGGCTGTCCCTCAGACAAGAGAGCAGAACTTATC | 420 |
| Db | 360 GGGCAATTAAGCAATTTCTCTTTTGGCTGTCCCTCAGACAAGAGAGCAGAACTTATC | 419 |
| QY | 421 GGGCACCGAGATPACATCTCTCAGTGAACAAGTTGACAAAGGCTTATGGAAATGCTGA | 480 |
| Db | 420 GGGCACCGAGATPACATCTCTCAGTGAACAAGTTGACAAAGGCTTATGGAAATGCTGA | 479 |
| QY | 481 TGGGATTAATCTCAGCTTGTGAAGCTTCAAGTTTCTTCCCTCATTTCAACCTGTGAAG | 540 |
| Db | 480 TGGGATTAATCTCAGCTTGTGAAGCTTCAAGTTTCTTCCCTCATTTCAACCTGTGAAG | 539 |
| QY | 541 CCAAGTTCTGTAAAGAAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTGAATTTAGA | 600 |
| Db | 540 CCAAGTTCTGTAAAGAAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTGAATTTAGA | 599 |
| QY | 601 TCTTCAGACCCCTCTCGGCACAATTCAAATTAAGGCACAAACATATACCTTCCATGAA | 660 |
| Db | 600 TCTTCAGACCCCTCTCGGCACAATTCAAATTAAGGCACAAACATATACCTTCCATGAA | 659 |
| QY | 661 GCAACAACAGACTTTTGAAGAGCAACAATGACTGTGAATTGAAGCCTTGAAGAAATG | 720 |
| Db | 660 GCAACAACAGACTTTTGAAGAGCAACAATGACTGTGAATTGAAGCCTTGAAGAAATG | 719 |
| QY | 721 AAGCTTTGAAGAAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCAATGTGTGA | 780 |
| Db | 720 AAGCTTTGAAGAAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCAATGTGTGA | 779 |
| QY | 841 TGAATTTAAGTTCGATTCGTTCAGAGAAATGATTAATATATACATTTTCCCT 890 | |
| Db | 840 TGAATTTAAGTTCGATTCGTTCAGAGAAATGATTAATATATACATTTTCCCT 889 | |
| RESULT 6 | | |
| ABL57350 standard; cDNA; 893 BP. | | |
| XX | ABL57350; | |
| XX | ABL57350; | |
| XX | 12-AUG-2002 (first entry) | |
| XX | Breast BS265 gene consensus sequence. | |
| DE | BS265; human; breast; cancer; tumour; metastasis; diagnosis; | |

| | |
|----|---------------------------------------------------------------------------|
| XX | gene therapy; expressed sequence tag; EST; gene; ss. |
| OS | Homo sapiens. |
| XX | |
| XX | Location/Qualifiers |
| FT | 1..123 |
| FT | /*tag= a |
| FT | /product= "BS265" |
| FT | /partial |
| FT | /note= "the CDS does not include a start codon" |
| XX | |
| PN | US2002034749-A1. |
| XX | |
| XX | 21-MAR-2002. |
| XX | |
| XX | 07-MAY-2001; 2001US-00850178. |
| XX | |
| XX | 18-NOV-1997; 97US-00972376. |
| PR | 18-NOV-1998; 98US-00193944. |
| XX | |
| XX | (BILL/) BILLINGEL P A. |
| PA | (COHE/) COHEN M. |
| PA | (COLP/) COLPITTS T L. |
| PA | (FRIE/) FRIEDMAN P N. |
| PA | (GORD/) GORDON J. |
| PA | (GRAM/) GRANADOS E N. |
| PA | (HODG/) HODGES S C. |
| PA | (KLAAS/) KLAAS M R. |
| PA | (KRAT/) KRATOCHVIL J D. |
| PA | (ROBE/) ROBERTS-RAPP L A. |
| PA | (RUSSEL/) RUSSELL J C. |
| PA | (STROU/) STROUPE S D. |
| XX | |
| PI | Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, |
| PI | Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp LA; |
| PI | Russell JC, Stroupe SD; |
| XX | |
| DR | WPI; 2002-403712/43. |
| DR | P-PSDB; ABB76272. |
| XX | |
| PT | New BS265 proteins and nucleic acids, useful for detecting, diagnosing, |
| PT | staging, monitoring, prognosticating, in vivo imaging, preventing, |
| PT | treating, or determining the predisposition of an individual to breast |
| PT | cancer. |
| XX | |
| XX | Claim 1; Page 38; 52pp; English. |
| PS | |
| XX | |
| CC | The present sequence is a consensus sequence of the human breast BS265 |
| CC | gene. Expressed sequence tags (ESTs) were derived from cDNA libraries |
| CC | made from breast tumor tissues, breast non-tumor tissues and numerous |
| CC | other tissues, and entered into a database as gene transcript images. |
| CC | They were then evaluated to identify EST sequences that were |
| CC | representative primarily of the breast tissue libraries, and were ranked |
| CC | according to their abundance in target libraries and absence from |
| CC | background libraries. 4 overlapping EST clones, together with a full- |
| CC | length sequence (see ABLS7345-49), were used to form a contig from which |
| CC | the present consensus sequence was derived. ESTs corresponding to the |
| CC | consensus sequence were found in 33.3% (9/27) of breast tissue libraries |
| CC | and in 0.6% (3/476) of non-breast libraries. The set of contiguous and |
| CC | partially overlapping cDNA sequences, designated as BS265 and transcribed |
| CC | from breast tissue, and the polypeptides encoded by them, are useful for |
| CC | detecting, diagnosing, staging, monitoring, prognosticating, in vivo |
| CC | imaging, preventing, treating, or determining the predisposition of an |
| CC | individual to diseases and conditions of the breast, such as breast |
| CC | cancer. Also provided are antibodies which specifically bind to BS265 |
| CC | proteins, and agonists or inhibitors which prevent action of the |
| CC | proteins, and which are useful for treatment of breast disease, |
| CC | especially tumors and metastases |
| XX | |
| SQ | Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other; |

Query Match

98.7%; Score 878; DB 6; Length 893;

Best Local Similarity

99.9%; Pred. No. 1,76-284;

[illegible]

CC The present invention describes an isolated polypeptide comprising an
 CC immunogenic portion of an ovarian carcinoma protein (or its variants).
 CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
 CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
 CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
 CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
 CC cancer. AA69691 to AA70077 and AA81552 to AA81557 represent human
 CC ovarian carcinoma polynucleotides and proteins used in the
 CC exemplification of the present invention
 CC

XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 3; Length 2627;

Best Local Similarity 99.9%; Pred. No. 3.1e-284;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGAGCTTAAGACTCAAGTTTCAATA 60
 DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGAGCTTAAGACTCAAGTTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGCTGAGCTGGGGGATTTTGCCGCCATCTCCGGGGGAATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGCTGAGCTGGGGGATTTTGCCGCCATCTCCGGGGGAATGTC 1840
 QY 121 TGAAGCAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
 DB 1841 TGAAGCAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
 QY 181 TAGTGATTAAGGCGCAGGGATGCTGCTCAACCTCCATGATGACAGGAGACGTTCTCCCA 240
 DB 1901 TAGTGATTAAGGCGCAGGGATGCTGCTCAACCTCCATGATGACAGGAGACGTTCTCCCA 1959
 QY 241 TTACAACTACCCCAATCCGAAGTGTCAACTGTGTGACAGACCTAAGAAACCTTGTTTGAAT 300
 DB 1960 TTACAACTACCCCAATCCGAAGTGTCAACTGTGTGACAGACCTAAGAAACCTTGTTTGAAT 2019
 QY 301 AGAAAAAGGCGCTGAAAAAGAGGAGGCAAAATCTGTCTCTCTCTCAATTAGTCATT 360
 DB 2020 AGAAAAAGGCGCTGAAAAAGAGGAGGCAAAATCTGTCTCTCTCTCAATTAGTCATT 2079
 QY 361 GGGAAATTAAGCATCTGTCTTCTTGGCTGTGCTGCTCAGACACAGAGCCAGAACTTATC 420
 DB 2080 GGGAAATTAAGCATCTGTCTTCTTGGCTGTGCTGCTCAGACACAGAGCCAGAACTTATC 2139
 QY 421 GGGCAGCAGGATTAACATCTCTCAGTAAAGAGTGAAGAGGCTTATGGAATGCTGA 480
 DB 2140 GGGCAGCAGGATTAACATCTCTCAGTAAAGAGTGAAGAGGCTTATGGAATGCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTGTGAGCTTGAAGTTTCTTCCCTTCAATCTACCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTGTGAGCTTGAAGTTTCTTCCCTTCAATCTACCTGCAAG 2259
 QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAAGTTTCTTACTCTGAATTAA 600
 DB 2260 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAAGTTTCTTACTCTGAATTAA 2319
 QY 601 TCTCCAGACCTCTCGGCACAATTCAAATTAAAGGCAACAAATATACCTTCCATGA 660
 DB 2320 TCTCCAGACCTCTCGGCACAATTCAAATTAAAGGCAACAAATATACCTTCCATGA 2379
 QY 661 GCACACACAGACTTTGAAAGCAAGGACATGACTCTGTAATTAAGGCGCTTGAAGAAATG 720
 DB 2380 GCACACACAGACTTTGAAAGCAAGGACATGACTCTGTAATTAAGGCGCTTGAAGAAATG 2439
 QY 721 AAGCTTTGAAGAAAAAATACCTTTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 780
 DB 2440 AAGCTTTGAAGAAAAAATACCTTTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 2499
 QY 781 ACCACTGCGCTCTGAGACCTTGAGGCAAGGATGATGATATCATGTTGTTATAGAAAC 840
 DB 2500 ACCACTGCGCTCTGAGACCTTGAGGCAAGGATGATGATATCATGTTGTTATAGAAAC 2559
 QY 841 TGAATTTAGAGTTCTGATGCTTCAGAGAAATGATTAATATACATTTCT 890

DB 2560 TGAATTTAGAGTTCTGATGCTTCAGAGAAATGATTAATATACATTTCT 2609

RESULT 9

AAH55681

ID AAH55681 standard; DNA; 2627 BP.

AAH55681;

04-SEP-2001 (first entry)

Human ovarian tumour-derived antigen OBE DNA sequence.

Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;

antigen; OBE; ds.

Homo sapiens.

WO200140269-A2.

07-JUN-2001.

29-NOV-2000; 2000WO-US032520.

30-NOV-1999; 99US-00451651.

22-FEB-2000; 2000US-00510662.

10-MAR-2000; 2000US-00523586.

07-APR-2000; 2000US-00545068.

15-MAY-2000; 2000US-00571025.

(CORI-) CORIXA CORP.

Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;

WPI; 2001-356154/37.

N-PSDB; AAB99204; AAB99205.

Breast tumor polypeptides and the nucleic acids that encode them, useful

for the prevention, diagnosis and treatment of breast cancer.

Claim 24; Page 189; 22pp; English.

The present invention relates to human breast tumour protein coding

sequences (see AAH5479-AAH5513, AAH5517-AAH5679 and AAH5682-

AAH5762). The breast tumour protein DNA sequences may be used in the

prevention, diagnosis and treatment of diseases associated with

CC inappropriate expression of the breast tumour protein e.g. breast cancer.

CC The present sequence is a human ovarian tumour-derived antigen coding

sequence, which was used in an example from the present invention

XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 4; Length 2627;

Best Local Similarity 99.9%; Pred. No. 3.1e-284;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGAGCTTAAGACTCAAGTTTCAATA 60
 DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGAGCTTAAGACTCAAGTTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGCTGAGCTGGGGGATTTTGCCGCCATCTCCGGGGGAATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGCTGAGCTGGGGGATTTTGCCGCCATCTCCGGGGGAATGTC 1840
 QY 121 TGAAGCAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
 DB 1841 TGAAGCAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
 QY 181 TAGTGATTAAGGCGCAGGGATGCTGCTCAACCTCCATGATGACAGGAGACGTTCTCCCA 240
 DB 1901 TAGTGATTAAGGCGCAGGGATGCTGCTCAACCTCCATGATGACAGGAGACGTTCTCCCA 1959

QY 241 TTACAACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGTGTTTGTAGT 300
 DB 1960 TTACAACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGTGTTTGTAGT 2019
 QY 301 AGAAAGGCGCTTGAAAGAGGGGAGCCAAATCTGTCTGTCTTCTCACTAATAGTCATT 360
 DB 2020 AGAAAGGCGCTTGAAAGAGGGGAGCCAAATCTGTCTGTCTTCTCACTAATAGTCATT 2079
 QY 361 GGGCAATTAAGCAATCTGTCTTGTGCTGCTGCTGAGCAAGAGGAGCCGAATCTATC 420
 DB 2080 GGGCAATTAAGCAATCTGTCTTGTGCTGCTGAGCAAGAGGAGCCGAATCTATC 2139
 QY 421 GGGCACCAGATACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTCTGA 480
 DB 2140 GGGCACCAGATACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATTCACCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATTCACCTGCAAG 2259
 QY 541 CCAAGTTCTGTAAAGAAATGCCGAGTTCTAGCTCAGGTTTCTTACTTGAAATTTAGA 600
 DB 2260 CCAAGTTCTGTAAAGAAATGCCGAGTTCTAGCTCAGGTTTCTTACTTGAAATTTAGA 2319
 QY 601 TCTCCAGACCCCTTCTGTGGCCAAATTCAAATTAAGCAACAAATATACCTTCCATGAA 660
 DB 2320 TCTCCAGACCCCTTCTGTGGCCAAATTCAAATTAAGCAACAAATATACCTTCCATGAA 2379
 QY 661 GCAACACAGACTTTTGAAGAGCAAGCAATGACTGCTTAATTAAGGAGGCTTGAAGAGATG 720
 DB 2380 GCAACACAGACTTTTGAAGAGCAAGCAATGACTGCTTAATTAAGGAGGCTTGAAGAGATG 2439
 QY 721 AACCTTGAAGAAAGAAATTAATTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTGA 780
 DB 2440 AACCTTGAAGAAAGAAATTAATTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTGA 2499
 QY 781 ACCACTGCTTCTGTGAGCACTTGGAGCCAGGTGACTGTATTAATGTTTATTAAGAAAC 840
 DB 2500 ACCACTGCTTCTGTGAGCACTTGGAGCCAGGTGACTGTATTAATGTTTATTAAGAAAC 2559
 QY 841 TGAATTTAGAGTTCTGATGCTTCAAGAAATGATTAATAATACATTTCT 890
 DB 2560 TGAATTTAGAGTTCTGATGCTTCAAGAAATGATTAATAATACATTTCT 2609
 RESULT 10
 ABN72971
 ID ABN72971 standard; DNA; 2627 BP.
 AC ABN72971;
 DT 02-JUL-2002 (first entry)
 DE Ovarian carcinoma polynucleotide O8B.
 KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
 OS Homo sapiens.
 PN WO200206317-A2.
 PD 24-JAN-2002.
 PF 17-JUL-2001; 2001WO-US022635.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00884441.
 (CORI-) CORIXA CORP.
 PA
 XX

PI Mitcham JL, King GE, Aislice PA, Filing SP, Retter MW, Fanger GR;
 PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
 XX WPI; 2002-164781/21.
 DR P-PSDB; ABP30900, ABP30901.
 XX
 PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
 PT protein or its variants, useful for stimulating an immune response in a
 PT patient and treating ovarian cancer.
 XX
 PS Example 2; Page 319-320; 408bp; English.
 XX
 CC This invention relates to polypeptides comprising an immunogenic portion
 CC of an ovarian carcinoma protein which acts as an immunostimulant and is
 CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations and antigen presenting cells that express
 CC the polypeptides are useful for stimulating an immune response in a
 CC patient and treating ovarian cancer. This sequence represents DNA related
 CC to the invention
 XX
 SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other:
 Query Match 98.7%; Score 878; DB 6; Length 2627;
 Best Local Similarity 99.9%; Pred. No. 3.1e-284;
 Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 CAAAGCTGTGAGCTTCTCTTCTTCAATCTGCTGAGCAAGCTAAGACTCAATTTCAATA 60
 DB 1721 CAAAGCTGTGAGCTTCTCTTCTTCAATCTGCTGAGCAAGCTAAGACTCAATTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGGATTTGGCCCCCATCTCGGGGGAAATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGGATTTGGCCCCCATCTCGGGGGAAATGTC 1840
 QY 121 TGAAGCAATTTTGTATCTCAATGAGGAGTGAAGAGATACAGTCTATACCAAC 180
 DB 1841 TGAAGCAATTTTGTATCTCAATGAGGAGTGAAGAGATACAGTCTATACCAAC 1900
 QY 181 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTCTCAATGATGAGGAGCTCTCCCA 240
 DB 1901 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTCTCAATGATGAGGAGCTCTCCCA 1959
 QY 241 TTACAACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGTGTTTGTAGT 300
 DB 1960 TTACAACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGTGTTTGTAGT 2019
 QY 301 AGAAAGGCGCTTGAAAGAGGGGAGCCAAATCTGTCTGTCTTCTCACTAATAGTCATT 360
 DB 2020 AGAAAGGCGCTTGAAAGAGGGGAGCCAAATCTGTCTGTCTTCTCACTAATAGTCATT 2079
 QY 361 GGGCAATTAAGCAATCTGTCTTGTGCTGCTGAGCAAGAGGAGCCGAATCTATC 420
 DB 2080 GGGCAATTAAGCAATCTGTCTTGTGCTGCTGAGCAAGAGGAGCCGAATCTATC 2139
 QY 421 GGGCACCAGATACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTCTGA 480
 DB 2140 GGGCACCAGATACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATTCACCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATTCACCTGCAAG 2259
 QY 541 CCAAGTTCTGTAAAGAAATGCCGAGTTCTAGCTCAGGTTTCTTACTTGAAATTTAGA 600
 DB 2260 CCAAGTTCTGTAAAGAAATGCCGAGTTCTAGCTCAGGTTTCTTACTTGAAATTTAGA 2319
 QY 601 TCTCCAGACCCCTTCTGTGGCCAAATTCAAATTAAGCAACAAATATACCTTCCATGAA 660
 DB 2320 TCTCCAGACCCCTTCTGTGGCCAAATTCAAATTAAGCAACAAATATACCTTCCATGAA 2379
 QY 661 GCAACACAGACTTTTGAAGAGCAAGCAATGACTGCTTAATTAAGGAGGCTTGAAGAGATG 720
 DB 2380 GCAACACAGACTTTTGAAGAGCAAGCAATGACTGCTTAATTAAGGAGGCTTGAAGAGATG 2439

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OY 721 AAGCTTTGAAGAAAAAGATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTTA 780
DB 2440 AAGCTTTGAAGAAAAAGATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTTA 2499
OY 781 ACCACTGCTCTCTGAGACCTTGAGCCAGCGTGACTGTATTACATGTTGTTATAGAAAAC 840
DB 2500 ACCACTGCTCTCTGAGACCTTGAGCCAGCGTGACTGTATTACATGTTGTTATAGAAAAC 2559
OY 841 TGAATTTAGATTCTGATCGTTCAAGAGATGATTTAATATACATTTCT 890
DB 2560 TGAATTTAGATTCTGATCGTTCAAGAGATGATTTAATATACATTTCT 2609

RESULT 11
ADA08544
ID ADA08544 standard; cDNA; 2627 BP.
XX
AC ADA08544;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human ovarian carcinoma polynucleotide OSE.
XX
KW ss; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
DR WPI; 2003-532352/50.
XX
PT New isolated 0772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
PS Example 2; SEQ ID NO 391; 371pp; English.
XX
CC The invention relates to an isolated 0772P polypeptide, which has the
CC structure fully defined in the specification. The composition containing
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen polynucleotide.
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
XX
Query Match 98.7%; Score 878; DB 9; Length 2627;
Best Local Similarity 99.9%; Pred. No. 3.1e-284;

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Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 1 CAAGCTGAGGCTTCTCTTTCATCTCTGGTGAGACGTAAGACTCAGTTTCAATA 60
DB 1721 CAAGCTGAGGCTTCTCTTTCATCTCTGGTGAGACGTAAGACTCAGTTTCAATA 1780
OY 61 GCATCTAAGACAGTGGGACTCAGCTGGGATTTCCGCCCCCATCTCCGGGGAAATGTC 120
DB 1781 GCATCTAAGACAGTGGGACTCAGCTGGGATTTCCGCCCCCATCTCCGGGGAAATGTC 1840
OY 121 TGAAGACAATTTGGTTACTCCCAATGAGGAGTGGAGAGATACAGTCTACCAAC 180
DB 1841 TGAAGACAATTTGGTTACTCCCAATGAGGAGTGGAGAGATACAGTCTACCAAC 1900
OY 181 TAGTGATTAAGGCGCAGGAGATGCTGCTCACTCCCTACCATGTACAGGAGCTCTCCCA 240
DB 1901 TAGTGATTAAGGCGCAGGAGATGCTGCTCACTCCCTACCATGTACAGGAGCTCTCCCA 1959
OY 241 TTACAACTAACCCCAATCCGAAGTGTCACTGTGTGAGACTAAGAAACCTGTTTGAAGT 300
DB 1960 TTACAACTAACCCCAATCCGAAGTGTCACTGTGTGAGACTAAGAAACCTGTTTGAAGT 2019
OY 301 AGAAAAGGCGCTGGAAGAGGGGAGCCCAAAATGTCGTGCTGCTGACATTAAGTACT 360
DB 2020 AGAAAAGGCGCTGGAAGAGGGGAGCCCAAAATGTCGTGCTGCTGACATTAAGTACT 2079
OY 361 GGCAAATTAAGCATTTCTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 2080 GGCAAATTAAGCATTTCTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139
OY 421 GGGCACCAAGATTAACATCTCTGAGTGAACAGAGTTGAACAAGGCTTATGGAAATGCTTGA 480
DB 2140 GGGCACCAAGATTAACATCTCTGAGTGAACAGAGTTGAACAAGGCTTATGGAAATGCTTGA 2199
OY 481 TGGGATTAATCTTCACTTGTGAGCTTGAAGTTCTTATAGTTCTTCCCTTATCTACCTGCAAG 540
DB 2200 TGGGATTAATCTTCACTTGTGAGCTTGAAGTTCTTATAGTTCTTCCCTTATCTACCTGCAAG 2259
OY 541 CCAAGTTCTGTAAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTAGA 600
DB 2260 CCAAGTTCTGTAAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTAGA 2319
OY 601 TCTCCAGACCTTCTGCGCCACAAATTAAGGCAACAACTATACCTTCATGAA 660
DB 2320 TCTCCAGACCTTCTGCGCCACAAATTAAGGCAACAACTATACCTTCATGAA 2379
OY 661 GCACACACAGACTTTGAAAGCAAGACATGACTGTGAATTGAGGCTTGAAGAAATG 720
DB 2380 GCACACACAGACTTTGAAAGCAAGACATGACTGTGAATTGAGGCTTGAAGAAATG 2439
OY 721 AAGCTTTGAAGAAAAAGATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTTA 780
DB 2440 AAGCTTTGAAGAAAAAGATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTTA 2499
OY 781 ACCACTGCTCTCTGAGACCTTGAGCCAGCGTGACTGTATTACATGTTGTTATAGAAAAC 840
DB 2500 ACCACTGCTCTCTGAGACCTTGAGCCAGCGTGACTGTATTACATGTTGTTATAGAAAAC 2559
OY 841 TGAATTTAGATTCTGATCGTTCAAGAGATGATTTAATATACATTTCT 890
DB 2560 TGAATTTAGATTCTGATCGTTCAAGAGATGATTTAATATACATTTCT 2609

RESULT 12
ADP08887
ID ADP08887 standard; cDNA; 2627 BP.
XX
AC ADP08887;
XX
DT 12-FEB-2004 (first entry)
XX
DE cDNA encoding secreted ovarian carcinoma antigen seqid 391.
XX

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KM Gene therapy; protein therapy; vaccine; antibody inhibition;
 KM breast cancer; restorative therapy; diagnostic agent; immunoassay;
 KM secreted ovarian carcinoma antigen; gene; ss.
 XX Homo sapiens.
 OS
 PN US2003124140-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 17-JUL-2002; 2002US-00198053.
 XX
 PR 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00884441.
 PR 17-JUL-2001; 2001US-00907969.
 XX
 PA (CORI-) CORIXA CORP.
 PI Bangur CS, Retter MW, Fanger GR, Hill P;
 PI WPI; 2003-897152/82.
 DR P-PSDB; ADF08888, ADF08889.
 XX
 PT Oncogenic nucleic acids useful for the prevention, diagnosis and
 XX treatment of breast cancer.
 XX
 SS Example 2; SEQ ID NO 391; 399pp; English.
 XX
 CC The invention describes nucleic acids (I) and the polypeptides (II) they
 CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
 CC treating diseases related to their aberrant expression i.e. breast
 CC cancers. For example, (I) and (II) may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of (II) by expressing
 CC inactive proteins or to supplement the patients own production of (II).
 CC Additionally, (I) may be used to produce (II), by inserting (I) into a
 CC host cell and culturing the cell to express the protein (II). (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. The host cell may also be used as antigens in the production of
 CC antibodies against (II) and in assays to identify modulators of (II)'s
 CC expression and activity. The anti-(II) antibodies, agonists and
 CC antagonists may be used to regulate expression and activity and as
 CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
 CC immunoassay). This sequence represents a polynucleotide encoding a
 CC secreted ovarian carcinoma antigen.
 XX
 SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 10; Length 2627;
 Best Local Similarity 99.9%; Pred. No. 3.1e-284;
 Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 CAAGCTCTGAGGCTTCCCTTCATCCGCGTGAAGAGTAGAGCTGTTTCAATA 60
 DB 1721 CAGGCTCTGAGGCTTCCCTTCATCCGCGTGAAGAGTAGAGCTGTTTCAATA 1780
 QY 61 GCATCTAGAGCACTGAGCACTGAGGATGATTTGCCCCCATCTCCGGGGGAATGTC 120
 DB 1781 GCATCTAGAGCACTGAGCACTGAGGATGATTTGCCCCCATCTCCGGGGGAATGTC 1840
 QY 121 TGAAGCAATTTGTTTACTCTCAATGAGGAGTGAAGAGATACAGTGTCTACTACCAAC 180
 DB 1841 TGAAGCAATTTGTTTACTCTCAATGAGGAGTGAAGAGATACAGTGTCTACTACCAAC 1900

QY 181 TAGGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTACCTATGATAGAGGAGCTCCCCA 240
 DB 1901 TAGGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTACCTATGATAGAGGAGCTCCCCA 1959
 QY 241 TTACAACTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAGAGAACCTGTGTTGAGT 300
 DB 1960 TTACAACTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAGAGAACCTGTGTTGAGT 2019
 QY 301 AGAAAAAGGCGCTGGAAAAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACTAGTCATT 360
 DB 2020 AGAAAAAGGCGCTGGAAAAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACTAGTCATT 2079
 QY 361 GGCATAATAGCAATCTGTCTTGTGCTGTGCTGCTGAGCAAGAGAGCCAGAACTCATC 420
 DB 2080 GGCATAATAGCAATCTGTCTTGTGCTGTGCTGCTGAGCAAGAGAGCCAGAACTCATC 2139
 QY 421 GGGCACCAAGATTAACATCTCTCAGTGAAGAGAGTTGACAGGCTTATGGAAAAATGCTCTGA 480
 DB 2140 GGGCACCAAGATTAACATCTCTCAGTGAAGAGAGTTGACAGGCTTATGGAAAAATGCTCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTCCCTTCAATTCACCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTCCCTTCAATTCACCTGCAAG 2259
 QY 541 CCAAGTTCTGTAGAGAAAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTGAATTAGA 600
 DB 2260 CCAAGTTCTGTAGAGAAAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTGAATTAGA 2319
 QY 601 TCTCCAGACCTCTCTGCGCACAAATTCAAATTAAAGGCAACAAATATACCTTCCATGAA 660
 DB 2320 TCTCCAGACCTCTCTGCGCACAAATTCAAATTAAAGGCAACAAATATACCTTCCATGAA 2379
 QY 661 GCACACACAGACTTTTGAAGAGCAAGACATGACTCTGTAATTGAGCGCTTGAGGATG 720
 DB 2380 GCACACACAGACTTTTGAAGAGCAAGACATGACTCTGTAATTGAGCGCTTGAGGATG 2439
 QY 721 AAGCTTTGAAGAAAAAATACCTTGTTCAGGCCCCCTTCCAGACTGTTATGAGTTA 780
 DB 2440 AAGCTTTGAAGAAAAAATACCTTGTTCAGGCCCCCTTCCAGACTGTTATGAGTTA 2499
 QY 781 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTCAGTATTTACATGTTTATAGAAAAAC 840
 DB 2500 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTCAGTATTTACATGTTTATAGAAAAAC 2559
 QY 841 TGATTTTAAGATTTGATGCTTCAAGAGATGATTAATATACATTTCT 890
 DB 2560 TGATTTTAAGATTTGATGCTTCAAGAGATGATTAATATACATTTCT 2609

RESULT 13
 ADG46174
 ID ADG46174 standard; cDNA; 2627 BP.
 XX
 AC ADG46174;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human ovarian carcinoma polynucleotide #387.
 DE Human ovarian carcinoma; gene; ss; 08E; ovarian cancer;
 KM Human; ovarian carcinoma; gene; ss; 08E; ovarian cancer;
 KM secreted tumour antigen; cytostatic; 0772P.
 OS Homo sapiens.
 OS
 PN US2003165504-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 04-APR-2001; 2001US-00827271.
 XX
 PR 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.

PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
XX
XX (RETT/) RETTER M W.
XX (FANG/) FANGER G R.
XX
XX Retter MM, Fanger GR;
XX
XX WPI; 2003-898035/B2.
XX
XX
XX New isolated OBE or O772P polypeptides, useful for diagnosing,
XX preventing, treating and monitoring cancer, e.g. ovarian cancer,
XX stimulating the immune response in patient.
XX
XX Example 2; SEQ ID NO 391; 290pp; English.
XX
XX
XX The invention relates to human ovarian carcinoma polypeptides, designated
XX OBE or O772P, and the polynucleotides encoding them. The invention also
XX relates to methods for inhibiting the development of cancer, e.g. ovarian
XX cancer in a patient, methods for stimulating and/or expanding T cells and
XX methods for identifying secreted tumour antigens. The polypeptides,
XX compositions, antibodies to the polypeptides and methods are useful for
XX diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
XX cancer. The composition is particularly useful for stimulating an immune
XX response in patient. This sequence represents a human ovarian carcinoma
XX polynucleotide of the invention.
XX
XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 10; Length 2627;

Best Local Similarity 99.9%; Pred. No. 3.1e-284;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTTAAGACCTCAAGTTTCAATA 60
DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTTAAGACCTCAAGTTTCAATA 1780
QY 61 GGATCTAGAGAGAGTGGAGCTCAAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 120
DB 1781 GCAATCTAGAGAGAGTGGAGCTCAAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 1840
QY 121 TGAAGACAATTTTGGTTACCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
DB 1841 TGAAGACAATTTTGGTTACCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
QY 181 TAGTGATTAAGAGCCAGGAGTGTCTCAACTCTCAATGATTAACAGGAGCTTCCCA 240
DB 1901 TAGTGATTAAGAGCCAGGAGTGTCTCAACTCTCAATGATTAACAGGAGCTTCCCA 1959
QY 241 TTACAACCTACCAATCCGAAGTGTCAAGTGTCAAGAGCTAAGAAAACCTGGTTTGAAT 300
DB 1960 TTACAACCTACCAATCCGAAGTGTCAAGTGTCAAGAGCTAAGAAAACCTGGTTTGAAT 2019
QY 301 AGAAAAAGGCTGGAAGAAGAGGAGCCAAACAATCTGTCTCTCTCAATTAAGTCAAT 360
DB 2020 AGAAAAAGGCTGGAAGAAGAGGAGCCAAACAATCTGTCTCTCTCAATTAAGTCAAT 2079
QY 361 GGGCAATAAGCATTTCTCTTTGGCTGCTGCTTGAAGACAGAGAGCCAGAACTTATC 420
DB 2080 GGGCAATAAGCATTTCTCTTTGGCTGCTGCTTGAAGACAGAGAGCCAGAACTTATC 2139
QY 421 GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGGGAATGCTGA 480
DB 2140 GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGGGAATGCTGA 2199
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCAAGTTTCTTCCCTCAATTTACCTGCAAG 540
DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCAAGTTTCTTCCCTCAATTTACCTGCAAG 2259
QY 541 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600

DB 2260 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
QY 601 TCTCCAGACCCCTCTGCGCAACATTTCAATTAAGCAACAACATATACCTTCCATGAA 660
DB 2320 TCTCCAGACCCCTCTGCGCAACATTTCAATTAAGCAACAACATATACCTTCCATGAA 2379
QY 661 GCACACACAGACTTTTGAAGACAGACATGACTGCTTGAATTGAGGCTTGAAGAAATG 720
DB 2380 GCACACACAGACTTTTGAAGACAGACATGACTGCTTGAATTGAGGCTTGAAGAAATG 2439
QY 721 AAGCTTGAAGGAAAGAAATCTTTGTTCCAGCCCTCCCACTCTTCATGTTGA 780
DB 2440 AAGCTTGAAGGAAAGAAATCTTTGTTCCAGCCCTCCCACTCTTCATGTTGA 2499
QY 781 ACCACTGCTTCTCTGAGACTTGAAGCCAGAGTGACTGATTAACATGTTGTTAAGAAAAC 840
DB 2500 ACCACTGCTTCTCTGAGACTTGAAGCCAGAGTGACTGATTAACATGTTGTTAAGAAAAC 2559
QY 841 TGATTTTGAAGTTCTGATGCTTCAAGAGAAATGATTAATATACATTCTCT 890
DB 2560 TGATTTTGAAGTTCTGATGCTTCAAGAGAAATGATTAATATACATTCTCT 2609
RESULT 14
ADN40452
ID ADN40452 standard; cDNA; 2627 BP.
XX
XX ADN40452;
XX
XX
XX 12-AUG-2004 (first entry)
XX
XX
XX Human breast cancer associated cDNA sequence #203.
XX
XX Human; breast cancer; T cell; tumour protein; antigen presenting cell;
XX immune response; CD4+; CD8+; cytostatic; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2004101899-A1.
XX
XX
XX 27-MAY-2004.
XX
XX
XX 13-NOV-2003; 2003US-00714389.
XX
XX
XX 30-NOV-1999; 99US-00451651.
XX 22-FEB-2000; 2000US-00510662.
XX 10-MAR-2000; 2000US-00523586.
XX 07-APR-2000; 2000US-00545068.
XX 15-MAY-2000; 2000US-00571025.
XX 06-FEB-2001; 2001US-00778320.
XX
XX
XX (CORI-) CORIXA CORP.
XX
XX
XX Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;
XX McNeill PD;
XX
XX WPI; 2004-399689/37.
XX P-PSDB; ADN40453, ADN40454.
XX
XX
XX New polynucleotides, useful for treating and diagnosing cancer,
XX particularly breast cancer by stimulating immune response in a patient
XX and inhibiting the development of cancer.
XX
XX
XX Claim 1; SEQ ID NO 207; 151pp; English.
XX
XX The present invention relates to polynucleotide and polypeptide sequences
XX associated with breast cancer. Also disclosed are expression vectors
XX comprising the polynucleotide sequences of the invention operably linked
XX to an expression control sequence, host cells comprising the vector,
XX antibodies (or antigen binding fragments of antibodies) specifically
XX binding the polypeptides of the invention, fusion proteins comprising at
XX least one of the polypeptides, stimulating and/or expanding T cells
XX specific for a tumour protein. The polynucleotide sequences, polypeptide

CC sequences, and antigen presenting cells can be administered
 CC therapeutically/prophylactically to induce an immune response. They can
 CC be included with a physiological carrier/immunostimulant in compositions
 CC such as vaccines, particularly to treat or prevent cancers such as breast
 CC cancer. They can also be used to inhibit the development of cancer by
 CC incubating one or more of them with CD4+ and/or CD8+ T cells isolated
 CC from a patient, such that the T cells proliferate, and administering the
 CC proliferated T cells to the patient. The polynucleotide sequences are
 CC useful for detecting cancer in a patient, producing fusion proteins,
 CC producing T cell populations and antigen presenting cells. The present
 CC sequence represents a polynucleotide sequence of the invention.

XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 12; Length 2627;

Best Local Similarity 99.9%; Pred. No. 3.1e-284;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGCAGTAAAGACCTCAGTTTCAATA 60
 DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGCAGTAAAGACCTCAGTTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGGATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGGATGTC 1840
 QY 121 TGAAGCAATTTTGTTAAGTCAATGAGGAGTGGAGAGATGATGCTACTACCAAC 180
 DB 1841 TGAAGCAATTTTGTTAAGTCAATGAGGAGTGGAGAGATGATGCTACTACCAAC 1900
 QY 181 TAGTGATTAAGGCGAGGAGTGTCTCAACCTCTCACTGATGACAGGAGCTGCCCA 240
 DB 1901 TAGTGATTAAGGCGAGGAGTGTCTCAACCTCTCACTGATGACAGGAGCTGCCCA 1959
 QY 241 TTACAACTACCCCAATCCGAAGTGTCACTGTGACAGACTAAGAAACCTGTGTTAGT 300
 DB 1960 TTACAACTACCCCAATCCGAAGTGTCACTGTGACAGACTAAGAAACCTGTGTTAGT 2019
 QY 301 AGAAAGGCGCTGGAAAGAGGAGCCCAACAATCTGTCTGCTTCCCAATTATGTCAT 360
 DB 2020 AGAAAGGCGCTGGAAAGAGGAGCCCAACAATCTGTCTGCTTCCCAATTATGTCAT 2079
 QY 361 GGGCAATTAAGCATTTCTCTTCTTGGCTGCTGCTGACGACAGAGAGCCAGAACTATC 420
 DB 2080 GGGCAATTAAGCATTTCTCTTCTTGGCTGCTGCTGACGACAGAGAGCCAGAACTATC 2139
 QY 421 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAATGCTCGA 480
 DB 2140 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAATGCTCGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTTCTTCCCTTCACTTACCTGCA 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAAGTTCTTCCCTTCACTTACCTGCA 2259
 QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTAGCTCAGGTTTCTTACTGTAATTAGA 600
 DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTAGCTCAGGTTTCTTACTGTAATTAGA 2319
 QY 601 TCTCCAGACCTTCTGTCGACCAATTCAAATTAAAGCAAAACATTAACCTTCAATGA 660
 DB 2320 TCTCCAGACCTTCTGTCGACCAATTCAAATTAAAGCAAAACATTAACCTTCAATGA 2379
 QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTGAGGCTTGAAGAGATG 720
 DB 2380 GCACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTGAGGCTTGAAGAGATG 2439
 QY 721 AAGCTTGAAGAAAGAAATACCTTGTGTTCCAGCCCTTCCACACTCTTCAATGTTGA 780
 DB 2440 AAGCTTGAAGAAAGAAATACCTTGTGTTCCAGCCCTTCCACACTCTTCAATGTTGA 2499
 QY 781 ACCACTGCTTCTCTGAGCAGTGGAGCCAGTGAAGTATTAATGTTGTTATGAAGAAC 840
 DB 2500 ACCACTGCTTCTCTGAGCAGTGGAGCCAGTGAAGTATTAATGTTGTTATGAAGAAC 2559

QY 841 TGAATTTAGAGTCTGTGATGCTTCAAGAGATGATTAATATACATTTTCT 890
 DB 2560 TGAATTTAGAGTCTGTGATGCTTCAAGAGATGATTAATATACATTTTCT 2609

RESULT 15

ADP81075
 ID ADP81075 standard; DNA; 2690 BP.

AC ADP81075;

DT 09-SEP-2004 (first entry)

DE Human ovarian specific gene, SEQ ID NO 109.

KW normal; neoplastic; ovarian; ovarian specific nucleic acid; OONA;
 KW metastatic; cancer; vaccine; cytosolic; human; gene; ds.

OS Homo sapiens.

PN W02004053079-A2.

PD 24-JUN-2004.

PF 08-DEC-2003; 2003WO-US038855.

PR 06-DEC-2002; 2002US-0431301P.

PR 06-DEC-2002; 2002US-0431321P.

PR 30-JUN-2003; 2003US-0484584P.

PR 07-NOV-2003; 2003US-0518607P.

XX (DIAD-) DIADEXUS INC.

PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;

DR WPI; 2004-468850/44.

XX P-PSDB; ADP81235, ADP81236.

PT New ovarian specific nucleic acid molecules and polypeptides useful for

PS diagnosing, preventing or treating ovarian cancer, for producing

XX transgenic animals or cells, or for research purposes.

PS Claim 1; SEQ ID NO 109; 754bp; English.

CC The invention relates to novel isolated nucleic acid molecules and

CC polypeptides present in normal and neoplastic ovarian cells. These

CC comprise a nucleic acid sequence encoding any of the 167 amino acid

CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the

CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of

CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined

CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention

CC further comprises: a method for determining the presence of a ovarian

CC specific nucleic acid (OSNA) in a sample; a vector comprising the above

CC nucleic acid molecule; a host cell comprising the vector; a method for

CC producing a polypeptide encoded by the above nucleic acid molecule; a

CC polypeptide encoded by the nucleic acid molecule cited above; an antibody

CC or its fragment that specifically binds to the above polypeptide; a

CC method for determining the presence of an ovarian specific protein in a

CC sample; a method for diagnosing or monitoring the presence and metastases

CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or

CC presence of cancer in a patient; the kit comprising a means for

CC determining the presence of the above nucleic acid molecule or

CC polypeptide; a method of treating a patient with ovarian cancer; and a

CC vaccine comprising the above polypeptide or nucleic acid encoding the

CC polypeptide. The isolated nucleic acid molecules and polypeptides have

CC cytostatic activity. The isolated polypeptides may be used to create a

CC vaccine. The isolated nucleic acid molecules and polypeptides can be used

CC for diagnosing or monitoring the presence and metastases of ovarian

CC cancer and treating ovarian cancer. This polynucleotide sequence

CC represents an ovarian specific gene of the invention.

XX Sequence 2690 BP; 760 A; 611 C; 603 G; 716 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 12; Length 2690;
Best Local Similarity 99.9%; Pred. No. 3.2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY      1 CAAGCTCTGAGGCTTCTCTTCCATCTCTGCTGACAGCTTAAGACTCAGTTTCAATA 60
DB      1801 CAAGCTCTGAGGCTTCTCTTCCATCTCTGCTGACAGCTTAAGACTCAGTTTCAATA 1860
QY      61 GCATCTAGAGCAGTGGGACTCAGCTGGGGGATTTGCCCCCATCTCCGGGGGAATGTC 120
DB      1861 GCATCTAGAGCAGTGGGACTCAGCTGGGGGATTTGCCCCCATCTCCGGGGGAATGTC 1920
QY      121 TGAAGCAATTTTGTTTACCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
DB      1921 TGAAGCAATTTTGTTTACCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1980
QY      181 TAGTGATTAAGGCCAGGGATGCTGCTCAACTCTACCATGTACAGGAGCTCTCCCA 240
DB      1981 TAGTGATTAAGGCCAGGGATGCTGCTCAACTCTACCATGTACA-GGACGTCTCCCA 2039
QY      241 TTACAACTACCCCAATCCGAAGTCAACTGTGTACAGACTAAGAAACCCGGTTTGAAT 300
DB      2040 TTACAACTACCCCAATCCGAAGTCAACTGTGTACAGACTAAGAAACCCGGTTTGAAT 2099
QY      301 AGAAAAGGCGCTGGAAGAAGGGAGCCAA CAAATCTGTCTGTCTCTCA CATTAGTCATT 360
DB      2100 AGAAAAGGCGCTGGAAGAAGGGAGCCAA CAAATCTGTCTGTCTCTCA CATTAGTCATT 2159
QY      361 GGCMAATAAGCATTTCTGTCTTTGGCTGTCTGTCTGACACAGAGAGCCAGAACTTATC 420
DB      2160 GGCMAATAAGCATTTCTGTCTTTGGCTGTCTGTCTGACACAGAGAGCCAGAACTTATC 2219
QY      421 GGGCACAGAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGGCTATGGGAAATGCTGA 480
DB      2220 GGGCACAGAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGGCTATGGGAAATGCTGA 2279
QY      481 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTTCTTCCCTTCATCTACCTGCAAG 540
DB      2280 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTTCTTCCCTTCATCTACCTGCAAG 2339
QY      541 CCAAGTTCTGTGAAGAGAAATGCTGAGTTCTAGCTCAGGTTTTCTTACTCTGAATTAGA 600
DB      2340 CCAAGTTCTGTGAAGAGAAATGCTGAGTTCTAGCTCAGGTTTTCTTACTCTGAATTAGA 2399
QY      601 TCTCCAGACCTTCTCGGCCACAATTCAATTAAAGCAACAACATATACCTTCATGAA 660
DB      2400 TCTCCAGACCTTCTCGGCCACAATTCAATTAAAGCAACAACATATACCTTCATGAA 2459
QY      661 GCACACACAGACTTTTGAAGAAGCAATGACTGTTGAATTGAGGCTTGAGGAATG 720
DB      2460 GCACACACAGACTTTTGAAGAAGCAATGACTGTTGAATTGAGGCTTGAGGAATG 2519
QY      721 AAGCTTTGAAGAAAAGATACTTTTGTTCAGCCCCCTTCCACACTCTTCATGTGTTA 780
DB      2520 AAGCTTTGAAGAAAAGATACTTTTGTTCAGCCCCCTTCCACACTCTTCATGTGTTA 2579
QY      781 ACCACTGCTTCTCTGAGCCTTGAGCCAGGTGACTGTATCATGTGTTATAGAAAAC 840
DB      2580 ACCACTGCTTCTCTGAGCCTTGAGCCAGGTGACTGTATCATGTGTTATAGAAAAC 2639
QY      841 TGAATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTTCCCT 890
DB      2640 TGAATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTTCCCT 2689
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Search completed: May 30, 2005, 10:27:11
Job time : 548.854 secs

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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:54:34 / Search time 164.951 Seconds
(without alignments)
8828.602 Million cell updates/sec

Title: US-09-763-978B-11

Perfect score: 890

Sequence: 1 caagctctgagctctctcct.....tgatataatatacttctcct 890

Scoring table: IDENTITY_NUC

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 878 | 98.7 | 2627 | 3 | US-09-404-879A-391 |
| 2 | 878 | 98.7 | 2627 | 4 | US-09-667-857-391 |
| 3 | 866 | 97.3 | 1567 | 3 | US-09-404-879A-74 |
| 4 | 866 | 97.3 | 1567 | 4 | US-09-338-933-74 |
| 5 | 866 | 97.3 | 1567 | 4 | US-09-215-681-74 |
| 6 | 866 | 97.3 | 1567 | 4 | US-09-216-003A-74 |
| 7 | 866 | 97.3 | 1567 | 4 | US-09-667-857-74 |
| 8 | 448.2 | 50.4 | 461 | 3 | US-09-404-879A-27 |
| 9 | 448.2 | 50.4 | 461 | 4 | US-09-338-933-27 |
| 10 | 448.2 | 50.4 | 461 | 4 | US-09-215-681-27 |
| 11 | 448.2 | 50.4 | 461 | 4 | US-09-216-003A-27 |
| 12 | 448.2 | 50.4 | 461 | 4 | US-09-667-857-27 |
| 13 | 433.8 | 48.7 | 695 | 3 | US-09-040-984-15 |
| 14 | 433.8 | 48.7 | 695 | 3 | US-09-123-912-15 |
| 15 | 433.8 | 48.7 | 695 | 3 | US-09-643-597-15 |
| 16 | 433.8 | 48.7 | 695 | 4 | US-09-480-884A-15 |
| 17 | 433.8 | 48.7 | 695 | 4 | US-09-542-615A-15 |
| 18 | 433.8 | 48.7 | 695 | 4 | US-09-606-421B-15 |
| 19 | 433.8 | 48.7 | 695 | 4 | US-09-221-107-15 |
| 20 | 433.8 | 48.7 | 695 | 4 | US-09-466-396A-15 |
| 21 | 433.8 | 48.7 | 695 | 4 | US-09-476-496A-15 |
| 22 | 433.8 | 48.7 | 695 | 4 | US-09-630-940B-15 |
| 23 | 433.8 | 48.7 | 695 | 4 | US-09-285-479-15 |
| 24 | 75.8 | 8.5 | 132438 | 4 | US-09-949-016-14349 |
| 25 | 75.8 | 8.5 | 132438 | 4 | US-09-949-016-14350 |
| 26 | 75.8 | 8.5 | 151089 | 4 | US-09-949-016-14348 |
| 27 | 75.8 | 8.5 | 524032 | 4 | US-09-949-016-16928 |

| | | | | | | |
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| C 28 | 75.8 | 8.5 | 524032 | 4 | US-09-949-016-16929 | Sequence 16929, A |
| C 29 | 75.8 | 8.5 | 524032 | 4 | US-09-949-016-16930 | Sequence 16930, A |
| C 30 | 75.8 | 8.5 | 524032 | 4 | US-09-949-016-16931 | Sequence 16931, A |
| C 31 | 75.8 | 8.5 | 529885 | 4 | US-09-949-016-14340 | Sequence 14340, A |
| C 32 | 75.8 | 8.5 | 529885 | 4 | US-09-949-016-14341 | Sequence 14341, A |
| C 33 | 75.8 | 8.5 | 529885 | 4 | US-09-949-016-14342 | Sequence 14342, A |
| C 34 | 75.8 | 8.5 | 529885 | 4 | US-09-949-016-14343 | Sequence 14343, A |
| C 35 | 75.8 | 8.5 | 529885 | 4 | US-09-949-016-14344 | Sequence 14344, A |
| C 36 | 75.8 | 8.5 | 529885 | 4 | US-09-949-016-14345 | Sequence 14345, A |
| C 37 | 75.8 | 8.5 | 529885 | 4 | US-09-949-016-14346 | Sequence 14346, A |
| C 38 | 75.8 | 8.5 | 529885 | 4 | US-09-949-016-14347 | Sequence 14347, A |
| C 39 | 73.2 | 8.2 | 601 | 4 | US-09-949-016-184694 | Sequence 184694, A |
| C 40 | 73.2 | 8.2 | 88557 | 4 | US-09-949-016-17028 | Sequence 17028, A |
| C 41 | 72.6 | 8.2 | 247299 | 4 | US-09-949-016-17590 | Sequence 17590, A |
| C 42 | 72 | 8.1 | 601 | 4 | US-09-949-016-73026 | Sequence 73026, A |
| C 43 | 72 | 8.1 | 601 | 4 | US-09-949-016-73027 | Sequence 73027, A |
| C 44 | 72 | 8.1 | 221545 | 4 | US-09-949-016-13875 | Sequence 13875, A |
| C 45 | 67 | 7.5 | 218 | 4 | US-09-573-080A-317 | Sequence 317, App |

ALIGNMENTS

| | | | | | | |
|------------------------------------------------------------------|------|--------------------------------------------------------|------|--|--|--|
| RESULT 1 | | | | | | |
| US-09-404-879A-391 | | | | | | |
| Sequence 391, Application US/09404879A | | | | | | |
| Patent No. 6468546 | | | | | | |
| GENERAL INFORMATION: | | | | | | |
| APPLICANT: Mitcham, Jennifer L. | | | | | | |
| APPLICANT: King, Gordon E. | | | | | | |
| APPLICANT: Algate, Paul A. | | | | | | |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND | | | | | | |
| FILE REFERENCE: 210121.462C2 | | | | | | |
| CURRENT APPLICATION NUMBER: US/09/404, 879A | | | | | | |
| CURRENT FILING DATE: 1999-09-24 | | | | | | |
| NUMBER OF SEQ ID NOS: 393 | | | | | | |
| SOFTWARE: FastSeq for Windows Version 3.0 | | | | | | |
| SEQ ID NO 391 | | | | | | |
| LENGTH: 2627 | | | | | | |
| TYPE: DNA | | | | | | |
| ORGANISM: Homo sapiens | | | | | | |
| US-09-404-879A-391 | | | | | | |
| Query Match | | | | | | |
| Best Local Similarity 98.7%; Score 878; DB 3; Length 2627; | | | | | | |
| Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1; | | | | | | |
| QY | 1 | CAAGCTGAGAGCTTCTCCCTTCATCCGCGGAGAGCTAGACCTGATTCATTA | 60 | | | |
| DB | 1721 | CAAGCTGAGAGCTTCTCCCTTCATCCGCGGAGAGCTAGACCTGATTCATTA | 1780 | | | |
| QY | 61 | GCATCTAGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG | 120 | | | |
| DB | 1781 | GCATCTAGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG | 1840 | | | |
| QY | 121 | TGAAGCAATTTTGTACTCTCATAGAGAGTGAAGAGATATCACTGATCACTAC | 180 | | | |
| DB | 1841 | TGAAGCAATTTTGTACTCTCATAGAGAGTGAAGAGATATCACTGATCACTAC | 1900 | | | |
| QY | 181 | TAGTGATTAAGGCGAGGAGTGTCTCAACCTCCATGATGAGGAGCGCTCCCA | 240 | | | |
| DB | 1901 | TAGTGATTAAGGCGAGGAGTGTCTCAACCTCCATGATGAGGAGCGCTCCCA | 1959 | | | |
| QY | 241 | TTACAACTACCAATCCGAGAGTGTCACTGTGTCAAGAGTGAAGAACTGTTGAGT | 300 | | | |
| DB | 1960 | TTACAACTACCAATCCGAGAGTGTCACTGTGTCAAGAGTGAAGAACTGTTGAGT | 2019 | | | |
| QY | 301 | AGAAAAGGCGCTGAGAGAGGAGGAGCAAAATCTGTCTCTTCTCACTTATGATT | 360 | | | |
| DB | 2020 | AGAAAAGGCGCTGAGAGAGGAGGAGCAAAATCTGTCTCTTCTCACTTATGATT | 2079 | | | |
| QY | 361 | GGCAATTAAGCAATTCGTCTCTTGTGCTGCTGCTGAGCAGAGAGCAAGACTATC | 420 | | | |

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Db 2080 GGCATAATAGCATTCGTCTCTTTGGCTCTGCTCAGACAGAGAGCCAGAACTCTATC 2139
Qy 421 GGGCACAGAGTAATCATCTCTCACTGTAACAGAGTTGACAGAGCCCTATGGGAATGCTCTGA 480
Db 2140 GGGCACAGAGTAATCATCTCTCACTGTAACAGAGTTGACAGAGCCCTATGGGAATGCTCTGA 2199
Qy 481 TGGGATTAATCTTCAAGCTTGTAGAGCTTCAAGTTTCTTCCCTCAATTTACCTGCAAG 540
Db 2200 TGGGATTAATCTTCAAGCTTGTAGAGCTTCTAAGTTTCTTCCCTCAATTTACCTGCAAG 2259
Qy 541 CCAAGTTCTGTAAAGAAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 2260 CCAAGTTCTGTAAAGAAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
Qy 601 TCTCCAGACCTTCTCTGCGCACATTTCAATTAAGGCAAAACATATACCTTCCATGAA 660
Db 2320 TCTCCAGACCTTCTCTGCGCACATTTCAATTAAGGCAAAACATATACCTTCCATGAA 2379
Qy 661 GCACACAGACTTTTGAAGACAGACATGACTGCTGAATGAGGCTTGAGGAATG 720
Db 2380 GCACACAGACTTTTGAAGACAGACATGACTGCTGAATGAGGCTTGAGGAATG 2439
Qy 721 AAGCTTTGAAGAAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTCATGTGTA 780
Db 2440 AAGCTTTGAAGAAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTCATGTGTA 2499
Qy 781 ACCACTGCTTCTCTGAGACCTTGAGCCAGGTCATGTAATTAATGTTGTTATAGAAAAC 840
Db 2500 ACCACTGCTTCTCTGAGACCTTGAGCCAGGTCATGTAATTAATGTTGTTATAGAAAAC 2559
Qy 841 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 2609
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RESULT 2
US-09-667-857-391
Sequence 391, Application US/09667857
Patent No. 6699664
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Reiter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 391
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-667-857-391
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Query Match 98.7%; Score 878; DB 4; Length 2627;
Best Local Similarity 99.9%; Pred. No. 8.9e-267;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAAAGCTCTAGAGCTTCTCTTCCATCCGCGTGAAGAGTAGAGCTCAAGTTTCAATA 60
Db 1721 CAAAGCTCTAGAGCTTCTCTTCCATCCGCGTGAAGAGTAGAGCTCAAGTTTCAATA 1780
Qy 61 GCATCTAGAGCAGTGGAGACTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 120
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Db 1781 GCATCTAGAGCAGTGGAGACTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 1840
Qy 121 TGAAGACAATTTTGGTTACTCTCAATGAGGAGTGAGAGGATAAGTGTACTACTACAAC 180
Db 1841 TGAAGACAATTTTGGTTACTCTCAATGAGGAGTGAGAGGATAAGTGTACTACTACAAC 1900
Qy 181 TAGTGATTAAGGCCAGGAGATGCTGCTCAACCTCTCATATGTAAGGAGCTCTCCCA 240
Db 1901 TAGTGATTAAGGCCAGGAGATGCTGCTCAACCTCTCATATGTAAGGAGCTCTCCCA 1959
Qy 241 TTAACAATACCCCAATCCGCAATGTCTGTAAGCTGTGAGACTTAAGAAACCTGTTTGAAGT 300
Db 1960 TTAACAATACCCCAATCCGCAATGTCTGTAAGCTGTGAGACTTAAGAAACCTGTTTGAAGT 2019
Qy 301 AGAAAAGGCGCTGAAAAGAGGGAGCCAAACAATGTCTGCTCTTCTCTCAATTAAGTCAAT 360
Db 2020 AGAAAAGGCGCTGAAAAGAGGGAGCCAAACAATGTCTGCTCTTCTCTCAATTAAGTCAAT 2079
Qy 361 GGCATAATAGCATTCGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
Db 2080 GGCATAATAGCATTCGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139
Qy 421 GGGCACAGAGTAATCATCTCTCACTGTAACAGAGTTGACAGAGCCCTATGGGAATGCTCTGA 480
Db 2140 GGGCACAGAGTAATCATCTCTCACTGTAACAGAGTTGACAGAGCCCTATGGGAATGCTCTGA 2199
Qy 481 TGGGATTAATCTTCAAGCTTGTAGAGCTTCAAGTTTCTTCCCTCAATTTACCTCTGCAAG 540
Db 2200 TGGGATTAATCTTCAAGCTTGTAGAGCTTCAAGTTTCTTCCCTCAATTTACCTCTGCAAG 2259
Qy 541 CCAAGTTCTGTAAAGAAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 2260 CCAAGTTCTGTAAAGAAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
Qy 601 TCTCCAGACCTTCTCTGCGCACATTTCAATTAAGGCAAAACATATACCTTCCATGAA 660
Db 2320 TCTCCAGACCTTCTCTGCGCACATTTCAATTAAGGCAAAACATATACCTTCCATGAA 2379
Qy 661 GCACACAGACTTTTGAAGACAGACATGACTGCTGAATGAGGCTTGAGGAATG 720
Db 2380 GCACACAGACTTTTGAAGACAGACATGACTGCTGAATGAGGCTTGAGGAATG 2439
Qy 721 AAGCTTTGAAGAAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTCATGTGTA 780
Db 2440 AAGCTTTGAAGAAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTCATGTGTA 2499
Qy 781 ACCACTGCTTCTCTGAGACCTTGAGCCAGGTCATGTAATTAATGTTGTTATAGAAAAC 840
Db 2500 ACCACTGCTTCTCTGAGACCTTGAGCCAGGTCATGTAATTAATGTTGTTATAGAAAAC 2559
Qy 841 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 2609
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RESULT 3
US-09-404-879A-74
Sequence 74, Application US/09404879A
Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Reiter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
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ORGANISM: Homo sapien
US-09-404-879A-74

Query Match 97.3%; Score 866; DB 3; Length 1567;
Best Local Similarity 99.8%; Pred. No. 4,3e-263;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 1 CAAGCTTGAGGCTTCTCCCTTCATCTGCGTGGACGATTAAGACCTGATTTCATA 60
DB 679 CAAGCTTGAGGCTTCTCCCTTCATCTGCGTGGACGATTAAGACCTGATTTCATA 738
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGATGATTTCCGCCCATCTCCGGGGAAATGTC 120
DB 739 GCATCTAGAGCAGTGGAGCTCAGCTGGGATGATTTCCGCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGACAATTTTGTGTTACTCTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC 180
DB 799 TGAAGACAATTTT-GTTACCTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC 857
QY 181 TAGTGAATAAAGCCAGGAGTGCCTCAACCTCTCACTGATACAGGAGCTGTCGCCA 240
DB 858 TAGTGAATAAAGCCAGGAGTGCCTCAACCTCTCACTGATACAGGAGCTGTCGCCA 916
QY 241 TTAACAATAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGATTTGAGT 300
DB 917 TTAACAATAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGATTTGAGT 976
QY 301 AGAAAGAGGCTTGAAAGAGGAGGCCAACAAATCTGTCTCTCTCACTAATTAATGTCATT 360
DB 977 AGAAAGAGGCTTGAAAGAGGAGGCCAACAAATCTGTCTCTCTCTCACTAATTAATGTCATT 1036
QY 361 GGAATAAAGCAATTCCTCTTGGCTGCTGCTGAGCAAGAGACCGAACTCTATC 420
DB 1037 GGAATAAAGCAATTCCTCTTGGCTGCTGCTGAGCAAGAGACCGAACTCTATC 1096
QY 421 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTATGGGAAATGCTGA 480
DB 1097 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTCTTCTCTCTCACTACCTGCAAG 540
DB 1157 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTCTTCTCTCTCACTACCTGCAAG 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGTTTCTTCTGAAATTTAGA 600
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGTTTCTTCTGAAATTTAGA 1276
QY 601 TCTCAGACCTTCTCTGGCCAAATTTCAATTAAGCAACAATATATACCTTCATGAA 660
DB 1277 TCTCAGACCTTCTCTGGCCAAATTTCAATTAAGCAACAATATATACCTTCATGAA 1336
QY 661 GCAACACACAGACTTTTGAAGCAAGCAATGACTGTGATTAAGAGCCTTGAAGATG 720
DB 1337 GCAACACACAGACTTTTGAAGCAAGCAATGACTGTGATTAAGAGCCTTGAAGATG 1396
QY 721 AAGCTTTGAAGGAAAAAATATCTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTA 780
DB 1397 AAGCTTTGAAGGAAAAAATATCTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTA 1456
QY 781 ACCACTGCTTCTCTGAGCCTTGGAGCCAGGTGACTGTATTAACATGTTTATAGAAAC 840
DB 1457 ACCACTGCTTCTCTGAGCCTTGGAGCCAGGTGACTGTATTAACATGTTTATAGAAAC 1516
QY 841 TGAATTTAGAGTTCTGATGTTTCAAGAAATGATTAATATACATTTCT 890
DB 1517 TGAATTTAGAGTTCTGATGTTTCAAGAAATGATTAATATACATTTCT 1566
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RESULT 4
US-09-338-933-74
; Sequence 74, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ. ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-338-933-74

Query Match 97.3%; Score 866; DB 4; Length 1567;
Best Local Similarity 99.8%; Pred. No. 4,3e-263;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 1 CAAGCTTGAGGCTTCTCCCTTCATCTGCGTGGACGATTAAGACCTGATTTCATA 60
DB 679 CAAGCTTGAGGCTTCTCCCTTCATCTGCGTGGACGATTAAGACCTGATTTCATA 738
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGATGATTTCCGCCCATCTCCGGGGAAATGTC 120
DB 739 GCATCTAGAGCAGTGGAGCTCAGCTGGGATGATTTCCGCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGACAATTTTGTGTTACTCTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC 180
DB 799 TGAAGACAATTTT-GTTACCTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC 857
QY 181 TAGTGAATAAAGCCAGGAGTGCCTCAACCTCTCACTGATACAGGAGCTGTCGCCA 240
DB 858 TAGTGAATAAAGCCAGGAGTGCCTCAACCTCTCACTGATACAGGAGCTGTCGCCA 916
QY 241 TTAACAATAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGATTTGAGT 300
DB 917 TTAACAATAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGATTTGAGT 976
QY 301 AGAAAGAGGCTTGAAAGAGGAGGCCAACAAATCTGTCTCTCTCACTAATTAATGTCATT 360
DB 977 AGAAAGAGGCTTGAAAGAGGAGGCCAACAAATCTGTCTCTCTCTCACTAATTAATGTCATT 1036
QY 361 GGAATAAAGCAATTCCTCTTGGCTGCTGCTGAGCAAGAGACCGAACTCTATC 420
DB 1037 GGAATAAAGCAATTCCTCTTGGCTGCTGCTGAGCAAGAGACCGAACTCTATC 1096
QY 421 TTAACAATAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGATTTGAGT 480
DB 1097 TTAACAATAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGATTTGAGT 1156
QY 481 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTCTTCTCTCTCACTACCTGCAAG 540
DB 1157 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTCTTCTCTCTCACTACCTGCAAG 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGTTTCTTCTGAAATTTAGA 600
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGTTTCTTCTGAAATTTAGA 1276
QY 601 TCTCAGACCTTCTCTGGCCAAATTTCAATTAAGCAACAATATATACCTTCATGAA 660
DB 1277 TCTCAGACCTTCTCTGGCCAAATTTCAATTAAGCAACAATATATACCTTCATGAA 1336
QY 661 GCAACACACAGACTTTTGAAGCAAGCAATGACTGTGATTAAGAGCCTTGAAGATG 720
DB 1337 GCAACACACAGACTTTTGAAGCAAGCAATGACTGTGATTAAGAGCCTTGAAGATG 1396
QY 721 AAGCTTTGAAGGAAAAAATATCTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTA 780
DB 1397 AAGCTTTGAAGGAAAAAATATCTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTA 1456
QY 781 ACCACTGCTTCTCTGAGCCTTGGAGCCAGGTGACTGTATTAACATGTTTATAGAAAC 840
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Db 1457 ACCACTGCTTCCTGGACCTTGAGCCACGGTGAAGTATTAATGTTTATAGAAAC 1516
QY 841 TGAATTTAGATTCTGATGATGCTTCAAGAGAAATGATTAATATACATTTCT 890
Db 1517 TGAATTTAGATTCTGATGATGCTTCAAGAGAAATGATTAATATACATTTCT 1566

RESULT 5
US-09-215-681-74
Sequence 74, Application US/09215681A
Patent No. 6528253
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
ORGANISM: Homo sapien
US-09-215-681-74

Query Match 97.3%; Score 866; DB 4; Length 1567;
Best Local Similarity 99.8%; Pred. No. 4.3e-263;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 CAAGCTCTGAGGCTTCCTCTTCATCCGCGGTGAGCACTAGACCTGATTTCAATA 60
Db 679 CAAGCTCTGAGGCTTCCTCTTCATCCGCGGTGAGCACTAGACCTGATTTCAATA 738
QY 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGTGATTTGCCCCCATCTCCGGGGAAATGTC 120
Db 739 GCATCTAGAGCAGTGGGAGCTCAGCTGGGTGATTTGCCCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC 180
Db 799 TGAAGCAATTTT-GTTACCTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC 857
QY 181 TAGTGATTAAGGCGGAGGATGCTGCTCAACCTCCCTCAATGATGAGGAGGAGCTCCCA 240
Db 858 TAGTGATTAAGGCGGAGGATGCTGCTCAACCTCCCTCAATGATGAGGAGGAGCTCCCA 916
QY 241 TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTTTGAAT 300
Db 917 TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTTTGAAT 976
QY 301 AAAAAAGGCTTGAAAAAGGGAGCCAACTGTGTCTGCTTCTCAATTAATGATTT 360
Db 977 AAAAAAGGCTTGAAAAAGGGAGCCAACTGTGTCTGCTTCTCAATTAATGATTT 1036
QY 361 GGGAAATTAAGCAATCTGCTTTGGCTGTGCTGCTAGAGACAGAGGCCAGAACTCTATC 420
Db 1037 GGGAAATTAAGCAATCTGCTTTGGCTGTGCTGCTAGAGACAGAGGCCAGAACTCTATC 1096
QY 421 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAATGCTGA 480
Db 1097 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCAGCTGTGTTGAGCTTCTAAGTTCTTTCCCTTCAATTTACCTTGCAAG 540
Db 1157 TGGGATTAATCTTCAGCTGTGTTGAGCTTCTAAGTTCTTTCCCTTCAATTTACCTTGCAAG 1216
QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTAGGTTTCTTACTCTGAATTTAA 600
Db 1217 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTAGGTTTCTTACTCTGAATTTAA 1276
QY 601 TCTCCAGACCTTCTGAGCCACAATTCATAATTAAAGCAACAACATATACCTTCATGAA 660

Db 1277 TCTCCAGACCTTCTGAGCCACAATTCATAATTAAAGCAACAACATATACCTTCATGAA 1336
QY 661 GCACACAGACTTTTGAAGCAAGACAAATGACCTGCTGAATGAGGCTTGAAGATG 720
Db 1337 GCACACAGACTTTTGAAGCAAGACAAATGACCTGCTGAATGAGGCTTGAAGATG 1396
QY 721 AAGCTTTGAAGAAAGAAATCTTTGTTTCCAGCCCTTCCTCCACACTCTTCATGTGTTA 780
Db 1397 AAGCTTTGAAGAAAGAAATCTTTGTTTCCAGCCCTTCCTCCACACTCTTCATGTGTTA 1456
QY 781 ACCACTGCTTCCTGGACCTTGGAGCCACGGTGAAGTATTAATGATTTGTTTAA 840
Db 1457 ACCACTGCTTCCTGGACCTTGGAGCCACGGTGAAGTATTAATGATTTGTTTAA 1516
QY 841 TGAATTTAGATTCTGATGATGCTTCAAGAGAAATGATTAATATACATTTCT 890
Db 1517 TGAATTTAGATTCTGATGATGCTTCAAGAGAAATGATTAATATACATTTCT 1566

RESULT 6
US-09-216-003A-74
Sequence 74, Application US/09216003A
Patent No. 6670463
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
NUMBER OF SEQ ID NOS: 310
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
ORGANISM: Homo sapiens
US-09-216-003A-74

Query Match 97.3%; Score 866; DB 4; Length 1567;
Best Local Similarity 99.8%; Pred. No. 4.3e-263;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 CAAGCTCTGAGGCTTCCTCTTCATCCGCGGTGAGCACTAGACCTGATTTCAATA 60
Db 679 CAAGCTCTGAGGCTTCCTCTTCATCCGCGGTGAGCACTAGACCTGATTTCAATA 738
QY 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGTGATTTGCCCCCATCTCCGGGGAAATGTC 120
Db 739 GCATCTAGAGCAGTGGGAGCTCAGCTGGGTGATTTGCCCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC 180
Db 799 TGAAGCAATTTT-GTTACCTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC 857
QY 181 TAGTGATTAAGGCGGAGGATGCTGCTCAACCTCCCTCAATGATGAGGAGGAGCTCCCA 240
Db 858 TAGTGATTAAGGCGGAGGATGCTGCTCAACCTCCCTCAATGATGAGGAGGAGCTCCCA 916
QY 241 TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTTTGAAT 300
Db 917 TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTTTGAAT 976
QY 301 AAAAAAGGCTTGAAAAAGGGAGCCAACTGTGTCTGCTTCTCAATTAATGATTT 360
Db 977 AAAAAAGGCTTGAAAAAGGGAGCCAACTGTGTCTGCTTCTCAATTAATGATTT 1036
QY 361 GGGAAATTAAGCAATCTGCTTTGGCTGTGCTGCTAGAGACAGAGGCCAGAACTCTATC 420
Db 1037 GGGAAATTAAGCAATCTGCTTTGGCTGTGCTGCTAGAGACAGAGGCCAGAACTCTATC 1096
QY 421 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAATGCTGA 480

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Db 1097 GGGACACAGATTAATCTCTCAGTGAACAGATTGACAGGCTATGGAATGCTGGA 1156
Qy 481 TGGATATATCTTGAAGCTTTGAGCTTCTAAGTTCTTCCCTTCACTTACCTGCAAG 540
Db 1157 TGGATATATCTTGAAGCTTTGAGCTTCTAAGTTCTTCCCTTCACTTACCTGCAAG 1216
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTTAGA 600
Db 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTTAGA 1276
Qy 601 TCTCCAGACCTTCTGCGCCACAATTCAAATTAAGGCAACAATATACCTTCATGAA 660
Db 1277 TCTCCAGACCTTCTGCGCCACAATTCAAATTAAGGCAACAATATACCTTCATGAA 1336
Qy 661 GCACACACAGACTTTTAAAGCAAGCAATGATGCTGTAATGAGGCTTGAGGAATG 720
Db 1337 GCACACACAGACTTTTAAAGCAAGCAATGATGCTGTAATGAGGCTTGAGGAATG 1396
Qy 721 AAGCTTTGAAGAAAGAAATCTTGTTCAGGCCCCCTCCACACTCTTCATGTGTTA 780
Db 1397 AAGCTTTGAAGAAAGAAATCTTGTTCAGGCCCCCTCCACACTCTTCATGTGTTA 1456
Qy 781 ACCACTGCTTCTGGAACCTTGAGCCAGGTGACTGTATTAATGTTATGAAATG 840
Db 1457 ACCACTGCTTCTGGAACCTTGAGCCAGGTGACTGTATTAATGTTATGAAATG 1516
Qy 841 TGATTTAGAGTTCTGATCTTCAAGAGATGATTAATATACCTTCT 890
Db 1517 TGATTTAGAGTTCTGATCTTCAAGAGATGATTAATATACCTTCT 1566
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RESULT 7
US-09-667-857-74

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; Sequence 74, Application US/09667857
; Patent No. 6693664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-667-857-74
```

Query Match 97.3%; Score 866; DB 4; Length 1567;
Best Local Similarity 99.8%; Pred. No. 4.3e-263;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy 1 CAAGCTCTGAGGCTTCTCTTCCATCTCTCGTGAGACGTAAGACCTCACTTTTCAATA 60
Db 679 CAAGCTCTGAGGCTTCTCTTCCATCTCTCGTGAGACGTAAGACCTCACTTTTCAATA 738
Qy 61 GCATCTAGACAGAGGAGTCACTGAGGAGATTTGCGCCCATCTCGGGGGAATGTC 120
Db 739 GCATCTAGACAGTGGAGTCACTGAGGAGATTTGCGCCCATCTCGGGGGAATGTC 798
Qy 121 TGAAGCAATTTGTTACTCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
Db 121 TGAAGCAATTTGTTACTCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
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Db 799 TGAAGCAATTTT - GTTACTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 857
Qy 181 TAGTGAATAAGGCCAGAGGATGCTGCTCAACCTTCTCAATGATGAGGAGCTCTCCCA 240
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Qy 301 AGAAAGGCTGTGAAAGAGGAGGCAACAAATCTGTCTGCTTCTCACTAGTATTCAT 360
Db 977 AGAAAGGCTGTGAAAGAGGAGGCAACAAATCTGTCTGCTTCTCACTAGTATTCAT 1036
Qy 361 GGCATAATGACATTTCTGCTTCTTGGCTGTGCTGCTTCAAGCAAGAGCCGAATCTATC 420
Db 1037 GGCATAATGACATTTCTGCTTCTTGGCTGTGCTGCTTCAAGCAAGAGCCGAATCTATC 1096
Qy 421 GGGCACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGGAATGCTGA 480
Db 1097 GGGCACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGGAATGCTGA 1156
Qy 481 TGGATATATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCAATCTACCTGCAAG 540
Db 1157 TGGATATATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCAATCTACCTGCAAG 1216
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTTAGA 600
Db 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTTAGA 1276
Qy 601 TCTCCAGACCTTCTGCGCCACAATTCAAATTAAGGCAACAATATACCTTCATGAA 660
Db 1277 TCTCCAGACCTTCTGCGCCACAATTCAAATTAAGGCAACAATATACCTTCATGAA 1336
Qy 661 GCACACACAGACTTTTAAAGCAAGCAATGATGCTGTAATGAGGCTTGAGGAATG 720
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Qy 781 ACCACTGCTTCTGGAACCTTGAGCCAGGTGACTGTATTAATGTTATGAAATG 840
Db 1457 ACCACTGCTTCTGGAACCTTGAGCCAGGTGACTGTATTAATGTTATGAAATG 1516
Qy 841 TGATTTAGAGTTCTGATCTTCAAGAGATGATTAATATACCTTCT 890
Db 1517 TGATTTAGAGTTCTGATCTTCAAGAGATGATTAATATACCTTCT 1566
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RESULT 8

US-09-404-879A-27/c
; Sequence 27, Application US/09404879A
; Patent No. 6468546

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; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
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OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-27

Query Match 50.4%; Score 448.2; DB 3; Length 461;
Best Local Similarity 99.1%; Pred. No. 2.6e-131;
Matches 458; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGATGGAT 486
DB 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAAGGCTTATGGAAATGCTGATGGAT 403
QY 487 TATCTTCACTTGTGAGCTTCTTAAGTTCTTCCCTTCACTTCACTTCACTTCACTTCA 546
DB 402 TATCTTCACTTGTGAGCTTCTTAAGTTCTTCCCTTCACTTCACTTCACTTCACTTCA 343
QY 547 TCTGTAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTCACTTCACTTCACTTCACTTCA 606
DB 342 TCTGTAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTCACTTCACTTCACTTCACTTCA 283
QY 607 GACCTTCTGCGCCCAATTCATTAAGGCAACAAATATACCTTCATGAGCAAC 666
DB 282 GACCTTCTGCGCCCAATTCATTAAGGCAACAAATATACCTTCATGAGCAAC 223
QY 667 ACAGCTTTTGAAGCAAGCAATGACTGCTGAATTAAGGCTTGAAGCAATGAGCTT 726
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QY 727 TGAAGAAAGAAATCTTGTTCAGGCCCCCTTCCACATCTTCACTTCACTTCACTTCA 786
DB 162 TGAAGAAAGAAATCTTGTTCAGGCCCCCTTCCACATCTTCACTTCACTTCACTTCA 103
QY 787 GCTTCTGAGCACTTGAAGCAAGCAAGTGAATTAAGGCTTGAAGCAATGAGCTT 846
DB 102 GCTTCTGAGCACTTGAAGCAAGCAAGTGAATTAAGGCTTGAAGCAATGAGCTT 43
QY 847 TAGAGTTCTGATCGTTCAAGAGATTAATATACCTTTC 888
DB 42 YAGAGTTCTGATCGTTCAAGAGATTAATATACCTTTC 1

RESULT 9

US-09-338-933-27/C
Sequence 27, Application US/09338933
Patent No. 6488931
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
NUMBER OF SEQ ID NOS: 1999-06-23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(461)
OTHER INFORMATION: n = A,T,C or G
US-09-338-933-27

Query Match 50.4%; Score 448.2; DB 4; Length 461;
Best Local Similarity 99.1%; Pred. No. 2.6e-131;
Matches 458; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGATGGAT 486
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DB 402 TATCTTCACTTGTGAGCTTCTTAAGTTCTTCCCTTCACTTCACTTCACTTCACTTCA 343

QY 547 TCTGTAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTCACTTCACTTCACTTCACTTCA 606
DB 342 TCTGTAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTCACTTCACTTCACTTCACTTCA 283

QY 607 GACCTTCTGCGCCCAATTCATTAAGGCAACAAATATACCTTCATGAGCAAC 666
DB 282 GACCTTCTGCGCCCAATTCATTAAGGCAACAAATATACCTTCATGAGCAAC 223

QY 667 ACAGCTTTTGAAGCAAGCAATGACTGCTGAATTAAGGCTTGAAGCAATGAGCTT 726
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DB 162 TGAAGAAAGAAATCTTGTTCAGGCCCCCTTCCACATCTTCACTTCACTTCACTTCA 103

QY 787 GCTTCTGAGCACTTGAAGCAAGCAAGTGAATTAAGGCTTGAAGCAATGAGCTT 846
DB 102 GCTTCTGAGCACTTGAAGCAAGCAAGTGAATTAAGGCTTGAAGCAATGAGCTT 43

QY 847 TAGAGTTCTGATCGTTCAAGAGATTAATATACCTTTC 888
DB 42 YAGAGTTCTGATCGTTCAAGAGATTAATATACCTTTC 1

RESULT 10

US-09-215-681-27/C
Sequence 27, Application US/09215681A
Patent No. 6528253
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Brudakis, Tony N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
NUMBER OF SEQ ID NOS: 1998-12-17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(461)
OTHER INFORMATION: n = A,T,C or G
US-09-215-681-27

Query Match 50.4%; Score 448.2; DB 4; Length 461;
Best Local Similarity 99.1%; Pred. No. 2.6e-131;
Matches 458; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGATGGAT 486
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DB 402 TATCTTCACTTGTGAGCTTCTTAAGTTCTTCCCTTCACTTCACTTCACTTCACTTCA 343
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| Db | 1 | ACTAGTGATTAAGGCCAGAGGATGCTGCTCAACCTCTACATGTATAGAGGACGCTCTCC | 60 | |
| QY | 239 | CATTTACACTACCCAAATCCGAAGTGTCAACTGTGTGACGACTTAAGAAACCCGTGTTTGA | 298 | |
| Db | 61 | CATTACAACTACCCAAATCCGAAGTGTCAACTGTGTGACGACTTAAGAAACCCGTGTTTGA | 120 | |
| QY | 299 | GTAGAAAAGGCGCTGAAAGAGGGAGCCAAATCTGTCTTCTTCCACATTAGTCA | 358 | |
| Db | 121 | TTAATAAAGGCGCTGAAAGAGGGAGCC-AATAATCTGTCTTCTTCCACATTANTCN | 179 | |
| QY | 359 | TTGGCAATTAAGCAATTCTGTCTCTTTGGCTGCTGCTCAGCAAGAGAGCCGAACCTTA | 418 | |
| Db | 180 | TTGGCAATTAAGCAATTCTGTCTCTTTGGCTGCTGCTCAGCAAAACCAAAANCAACTCA | 239 | |
| QY | 419 | TGGGCAACAGGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCGTATGGGAAATGCGT | 478 | |
| Db | 240 | TGNGGC-CAGGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCGTATGGGAAATGCGN | 298 | |
| QY | 479 | GATGGATTTATCTTCAGCTTGTGTGAGCTTCTAAGTTCTCTTCCCTTCATCTCACTCGCA | 538 | |
| Db | 299 | GATGGATTTATCTTCAGCTTGTGTGAGCTTCTAAGTTCTCTTCCCTTCATCTCACTCGCC | 358 | |
| QY | 539 | AGCCAACTTCTGTATAAGAAATGCGTCAAGTTCTAGCTCAAGGTTTCTTAAGTGAATTTA | 598 | |
| Db | 359 | AGCCNAGTCTGTGTAAAGAAATGCGNCAATTCNAACCCGAGTTTCTTAAGTGAATTTA | 418 | |

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1      RESULT 14
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3      ; Sequence 15: Application US/09123912A
4      ; Patent No. 6312695
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Reed, Steven G.
7      ; APPLICANT: Wang, Tonglong
8      ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
9      ; FILE REFERENCE: 210121.455C1
10     ; CURRENT APPLICATION NUMBER: US/09/123,912A
11     ; CURRENT FILING DATE: 1998-07-27
12     ; PRIOR APPLICATION NUMBER: 09/040,802
13     ; PRIOR FILING DATE: 1998-03-18
14     ; NUMBER OF SEQ. ID NOS: 114
15     ; SOFTWARE: PatentIn Ver. 2.0
16     ; SEQ ID NO 15
17     ; LENGTH: 695
18     ; TYPE: DNA
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25     ; LOCATION: (172)
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51     ; NAME/KEY: modified_base
52     ;

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3 LOCATION: (455)
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5 NAME/KEY: modified_base
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68 NAME/KEY: modified_base
69 LOCATION: (651)
70 OTHER INFORMATION: Where n is a, c, g or t

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; NAME/KEY: modified_base
; LOCATION: (652)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (657)

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Query Match      48.7%; Score 433.8; DB 3; Length 695;
Best Local Similarity 80.2%; Pred. No. 1.2e-126;
Matches 551; Conservative 0; Mismatches 126; Indels 10; Gaps 7;

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QY 179 ACTAGTGATTAAGGCCAGGAGATGCTGCTCAACCTCTCCATGTAACAGGAGAGCTCTCC 238
DB 1 ACTAGTGATTAAGGCCAGGAGATGCTGCTCAACCTCTCCATGTAACAGGAGAGCTCTCC 60
QY 239 CATTAACAATCCCAATCCGAAGTGCATGTCAGAGACTAAGAAACCTGGTTTGA 298
DB 61 CATTAACAATCCCAATCCGAAGTGCATGTCAGAGACTAAGAAACCTGGTTTGA 120
QY 299 GTAGAAAAGGCGCTGGAAAAGGGAGCCAAACATCTGTCTCTCTCCTCCTCAGATTAGTCA 358
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DB 240 TCGGAC-CCAGGAATACATCTCNCATTAACAAATTGANCAGAGGCTATGGGAAATGCTCN 298
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DB 299 GATGGATTATCTTCAGCTTGTGAGCTTCTAAGTTCTTCTCTCTCATTTACCTTGA 358
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QY 778 TTAACCACTGCTCTCTGG-ACCTTGAGGCAAGGAGTATTAATGTTGTTATGA 836
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RESULT 15
US-09-643-597-15

; Sequence 15, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongrong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skelky, Yasir A.W.

```

; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(695)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-15

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Query Match      48.7%; Score 433.8; DB 3; Length 695;
Best Local Similarity 80.2%; Pred. No. 1.2e-126;
Matches 551; Conservative 0; Mismatches 126; Indels 10; Gaps 7;

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QY 179 ACTAGTGATTAAGGCCAGGAGATGCTGCTCAACCTCTCCATGTAACAGGAGAGCTCTCC 238
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19: /cgn2_6/prodata/2/pubpna/US10F_PUBCOMB.seq:*
20: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|-------------------|
| 1 | 878 | 98.7 | 893 | US-09-850-178-5 | Sequence 5, Appl1 |
| 2 | 878 | 98.7 | 893 | US-09-850-178-6 | Sequence 6, Appl1 |
| 3 | 878 | 98.7 | 2627 | US-09-778-320-207 | Sequence 207, App |
| 4 | 878 | 98.7 | 2627 | US-09-910-689-207 | Sequence 207, App |
| 5 | 878 | 98.7 | 2627 | US-09-884-441-391 | Sequence 391, App |
| 6 | 878 | 98.7 | 2627 | US-09-907-969-391 | Sequence 391, App |
| 7 | 878 | 98.7 | 2627 | US-09-827-271-391 | Sequence 391, App |
| 8 | 878 | 98.7 | 2627 | US-10-010-742-207 | Sequence 207, App |
| 9 | 878 | 98.7 | 2627 | US-10-198-053-391 | Sequence 391, App |
| 10 | 878 | 98.7 | 2627 | US-10-714-389-207 | Sequence 207, App |
| 11 | 878 | 98.7 | 2627 | US-10-717-296-207 | Sequence 207, App |

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|----|-------|------|------|---------------------|---------------------|
| 12 | 878 | 98.7 | 2627 | US-10-860-790-391 | Sequence 391, App |
| 13 | 878 | 98.7 | 3357 | US-10-023-339-2 | Sequence 2, Appl1 |
| 14 | 877.6 | 98.6 | 2603 | US-09-896-738-1 | Sequence 1, Appl1 |
| 15 | 876.4 | 98.5 | 2626 | US-09-877-065-7 | Sequence 7, Appl1 |
| 16 | 867 | 97.4 | 2591 | US-09-850-178-23 | Sequence 23, Appl1 |
| 17 | 866 | 97.3 | 1567 | US-09-884-441-74 | Sequence 74, Appl1 |
| 18 | 866 | 97.3 | 1567 | US-09-907-969-74 | Sequence 74, Appl1 |
| 19 | 866 | 97.3 | 1567 | US-09-827-271-74 | Sequence 74, Appl1 |
| 20 | 866 | 97.3 | 1567 | US-10-198-053-74 | Sequence 74, Appl1 |
| 21 | 866 | 97.3 | 1567 | US-10-860-790-74 | Sequence 74, Appl1 |
| 22 | 856.6 | 96.2 | 2626 | US-10-023-339-9 | Sequence 9, Appl1 |
| 23 | 807 | 90.7 | 846 | US-09-814-353-21446 | Sequence 21446, A |
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| 26 | 626.2 | 70.4 | 1811 | US-10-097-340-331 | Sequence 331, App |
| 27 | 626.2 | 70.4 | 1811 | US-10-177-293-163 | Sequence 163, App |
| 28 | 626.2 | 70.4 | 1811 | US-10-173-999-71 | Sequence 71, Appl1 |
| 29 | 552 | 62.0 | 563 | US-09-867-701-3948 | Sequence 3948, App |
| 30 | 544 | 61.1 | 555 | US-09-833-790-388 | Sequence 388, App |
| 31 | 517 | 58.1 | 1596 | US-10-198-846-13583 | Sequence 13583, A |
| 32 | 494.6 | 55.6 | 858 | US-09-867-701-1498 | Sequence 1498, App |
| 33 | 494 | 55.5 | 524 | US-09-867-701-2301 | Sequence 2301, App |
| 34 | 487.8 | 54.8 | 578 | US-09-814-353-17682 | Sequence 17682, A |
| 35 | 480 | 53.9 | 491 | US-09-850-178-3 | Sequence 3, Appl1 |
| 36 | 471.8 | 53.0 | 1891 | US-10-097-340-347 | Sequence 347, App |
| 37 | 466.2 | 52.4 | 486 | US-09-867-701-1482 | Sequence 1482, App |
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| 40 | 448.2 | 50.4 | 461 | US-09-827-271-27 | Sequence 27, Appl1 |
| 41 | 448.2 | 50.4 | 461 | US-10-198-053-27 | Sequence 27, Appl1 |
| 42 | 448.2 | 50.4 | 461 | US-10-860-790-27 | Sequence 27, Appl1 |
| 43 | 446.4 | 50.2 | 757 | US-09-814-353-5006 | Sequence 5006, App |
| 44 | 446.4 | 50.2 | 757 | US-09-814-353-11298 | Sequence 11298, App |
| 45 | 440 | 49.4 | 442 | US-09-867-701-2832 | Sequence 2832, App |

ALIGNMENTS

RESULT 1
US-09-850-178-5
Sequence 5, Application US/09850178
Patent No. US20020034749A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colipites, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Ruseell, John C.
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Kras, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Stroupe, Stephen D.
APPLICANT: Gordon, Julian
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
FILE REFERENCE: 6251.US.P1
FILE REFERENCE: DETECTING DISEASES OF THE BREAST
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-850-178-5
Query Match 98.7%; Score 878; DB 9; Length 893;

Best Local Similarity 99.9%; Pred. No. 3.3e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTCATCTCGCGGAGCAGCTAGAGCTTTCATTA 60
DB 1 CAAGCTGAGGCTTCTCTTCATCTCGCGGAGCAGCTAGAGCTTTCATTA 60
QY 61 GCATCTAGAGCAGTGGGAGCTGAGCTGGGGTGAATTTGCCGCCCATCTCCGGGGAAATGTC 120
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QY 421 GGGCACAAGGATTAACATCTCTCAGTGAAGAGTGTGACAGAGCTTAAGGAAATGCTGA 480
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RESULT 2
US-09-850-178-6
; Sequence No. US20020034749A1
; Patent No. US20020034749A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colipites, Tracey L.

APPLICANT: Friedman, Paula N.
APPLICANT: Russell, John C.
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klaas, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Stroupe, Stephen D.
APPLICANT: Gordon, Juliano
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
DETECTING DISEASES OF THE BREAST.
FILE REFERENCE: 6251.US.PI
CURRENT APPLICATION NUMBER: US/09/850,178
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-850-178-6

Query Match 98.7%; Score 878; DB 9; Length 893;
Best Local Similarity 99.9%; Pred. No. 3.3e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTCATCTCGCGGAGCAGCTAGAGCTTTCATTA 60
DB 1 CAAGCTGAGGCTTCTCTTCATCTCGCGGAGCAGCTAGAGCTTTCATTA 60
QY 61 GCATCTAGAGCAGTGGGAGCTGAGCTGGGGTGAATTTGCCGCCCATCTCCGGGGAAATGTC 120
DB 61 GCATCTAGAGCAGTGGGAGCTGAGCTGGGGTGAATTTGCCGCCCATCTCCGGGGAAATGTC 120
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DB 121 TGAAGCAATTTTGGTTTACCTCATATAGGAGTGGAGAGATACAGTCTACTACCAAC 180
QY 181 TGTGTGATTAAGGCGCAGGAGTGTCTCAACCTCCATACATGACAGGAGCGTCCCA 240
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RESULT 3
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; Sequence 207, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778.320
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-320-207

Query Match 98.7%; Score 878; DB 9; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAAGCTCTGAGGCTTCTCTTCATCTCGCGTGAGACGTAAGACCTCACTTTCAATA 60
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Qy 361 GGAATTAAGCAATCTGTCTTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 420
Db 2080 GGAATTAAGCAATCTGTCTTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 2139

Qy 421 GGCACACAGATTAACATCTCTAGTAAACAGAGTGAACAAGGCTATGGAATGCTGA 480
Db 2140 GGCACACAGATTAACATCTCTAGTAAACAGAGTGAACAAGGCTATGGAATGCTGA 2199
Qy 481 TGGGATTAATCTTCACTGTTGAGCTTGAAGCTTGAAGTTCTTCCCTTCACTTACCTGCAAG 540
Db 2200 TGGGATTAATCTTCACTGTTGAGCTTGAAGCTTGAAGTTCTTCCCTTCACTTACCTGCAAG 2259
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Db 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTACTCAGGTTTCTTACTGTGAATTTAGA 2219
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RESULT 4
US-09-910-689-207
; Sequence 207, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910.689
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-689-207

Query Match 98.7%; Score 878; DB 9; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAAGCTCTGAGGCTTCTCTTCATCTCGCGTGAGACGTAAGACCTCACTTTCAATA 60
Db 1721 CAAGCTCTGAGGCTTCTCTTCATCTCGCGTGAGACGTAAGACCTCACTTTCAATA 1780
Qy 61 GCATCTAGAGCAGTGGGACACGCTGGGAGATTTGCCCCCATCTCCGGGGGAATGTC 120
Db 1781 GCATCTAGAGCAGTGGGACACGCTGGGAGATTTGCCCCCATCTCCGGGGGAATGTC 1840
Qy 121 TGAAGCAATTTTGTTTACTCATGAGAGTGAGAGAGATACAGTGTACTACCAAC 180

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Db      1841 TGAAGA CAAATTTGGTTACCTCAATGAGGAGTGAGAGATACAGTCTACTACCAAC 1900
Qy      181  TAGTGATTAAGAGCCGAGGATGCTGCTCAACCTCCATACCATGATGACGAGAGCTGCCCA 240
Db      1901 TAGTGATTAAGAGCCGAGGATGCTGCTCAACCTCCATACCATGATGACGAGAGCTGCCCA 1959
Qy      241  TTACAACTAACCAATCCGAATGCTCAACTGTGTCAAGACTAAGAAACCTGTGTTTGAAT 300
Db      1960 TTACAACTAACCAATCCGAATGCTCAACTGTGTCAAGACTAAGAAACCTGTGTTTGAAT 2019
Qy      301  AAAAAAGGCGCTGGAAGAGGAGGAGCAAAATCTGTCTCTCTCTCTCAATTAATCAAT 360
Db      2020 AAAAAAGGCGCTGGAAGAGGAGGAGCAAAATCTGTCTCTCTCTCAATTAATCAAT 2079
Qy      361  GCGAATAAGCAATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db      2080 GCGAATAAGCAATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2139
Qy      421  GGGCACCAGGATTAACATCTCTCAAGTGAACAGAGTTGACAAAGGCTTATGGAAAATGCTGA 480
Db      2140 GGGCACCAGGATTAACATCTCTCAAGTGAACAGAGTTGACAAAGGCTTATGGAAAATGCTGA 2199
Qy      481  TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCTCTCTCTCTCTCTCTCTCT 540
Db      2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCTCTCTCTCTCTCTCTCTCT 2259
Qy      541  CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTCTCTCTCTCTCTCTCT 600
Db      2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTCTCTCTCTCTCTCTCT 2319
Qy      601  TCTCCAGACCCCTTCTGCGCACAAATTAAGGCAACAAATATACCTTCCATGAA 660
Db      2320 TCTCCAGACCCCTTCTGCGCACAAATTAAGGCAACAAATATACCTTCCATGAA 2379
Qy      661  GACACACAGACTTTTGAAGAGAGCAATGCTGCTGAATGAGGCTTGAAGAAAG 720
Db      2380 GACACACAGACTTTTGAAGAGAGCAATGCTGCTGAATGAGGCTTGAAGAAAG 2439
Qy      721  AAGCTTTGAAGAAAGAAATATCTTGTTCAGGCCCTTCCACACTCTTCAATGTGTA 780
Db      2440 AAGCTTTGAAGAAAGAAATATCTTGTTCAGGCCCTTCCACACTCTTCAATGTGTA 2499
Qy      781  ACCACTGCTTCTCTGAGACCTTGAAGCAGGTCATGTAATGATGTTTATAGAAAC 840
Db      2500 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTCATGTAATGATGTTTATAGAAAC 2559
Qy      841  TGAATTTAGATTCGATGCTTCAAGAGAAATGATTAATATATCAATTTCT 890
Db      2560 TGAATTTAGATTCGATGCTTCAAGAGAAATGATTAATATATCAATTTCT 2609

RESULT 5
US-09-884-441-391
; Sequence 391, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF OVARIAN CANCER
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-441-391

Query Match      98.7%; Score 878; DB 9; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6.2e-284;
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Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy      1  CAAAGCTGAGAGCTTCTCTCTTCCATCTGAGTGAAGAGTCAAGAGCTCAATTTCAATA 60
Db      1721 CAAAGCTGAGAGCTTCTCTCTTCCATCTGAGTGAAGAGTCAAGAGCTCAATTTCAATA 1780
Qy      61  GCATTTAAGAGAGTGGAGCTCAAGTGGAGTATTTGGCCCCCATCTCCGGGGAAATGTC 120
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Db      1841 TGAAGACAAATTTGGTTTCTTCAATGAGGAGTGAAGAGGATTAAGTCTATCCAAAC 1900
Qy      181  TAGTGATTAAGAGCCGAGGATGCTGCTCAACCTCCATACCATGATGACGAGAGCTGCCCA 240
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Qy      241  TTACAACTAACCAATCCGAATGCTCAACTGTGTCAAGACTAAGAAACCTGTGTTTGAAT 300
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Qy      301  AAAAAAGGCGCTGGAAGAGGAGGAGCAAAATCTGTCTCTCTCTCTCTCTCTCTCTCTCT 360
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Qy      361  GCGAATAAGCAATCTGTCTCTTGTGGCTGCTCAGACACAGAGGCGAGAACTCTATC 420
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Qy      421  GGGCACCAGGATTAACATCTCTCAAGTGAACAGAGTTGACAAAGGCTTATGGAAAATGCTGA 480
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Qy      601  TCTCCAGACCCCTTCTGCGCACAAATTAAGGCAACAAATATACCTTCCATGAA 660
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Db      2380 GACACACAGACTTTTGAAGAGAGCAATGCTGCTGAATGAGGCTTGAAGAAAG 2439
Qy      721  AAGCTTTGAAGAAAGAAATATCTTGTTCAGGCCCTTCCACACTCTTCAATGTGTA 780
Db      2440 AAGCTTTGAAGAAAGAAATATCTTGTTCAGGCCCTTCCACACTCTTCAATGTGTA 2499
Qy      781  ACCACTGCTTCTCTGAGACCTTGAAGCAGGTCATGTAATGATGTTTATAGAAAC 840
Db      2500 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTCATGTAATGATGTTTATAGAAAC 2559
Qy      841  TGAATTTAGATTCGATGCTTCAAGAGAAATGATTAATATATCAATTTCT 890
Db      2560 TGAATTTAGATTCGATGCTTCAAGAGAAATGATTAATATATCAATTTCT 2609

RESULT 6
US-09-907-969-391
; Sequence 391, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
```



```
Db      2260 CCAAGTCTGTGAAGAAATGCGCTGATCTGACTCAGGCTTTCTTACTCTGAATTAGA 2319
Qy      601 TCTCCAGACCCCTTCTGCGCACAATTCATTAAAGGCAACAAACATATATACCTTCCATGA 660
Db      2320 TCTCCAGACCCCTTCTGCGCACAATTCATTAAAGGCAACAAACATATATACCTTCCATGA 2379
Qy      661 GCACACACAGACTTTTGAAGAGCAATGACTGCTTGAATTGAGGCTTGAGAGATG 720
Db      2380 GCACACACAGACTTTTGAAGAGCAATGACTGCTTGAATTGAGGCTTGAGAGATG 2439
Qy      721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTA 780
Db      2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTA 2499
Qy      781 ACCACTGCTTCTGAGACCTTGAGCAGCGTGACTGTATTACATGTTGTATAGAAAC 840
Db      2500 ACCACTGCTTCTGAGACCTTGAGCAGCGTGACTGTATTACATGTTGTATAGAAAC 2559
Qy      841 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
Db      2560 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 2609
```

RESULT 8

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US-10-010-742-207
; Sequence 207, Application US/10010742
; Publication No. US20020146727A1
GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-742-207
```

```
Query Match      98.7%; Score 878; DB 13; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      1 CAAAGCTGAGGCTTCTCTTCCATCTCGCGCGTGAAGAGCTTAAGACTTCAATTAATA 60
Db      1721 CAAAGCTGAGGCTTCTCTTCCATCTCGCGCGTGAAGAGCTTAAGACTTCAATTAATA 1780
Qy      61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 120
Db      1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 1840
Qy      121 TGAAGCAATTTTGTACTCAATAGAGGAGTGAAGAGATACAGTGTACTTACCAAC 180
Db      1841 TGAAGCAATTTTGTACTCAATAGAGGAGTGAAGAGATACAGTGTACTTACCAAC 1900
Qy      181 TGTGATTAAGGCGCAGGATGCTGCTCAACCTCCATACATGACAGGAGCGTCTCCCA 240
Db      1901 TGTGATTAAGGCGCAGGATGCTGCTCAACCTCCATACATGACAGGAGCGTCTCCCA 1959
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```
Qy      241 TTAACAATACCAATCCGAATGCTGTAACCTGTGACGACTAAGAAACCTGGTTTGAGT 300
Db      1960 TTAACAATACCAATCCGAATGCTGTAACCTGTGACGACTAAGAAACCTGGTTTGAGT 2019
Qy      301 AGAAAGGCGCTGGAAGAGGGGAGCCAAACAATGTGTGCTGCTTCTCATTAAGTATT 360
Db      2020 AGAAAGGCGCTGGAAGAGGGGAGCCAAACAATGTGTGCTGCTTCTCATTAAGTATT 2079
Qy      361 GGCATATAGCAATTCGTCTCTTTGGCTGCTGCTCCTCAACAAGAGGCGAGAACTATC 420
Db      2080 GGCATATAGCAATTCGTCTCTTTGGCTGCTGCTCCTCAACAAGAGGCGAGAACTATC 2139
Qy      421 GGGCACACAGATTAATCTCTCAAGTGAACAGAGTTGAACAAGGCTCTTAGGAAATGCTGTA 480
Db      2140 GGGCACACAGATTAATCTCTCAAGTGAACAGAGTTGAACAAGGCTCTTAGGAAATGCTGTA 2199
Qy      481 TGGGATTAATCTTCACTGTTGAGGCTTGAATTTCTTCCCTTCAATCTACCTGCAAG 540
Db      2200 TGGGATTAATCTTCACTGTTGAGGCTTGAATTTCTTCCCTTCAATCTACCTGCAAG 2259
Qy      541 CCAAGTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db      2260 CCAAGTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
Qy      601 TCTCCAGACCCCTTCTGCGCACAATTCATTAAAGGCAACAAACATATACCTTCCATGA 660
Db      2320 TCTCCAGACCCCTTCTGCGCACAATTCATTAAAGGCAACAAACATATACCTTCCATGA 2379
Qy      661 GCACACACAGACTTTTGAAGAGCAATGACTGCTGTAATTGAGGCTTGAGAAATG 720
Db      2380 GCACACACAGACTTTTGAAGAGCAATGACTGCTGTAATTGAGGCTTGAGAAATG 2439
Qy      721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTA 780
Db      2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTA 2499
Qy      781 ACCACTGCTTCTGAGACCTTGAGCAGCGTGACTGTATTACATGTTGTATAGAAAC 840
Db      2500 ACCACTGCTTCTGAGACCTTGAGCAGCGTGACTGTATTACATGTTGTATAGAAAC 2559
Qy      841 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
Db      2560 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 2609
```

RESULT 9

```
US-10-198-053-391
; Sequence 391, Application US/10198053
; Publication No. US20030124140A1
GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-053-391
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Query Match      98.7%; Score 878; DB 15; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Qy      1 CAAAGCTGAGGCTTCTCTTCCATCTCGCGTGAAGAGCTTAAGACTTCAATTAATA 60
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Db 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGACAGTAAGACTCAGTTTTCATA 1780
Qy 61 GCATCTAGAGCAGTGGGACCTCAGCTGGGGGATTTGGCCCCCATCTCCGGGGGAATGTC 120
Db 1781 GCATCTAGAGCAGTGGGACCTCAGCTGGGGGATTTGGCCCCCATCTCCGGGGGAATGTC 1840
Qy 121 TGAAGACAATTTTGGTTTACTCTCAATGAGGAGTGGAGGAGATACAGTGTACTACCAAC 180
Db 1841 TGAAGACAATTTTGGTTTACTCTCAATGAGGAGTGGAGGAGATACAGTGTACTACCAAC 1900
Qy 181 TAGTGATTAAGGCGCAGGAGTGTCTGCTCAACCTCTCAACATGTAAGAGGAGCTGTCCCA 240
Db 1901 TAGTGATTAAGGCGCAGGAGTGTCTGCTCAACCTCTCAACATGTAAGAGGAGCTGTCCCA 1959
Qy 241 TTTCACATACCCCAATCCGAGTGTCAACCTGTGCAAGACCTTAAGAAACCCGTGTTTGAAT 300
Db 1960 TTTCACATACCCCAATCCGAGTGTCAACCTGTGCAAGACCTTAAGAAACCCGTGTTTGAAT 2019
Qy 301 AGAAAAAGGCGCTGGAAAAAGAGGAGCCAAATCTGTCTGCTTCTCATTAGTCAAT 360
Db 2020 AGAAAAAGGCGCTGGAAAAAGAGGAGCCAAATCTGTCTGCTTCTCATTAGTCAAT 2079
Qy 361 GGCATAATAGCATTCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 420
Db 2080 GGCATAATAGCATTCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 2139
Qy 421 GGGCACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTTGA 480
Db 2140 GGGCACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTTGA 2199
Qy 481 TGGGATTAATCTCAGCTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 540
Db 2200 TGGGATTAATCTCAGCTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 2259
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGAATTTAGA 600
Db 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGAATTTAGA 2319
Qy 601 TCTCCAGACCCCTTCTGGCCCAATTTCAATTAAGGCAACAACTATACCTTCCATGAA 660
Db 2320 TCTCCAGACCCCTTCTGGCCCAATTTCAATTAAGGCAACAACTATACCTTCCATGAA 2379
Qy 661 GCACACACAGACTTTTGAAGCAAGACCAATGACCTGTAATTTGAGGCTTGAAGAAATG 720
Db 2380 GCACACACAGACTTTTGAAGCAAGACCAATGACCTGTAATTTGAGGCTTGAAGAAATG 2439
Qy 721 AAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCAATGTGTA 780
Db 2440 AAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCAATGTGTA 2499
Qy 781 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTGACTGTATTAATGTTTATTAAGAAAC 840
Db 2500 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTGACTGTATTAATGTTTATTAAGAAAC 2559
Qy 841 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCT 2609
```

```
RESULT 10
US-10-714-389-207
; Sequence 207, Application US/10714389
; Publication No. US20040101899A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
```

```
; FILE REFERENCE: 210121.491D1
; CURRENT APPLICATION NUMBER: US/10/714,389
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-389-207

Query Match 98.7%; Score 878; DB 18; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGACAGTAAGACTCAGTTTTCATA 60
Db 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGACAGTAAGACTCAGTTTTCATA 1780
Qy 61 GCATCTAGAGCAGTGGGACCTCAGCTGGGGGATTTGGCCCCCATCTCCGGGGGAATGTC 120
Db 1781 GCATCTAGAGCAGTGGGACCTCAGCTGGGGGATTTGGCCCCCATCTCCGGGGGAATGTC 1840
Qy 121 TGAAGACAATTTTGGTTTACTCTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC 180
Db 1841 TGAAGACAATTTTGGTTTACTCTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC 1900
Qy 181 TAGTGATTAAGGCGCAGGAGTGTCTGCTCAACCTCTCAACATGTAAGAGGAGCTGTCCCA 240
Db 1901 TAGTGATTAAGGCGCAGGAGTGTCTGCTCAACCTCTCAACATGTAAGAGGAGCTGTCCCA 1959
Qy 241 TTTCACATACCCCAATCCGAGTGTCAACCTGTGCAAGACCTTAAGAAACCCGTGTTTGAAT 300
Db 1960 TTTCACATACCCCAATCCGAGTGTCAACCTGTGCAAGACCTTAAGAAACCCGTGTTTGAAT 2019
Qy 301 AGAAAAAGGCGCTGGAAAAAGAGGAGCCAAATCTGTCTGCTTCTCATTAGTCAAT 360
Db 2020 AGAAAAAGGCGCTGGAAAAAGAGGAGCCAAATCTGTCTGCTTCTCATTAGTCAAT 2079
Qy 361 GGCATAATAGCATTCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 420
Db 2080 GGCATAATAGCATTCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 2139
Qy 421 GGGCACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTTGA 480
Db 2140 GGGCACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTTGA 2199
Qy 481 TGGGATTAATCTCAGCTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 540
Db 2200 TGGGATTAATCTCAGCTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 2259
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGAATTTAGA 600
Db 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGAATTTAGA 2319
Qy 601 TCTCCAGACCCCTTCTGGCCCAATTTCAATTAAGGCAACAACTATACCTTCCATGAA 660
Db 2320 TCTCCAGACCCCTTCTGGCCCAATTTCAATTAAGGCAACAACTATACCTTCCATGAA 2379
Qy 661 GCACACACAGACTTTTGAAGCAAGACCAATGACCTGTAATTTGAGGCTTGAAGAAATG 720
Db 2380 GCACACACAGACTTTTGAAGCAAGACCAATGACCTGTAATTTGAGGCTTGAAGAAATG 2439
Qy 721 AAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCAATGTGTA 780
Db 2440 AAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCAATGTGTA 2499
Qy 781 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTGACTGTATTAATGTTTATTAAGAAAC 840
Db 2500 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTGACTGTATTAATGTTTATTAAGAAAC 2559
Qy 841 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCT 890
```


Db 2560 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTCTCT 2609

RESULT 11

US-10-717-296-207

/ Sequence 207, Application US/10717296

/ Publication No. US20040142361A1

/ GENERAL INFORMATION:

/ APPLICANT: Dillon, Davin C.

/ APPLICANT: Jiang, Yugu

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

/ TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

/ FILE REFERENCE: 210121.491C8

/ CURRENT APPLICATION NUMBER: US/10/717,296

/ NUMBER OF SEQ ID NOS: 313

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 207

/ LENGTH: 2627

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-717-296-207

Query Match 98.7%; Score 878; DB 18; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6.2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTCCATCCGCGGAGCAGCTAAGACCTCAGTTTCAATA 60

Db 1721 CAAGCTGAGGCTTCTCTTCCATCCGCGGAGCAGCTAAGACCTCAGTTTCAATA 1780

QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCATCTCCGGGGAAATGTC 120

Db 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCATCTCCGGGGAAATGTC 1840

QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180

Db 1841 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900

QY 181 TGTGATTAAGGCGGAGGATGCTCAACCTCCATCATGATGAGGAGGATGCTCCCA 240

Db 1901 TGTGATTAAGGCGGAGGATGCTCAACCTCCATCATGATGAGGAGGATGCTCCCA 1959

QY 241 TTAACAATCCCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 300

Db 1960 TTAACAATCCCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 2019

QY 301 AGAAAAAGGCGTGGAAAGGGGAGCCAAATCTGTCTGCTTCTCAATTAATGTCATT 360

Db 2020 AGAAAAAGGCGTGGAAAGGGGAGCCAAATCTGTCTGCTTCTCAATTAATGTCATT 2079

QY 361 GCGAATAAGCAATTCGTCTTTGGCTGCTCAGACAGAGAGCCAGAACTCTATC 420

Db 2080 GCGAATAAGCAATTCGTCTTTGGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139

QY 421 GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTTGACAAAGCTATGGAATGCTGA 480

Db 2140 GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTTGACAAAGCTATGGAATGCTGA 2199

QY 481 TGGGATTAATCTTCACTTTGAGCTTGAAGTTTCTTCCCTCAATTTACCTGCAAG 540

Db 2200 TGGGATTAATCTTCACTTTGAGCTTGAAGTTTCTTCCCTCAATTTACCTGCAAG 2259

QY 541 CCAAGTTCTGTAAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600

Db 2260 CCAAGTTCTGTAAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319

QY 601 TCTCCAGACCTTCTGCGCACAAATTCATTAAGGCAACAAACATATACCTTCCATGA 660

Db 2320 TCTCCAGACCTTCTGCGCACAAATTCATTAAGGCAACAAACATATACCTTCCATGA 2379

QY 661 GCACACACAGACTTTGAAAGCAGAGCAATGATCTGTAATGAGGCTTGAAGATG 720

Db 2380 GCACACACAGACTTTGAAAGCAGAGCAATGATCTGTAATGAGGCTTGAAGATG 2439

QY 721 AAGCTTGAAGAAAGATACTTGTTCAGCCGCCCTTCCACACTCTTCATGTGTTA 780

Db 2440 AAGCTTGAAGAAAGATACTTGTTCAGCCGCCCTTCCACACTCTTCATGTGTTA 2499

QY 781 ACCACTGCTTCTGAGACCTTGAAGCCAGGCTGATTAATCATGTTGTTATAGAAAC 840

Db 2500 ACCACTGCTTCTGAGACCTTGAAGCCAGGCTGATTAATCATGTTGTTATAGAAAC 2559

QY 841 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTCTCT 890

Db 2560 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTCTCT 2609

RESULT 12

US-10-860-790-391

/ Sequence 391, Application US/10860790

/ Publication No. US20050031634A1

/ GENERAL INFORMATION:

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: Reiter, Marc W.

/ APPLICANT: Ranger, Gary R.

/ APPLICANT: Hill, Paul

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

/ FILE REFERENCE: 210121.462C11

/ CURRENT APPLICATION NUMBER: US/10/860,790

/ NUMBER OF SEQ ID NOS: 624

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 391

/ LENGTH: 2627

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-860-790-391

Query Match 98.7%; Score 878; DB 19; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6.2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTCCATCCTGCTGAGCAGCTAAGACCTCAGTTTCAATA 60

Db 1721 CAAGCTGAGGCTTCTCTTCCATCCTGCTGAGCAGCTAAGACCTCAGTTTCAATA 1780

QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCATCTCCGGGGAAATGTC 120

Db 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCATCTCCGGGGAAATGTC 1840

QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180

Db 1841 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900

QY 181 TGTGATTAAGGCGGAGGATGCTCAACCTCCATCATGATGAGGAGGATGCTCCCA 240

Db 1901 TGTGATTAAGGCGGAGGATGCTCAACCTCCATCATGATGAGGAGGATGCTCCCA 1959

QY 241 TTAACAATCCCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 300

Db 1960 TTAACAATCCCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 2019

QY 301 AGAAAAAGGCGTGGAAAGGGGAGCCAAATCTGTCTGCTTCTCAATTAATGTCATT 360

Db 2020 AGAAAAAGGCGTGGAAAGGGGAGCCAAATCTGTCTGCTTCTCAATTAATGTCATT 2079

QY 361 GCGAATAAGCAATTCGTCTTTGGCTGCTCAGACAGAGAGCCAGAACTCTATC 420

Db 2080 GCGAATAAGCAATTCGTCTTTGGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139

QY 421 GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTTGACAAAGCTATGGAATGCTGA 480

Db 2140 GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTTGACAAAGCTATGGAATGCTGA 2199

QY 481 TGGATTATCTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCACTCGAAG 540
DB 2200 TGGATTATCTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCACTCGAAG 2259
QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGTTTCTTACTGAAATTTAGA 600
DB 2260 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGTTTCTTACTGAAATTTAGA 2319
QY 601 TCTCCAGACCCCTTCCTGCGCAATTCGAATTAAGGCAACAAATATACCTTCATGAA 660
DB 2320 TCTCCAGACCCCTTCCTGCGCAATTCGAATTAAGGCAACAAATATACCTTCATGAA 2379
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTAAGGCGCTTGAGAAATG 720
DB 2380 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTAAGGCGCTTGAGAAATG 2439
QY 721 AACCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCTTCCCACTCTTCATGTTGA 780
DB 2440 AACCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCTTCCCACTCTTCATGTTGA 2499
QY 781 ACCACTGCTTCTCTGAGCTTTGAGCGCAAGTGAATTAATTAATTAATTAATTAATTA 840
DB 2500 ACCACTGCTTCTCTGAGCTTTGAGCGCAAGTGAATTAATTAATTAATTAATTAATTA 2559
QY 841 TGAATTTAGAGTTCTGATCGTTCAAGAAATGAATTAATTAATTAATTAATTAATTA 890
DB 2560 TGAATTTAGAGTTCTGATCGTTCAAGAAATGAATTAATTAATTAATTAATTAATTA 2609

RESULT 13

US-10-023-339-2
; Sequence 2, Application US/10023339
; Publication No. US20030208058A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: B7-Like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: F7124P1
; CURRENT APPLICATION NUMBER: US/10/023,339
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/20917
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3357
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-339-2

Query Match 98.7%; Score 878; DB 17; Length 3357;
Best Local Similarity 99.9%; Pred. No. 7,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAAGCTCTGAGGCTTCTCTTCATCTCTGCGTGAACAGTCAAGCTTCAGTTTCAATA 60
DB 2057 CAAAGCTCTGAGGCTTCTCTTCATCTCTGCGTGAACAGTCAAGCTTCAGTTTCAATA 2116
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGAGTATTTGCGCCCATCTCGGGGGAAATGTC 120
DB 2117 GCATCTAGAGCAGTGGAGCTCAGCTGGGAGTATTTGCGCCCATCTCGGGGGAAATGTC 2176
QY 121 TGAAGCAATTTGTTTACTCAATGAGGAGTGAAGAGATTAAGTGTACTACCAAC 180
DB 2177 TGAAGCAATTTGTTTACTCAATGAGGAGTGAAGAGATTAAGTGTACTACCAAC 2236
QY 181 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTTCTTAACATGTAACAGGAGCTGTCTCCCA 240
DB 2237 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTTCTTAACATGTAACAGGAGCTGTCTCCCA 2295

QY 241 TTCAACTACCAATCCGAAGTGTCACTGTGTAGACTATAGAAACCTGTTTGAAT 300
DB 2296 TTCAACTACCAATCCGAAGTGTCACTGTGTAGACTATAGAAACCTGTTTGAAT 2355
QY 301 AGAAAGGCGCTGAAAGAGGAGGCAACAAATGTGTCTGCTTCTCAATTAGTATT 360
DB 2356 AGAAAGGCGCTGAAAGAGGAGGCAACAAATGTGTCTGCTTCTCAATTAGTATT 2415
QY 361 GGCATAATAGCATTGTGTCTTCTTGGTGTGTCTGCTTCAAGACAGAGGCGAACTATC 420
DB 2416 GGCATAATAGCATTGTGTCTTCTTGGTGTGTCTGCTTCAAGACAGAGGCGAACTATC 2475
QY 421 GGGCACAGGATTAACATCTCTCAGTGAACAGTGTGAAGGCGTATGGAAATGCGTGA 480
DB 2476 GGGCACAGGATTAACATCTCTCAGTGAACAGTGTGAAGGCGTATGGAAATGCGTGA 2535
QY 481 TGGATTATCTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCACTCGAAG 540
DB 2536 TGGATTATCTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCACTCGAAG 2595
QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTTACTCAGGTTTCTTAATTAATTAATTA 600
DB 2596 CCAAGTTCTGTAGAGAAATGCTGAGTTTACTCAGGTTTCTTAATTAATTAATTA 2655
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DB 2656 TCTCCAGACCCCTTCCTGCGCAATTCGAATTAAGGCAACAAATATACCTTCATGAA 2715
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTAAGGCGCTTGAGAAATG 720
DB 2716 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTAAGGCGCTTGAGAAATG 2775
QY 721 AACCTTTGAAGAAAGAAATACCTTTGTTTCCAGCCCTTCCCACTCTTCATGTTGA 780
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QY 781 ACCACTGCTTCTCTGAGCTTTGAGCGCAAGTGAATTAATTAATTAATTAATTAATTA 840
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RESULT 14

US-09-896-738-1
; Sequence 1, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Fang, Mei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 00-513-A
; CURRENT APPLICATION NUMBER: US/09/896,738
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,645
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2603
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (53) .. (901)
US-09-896-738-1

Query Match 98.6%; Score 877.6; DB 9; Length 2603;
Best Local Similarity 99.8%; Pred. No. 8,5e-284;
Matches 888; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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| Db | 1751 | GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTCCGCCCCCATCTCCGGGGGAATGTC | 1810 |
| OY | 121 | TGAAGACAATTTTGTTACTCTCAATGAGAGAGTGGAGGAGTACAGTGTACTAACAC | 180 |
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| OY | 181 | TAGTGGATAAAGGCGCAGGAGATGCTCTCAACCTCCTCATGTACAGGGAAGTCTCCCA | 240 |
| Db | 1871 | TAGTGGATAAAGGCGCAGGAGATGCTCTCAACCTCCTCATGTACAGGGAAGTCTCCCA | 1929 |
| OY | 241 | TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTCCAGACTAAGAAACCTTGTTTTAGT | 300 |
| Db | 1930 | TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTCCAGACTAAGAAACCTTGTTTTAGT | 1989 |
| OY | 301 | AGAAAAGGCGCTGGAAAGAGGGGAGCCAAACAATGTGTCTGCTTCCCTCAATTAGTCA | 360 |
| Db | 1990 | AGAAAAGGCGCTGGAAAGAGGGGAGCCAAACAATGTGTCTGCTTCCCTCAATTAGTCA | 2049 |
| OY | 361 | GCGAATATAGCAATTTGTCTCTTTGGCTGTGCTCACAAGAGAGGCAACAATCTATC | 420 |
| Db | 2050 | GCGAATATAGCAATTTGTCTCTTTGGCTGTGCTCACAAGAGAGGCAACAATCTATC | 2109 |
| OY | 421 | GGGCACAGATACATCTTCTCAGTGAACAAGTTGACAGGCGCTATGGGAAATGCTGA | 480 |
| Db | 2110 | GGGCACACAGATACATCTTCTCAGTGAACAAGTTGACAGGCGCTATGGGAAATGCTGA | 2169 |
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| Db | 2170 | TGGATATATCTTCACTGTTGAGGCTTCTAAGTTCTTCCCTCATCTCAACCTGCAAG | 2229 |
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| Db | 2230 | CCAAGTTCTGTAAGAGAAATGCGTAGTTCTAGCTCAGGTTTTCTTACTGAAATTTAGA | 2289 |
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| Db | 2350 | GCACACACAGACTTTGAAAGCAAGCAATGACGCTGAATGAGGCGTTGAGGAATG | 2409 |
| OY | 721 | AAGCTTTAAGGAAAGAATACTTGTGTTCCAGGCGCCCTCCACACTCTTCATGTGTTA | 780 |
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| OY | 841 | TGATTTAGATTCGATCGTTCAAGAGAAATGATTAATATACATTTCT | 890 |
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| US-09-877-065-7 | | | |
| ; Sequence 7, Application US/09877065 | | | |
| ; Patent No. US2002005190A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: OPLE, ERIC | | | |
| ; APPLICANT: MCLACHLAN, KAREN | | | |
| ; APPLICANT: HEARD, CHERYL J. | | | |
| ; TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR | | | |
| ; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF OVARIAN CARCINOMAS | | | |
| ; FILE REFERENCE: 037003-0280631 | | | |

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Db      2418 AACCTTGAGAGAAAGAAATACCTTTGTTTCAGCCCTTCCACACTCTTCATGTGTA 2477
Qy      781  ACCACTGCCCTTCTGAGACCTTGGAGCCACGGTGACTGTATTACATGTTGTTATAGAAAC 840
Db      2478 ACCACTGCCCTTCTGAGACCTTGGAGCCACGGTGACTGTATTACATGTTGTTATAGAAAC 2537
Qy      841  TGAATTTAGAGTCTGATCGTTCAAGAGAAATGATTAAATATACATTTCCCT 890
Db      2538 TGAATTTAGAGTCTGATCGTTCAAGAGAAATGATTAAATATACATTTCCCT 2587

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Search completed: May 31, 2005, 10:07:38
 Job time : 613.64 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:48:09 ; Search time 3461.52 Seconds

(without alignments)
9786.800 Million cell updates/sec

Title: US-09-763-978B-11

Perfect score: 890
Sequence: 1 caagctctgagcttctcct.....tgatataatatacttctcct 890

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

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| 2 | 741.8 | 83.3 | 1018 | 5 | EX337228 BX337228 |
| 3 | 695 | 78.1 | 737 | 6 | CA313445 UI-CF-FNO |
| 4 | 666 | 74.8 | 700 | 5 | BU632767 UI-H-FEI- |
| 5 | 663 | 74.5 | 691 | 6 | CB241729 UI-CF-FNO |
| 6 | 662 | 74.4 | 691 | 6 | CA314865 UI-CF-FNO |
| 7 | 658.2 | 74.0 | 691 | 6 | BU608696 UI-CF-FNO |
| 8 | 637.8 | 71.7 | 660 | 6 | CB852235 UI-CF-FNO |
| 9 | 634.4 | 71.3 | 660 | 6 | CA426580 UI-H-FEI- |
| 10 | 632.2 | 71.0 | 679 | 6 | CA312678 UI-CF-FNO |
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| 17 | 511 | 57.4 | 529 | 2 | AM615203 lx78a06.x |
| 18 | 494.6 | 55.6 | 524 | 1 | AA075632 zmb8h04.r |
| 19 | 494 | 55.5 | 524 | 1 | AA171844 zmb8h04.s |
| 20 | 478.4 | 53.8 | 482 | 1 | AI683712 lx53809.x |
| 21 | 478 | 53.7 | 481 | 2 | AA470108 lx29h08.x |
| 22 | 466.2 | 52.4 | 486 | 1 | AA075579 zmb8h04.s |
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| C | 26 | 432 | 48.5 | 436 | 1 | AI638559 | AI638559 t550a07.x |
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| C | 33 | 403.2 | 45.3 | 416 | 1 | AI539668 | AI539668 lx71e07.x |
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| C | 39 | 354.6 | 39.8 | 382 | 2 | AM172459 | AM172459 lx39d04.x |
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| C | 41 | 333.4 | 37.5 | 352 | 1 | AA953518 | AA953518 om80b02.s |
| C | 42 | 328.4 | 36.9 | 355 | 6 | CA314209 | CA314209 UI-CF-FNO |
| C | 43 | 327 | 36.7 | 450 | 7 | H51315 | H51315 YP07E05.s1 |
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ALIGNMENTS

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LOCUS
DEFINITION
full-length cDNA clone CS0D1039YG21 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION
CR603772
VERSION
CR603772.1 GI:50484579
KEYWORDS
HTC; cDNA; cDNA
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE

REFERENCE
AUTHORS
Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 2431)

REFERENCE

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 2431
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/mol_type="mRNA"
/db_xref="taxon:9606"
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FEATURES

source

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Matches 859; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DEFINITION clone CS0D1039YG21 3-PRIME, mRNA sequence.
ACCESSION BX337228
KEYWORDS BX337228.2 GI:46283446
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1018)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30346952.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteil, CP 5705 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
742.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/8=CS0D1039AD11NP1&c=742.r.
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sites of the pCMVSPORT 6 vector. Library was normalized."
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Best Local Similarity 93.4%; Pred. No. 3,4e-210;
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QY 62 CATCTAGAGCACTGAGCACTGAGTGGGATTTGGCCCCC-ATCTCGGGGGAATGTC 120
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Db 809 CATCTAGAGCACTGAGCACTGAGTGGGATTTGGCCCCC-ATCTCGGGGGAATGTC 750
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QY 476 -CCGATGAGATTAATCTTCAAGCTGTGAGC--TTCTAGTTTCTTCCCTCATTTAC 533
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 700)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 623-700, >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

1..700
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/note="Organ: Chondrosarcoma; Vector: pT73-Pac
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Site 2: Not I; NCI CCGAP FBI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCTACGGAC. The cell lines were provided by Dr James
Martin from the University of Iowa.
TAG TISSUE=Human grade 2 chondrosarcoma cell line pool
TAG_LIB=UI-H-FBI
TAG_SEQ=CGCTACGGAC"

ORIGIN

Query Match 74.8%; Score 666; DB 5; Length 700;
Best Local Similarity 99.9%; Pred. No. 1, 5e-187;
Matches 677; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
213 TCCTACCATGTACAGGAGCGTCCCATTAACCACTCCGAGTGTCACTGTG 272
Db TCTTACCATGTACA-GGACGTCCTCCCATTAACAATCCGAGTGTCACTGTG 642
QY 273 TCAGAGCTAAGAAACCTGCTTTGAGTAAAGAGGCTGAGAAAGGGAGCCAAACA 332
Db 641 TCAGAGCTAAGAAACCTGCTTTGAGTAAAGAGGCTGAGAAAGGGAGCCAAACA 582
QY 333 ATCTGCTGCTTCTCACAATTAGTCACTGCTCTGCTTGGCTGCGG 392
Db 581 ATCTGCTGCTTCTCACAATTAGTCACTGCTCTGCTTGGCTGCGG 522
QY 393 CCTCAGACAGAGAGCCAGAACTCTATCGGGCCACAGATAACATCTTCAGTAAACAGA 452
Db 521 CCTCAGACAGAGAGCCAGAACTCTATCGGGCCACAGATAACATCTTCAGTAAACAGA 462
QY 453 GTTGAACAAGGCTTATGGGAAATGCTGATGGGATTATCTTCAGCTTGTGAGCTTTAAG 512
Db 461 GTTGAACAAGGCTTATGGGAAATGCTGATGGGATTATCTTCAGCTTGTGAGCTTTAAG 402

QY 513 TTTCTTCCCTTCATTTCTACCGTCGACCAAGTTCTGTAAAGAAATGCTGAGTTCTA 572
Db 401 TTTCTTCCCTTCATTTCTACCGTCGACCAAGTTCTGTAAAGAAATGCTGAGTTCTA 342
QY 573 GCTCAGGTTTCTTACTGTAATTTAGATCTTCAGACCCCTTCCTGGCCCAATTTAAATT 632
Db 341 GCTCAGGTTTCTTACTGTAATTTAGATCTTCAGACCCCTTCCTGGCCCAATTTAAATT 282
QY 633 AAGGACAAACATATATACCTTCATGAAGACACACAGACTTTTGAAGCAAGCAATG 692
Db 281 AAGGACAAACATATATACCTTCATGAAGACACACAGACTTTTGAAGCAAGCAATG 222
QY 693 ACTGCTGAATTTAGAGCCCTTGAGAAATGAGCTTTGAAGAAAGAAATATCTTTGTTC 752
Db 221 ACTGCTGAATTTAGAGCCCTTGAGAAATGAGCTTTGAAGAAAGAAATATCTTTGTTC 162
QY 753 GCCCCTTCCACACATCTTCATGTTTAAACACAGCTTCTCTGACCTTGGACCAAGGT 812
Db 161 GCCCCTTCCACACATCTTCATGTTTAAACACAGCTTCTCTGACCTTGGACCAAGGT 102
QY 813 GACTGATTTACATGTTGTTATGAAGAACTGATTTTGAAGTTCTGATCGTTCAAGAAATG 872
Db 101 GACTGATTTACATGTTGTTATGAAGAACTGATTTTGAAGTTCTGATCGTTCAAGAAATG 42
QY 873 ATTAATATATACATTTCT 890
Db 41 ATTAATATATACATTTCT 24

RESULT 5
CB241729/c 691 bp mRNA linear EST 12-FEB-2003
LOCUS
DEFINITION
UI-CF-FN0-afz-p-01-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
ACCESSION
CB241729.1 GI:28363373
VERSION
CB241729.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 691)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL
MEDLINE
PUBMED
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.researchgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

1..691
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FN0-afz-p-01-0-UI"

/tissue type="Human Lung Epithelial cells"
 /lab host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone lib="UI-CF-FN0"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: Score 1; Site_2: Not 1;
 UI-CF-FN0 is a subcloned cDNA library derived from two
 normalized Human lung epithelial cell libraries (EN1 and
 DU1). The library was subcloned according to Bernaldo,
 Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@uiowa.edu
 TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG LIB=UI-CF-FN0
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 74.4%; Score 663; DB 6; Length 691;
 Best Local Similarity 100.0%; Pred. No. 1.1e-186;
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

228 GAGCGTCTCCCTTACACTACCAATCCGAAGTCACTGTGTACAGACTTAAGAAC 287
 681 GAGCGTCTCCCTTACACTACCAATCCGAAGTCACTGTGTACAGACTTAAGAAC 622
 288 CCGTGTGTTGAGTGAAGAGGCGCTGGAAGAGGGGAGCCAAATCTGTCTGCTTCT 347
 621 CCGTGTGTTGAGTGAAGAGGCGCTGGAAGAGGGGAGCCAAATCTGTCTGCTTCT 562
 348 CACATTAGTCATTGGCAATTAACATCTCTCTTGTGCTGCTGCTGCTGCTGCTGCT 407
 561 CACATTAGTCATTGGCAATTAACATCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTG 502
 408 CCGAACTCTATGCGGACCAAGATTAACATCTCTGATGAACAGATTTGCAAGGCTTAT 467
 501 CCGAACTCTATGCGGACCAAGATTAACATCTCTGATGAACAGATTTGCAAGGCTTAT 442
 468 GGAATAGCTGATGGGATTAATCTGATGCTTGTGAGCTTCTAGTTCTTCCCTTCAT 527
 441 GGAATAGCTGATGGGATTAATCTGATGCTTGTGAGCTTCTAGTTCTTCCCTTCAT 382
 528 TCTACCTGCAAGCCAAATCTGTGAAGAAATGCTGATGCTTCTGATGCTTCTTCTTA 587
 381 TCTACCTGCAAGCCAAATCTGTGAAGAAATGCTGATGCTTCTGATGCTTCTTCTTA 322
 588 CTTGTAATTTAGTCTTCAGACCTTCTGCGCAATTAATTAAGGCAACAAATTA 647
 321 CTTGTAATTTAGTCTTCAGACCTTCTGCGCAATTAATTAAGGCAACAAATTA 262
 648 TACCTTCATGAAGCACACAGACTTTGAAGCAAGCAATGACTGCTGAATTTAG 707
 261 TACCTTCATGAAGCACACAGACTTTGAAGCAAGCAATGACTGCTGAATTTAG 202
 708 GCGTTGAGAAATGAAGCTTTGAAGAAATTAATTTTTCAGCCCTTCCACAC 767
 201 GCGTTGAGAAATGAAGCTTTGAAGAAATTAATTTTTCAGCCCTTCCACAC 142
 768 TCTTCAATGTTTAAACACCTGCTTCTGACCTTGAAGCAAGGCTGATTTAATGAT 827
 141 TCTTCAATGTTTAAACACCTGCTTCTGACCTTGAAGCAAGGCTGATTTAATGAT 82
 828 TGTATAGAAATGAATTTAGAGTCTGATGCTTGAAGCAAGCAATTAATTAATGAT 887
 81 TGTATAGAAATGAATTTAGAGTCTGATGCTTGAAGCAAGCAATTAATTAATGAT 22

QY 888 CCT 890
 DB 21 CCT 19

RESULT 6
 CA314865/c 691 bp mRNA linear EST 04-NOV-2002
 LOCUS CA314865/c
 DEFINITION UI-CF-FN0-afi-e-12-0-UI.81 UI-CF-FN0 Homo sapiens cDNA clone

ACCESSION
 CA314865
 VERSION
 CA314865.1 GI:24532963
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 691)
 Bernaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL
 MEDLINE
 PUBMED
 97044477
 8889548
 COMMENT
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 DNA Distribution: Researchers may obtain clones from Research
 Genetics (www.reagen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 618-691. >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 PolyA=yes.

FEATURES

source

Location/Qualifiers
 1. 691
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FN0-afi-e-12-0-UI"
 /tissue_type="Human Lung Epithelial cells"
 /lab host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone lib="UI-CF-FN0"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: Score 1; Site_2: Not 1;
 UI-CF-FN0 is a subcloned cDNA library derived from two
 normalized Human lung epithelial cell libraries (EN1 and
 DU1). The library was subcloned according to Bernaldo,
 Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@uiowa.edu
 TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG LIB=UI-CF-FN0
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 74.4%; Score 662; DB 6; Length 691;
 Best Local Similarity 99.8%; Pred. No. 2.3e-186;
 Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

228 GAGCGTCTCCCTTACACTACCAATCCGAAGTCACTGTGTACAGACTTAAGAAC 287
 681 GAGCGTCTCCCTTACACTACCAATCCGAAGTCACTGTGTACAGACTTAAGAAC 622
 288 CCGTGTGTTGAGTGAAGAGGCGCTGGAAGAGGGGAGCCAAATCTGTCTGCTTCT 347
 621 CCGTGTGTTGAGTGAAGAGGCGCTGGAAGAGGGGAGCCAAATCTGTCTGCTTCT 562
 348 CACATTAGTCATTGGCAATTAACATCTCTCTTGTGCTGCTGCTGCTGCTGCTGCT 407
 561 CACATTAGTCATTGGCAATTAACATCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTG 502
 408 CCGAACTCTATGCGGACCAAGATTAACATCTCTGATGAACAGATTTGCAAGGCTTAT 467

RESULT 8
CB852239/c
LOCUS CB852239 660 bp mRNA linear EST 22-APR-2003
DEFINITION UI-CF-FNO-aff-m-01-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
CB852239
ACCESSION UI-CF-FNO-aff-m-01-0-UI 3', mRNA sequence.
VERSION CB852239
KEYWORDS EST, GI:30047206
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 660)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PubMed 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul.mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..660
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-aff-m-01-0-UI"
/issue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1lb="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized human lung epithelial cell libraries (BN1 and
DN1). The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_SEQ=None found"

ORIGIN
Query Match 71.7%; Score 637.8; DB 6; Length 660;
Best Local Similarity 99.5%; Pred. No. 3.9e-179;
Matches 639; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

249 ACCCAATCCGAAGTCACTGTCAGACTAGAAAGGCTTTGAGTAGAAAGG 308
|||||
660 ACCCAATCCGAAGTCACTGTCAGACTAGAAAGGCTTTGAGTAGAAAGG 601
|||||
309 GCGTGAAGAGGGAGCCAAATCTGCTCTTCTCATTAGTCATTGGCAATA 368
|||||
600 GCGTGAAGAGGGAGCCAAATCTGCTCTTCTCATTAGTCATTGGCAATA 541
|||||
369 AGATTCTGCTCTTTGGCTGCTGCTCAGACACAGAGAGCCAAATCTATCGGGACCA 428
|||||
540 AGATTCTGCTCTTTGGCTGCTGCTCAGACACAGAGAGCCAAATCTATCGGGACCA 481
|||||
429 GGATAATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGATGGATTA 488
|||||

Db 480 GGATAATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGATGGATTA 421
|||||
Qy 489 TCTTCAGCTGTTGAGCTCTTAAGTTCTTCCCTTCATTTCACCTCGAAGCAAGTTC 548
|||||
Db 420 TCTTCAGCTGTTGAGCTCTTAAGTTCTTCCCTTCATTTCACCTCGAAGCAAGTTC 361
|||||
Qy 549 TGTAAAGAAATGCCGAGTTCAGTCAAGTTTCTTCTGATTTAGATTCACG 608
|||||
Db 360 TGTAAAGAAATGCCGAGTTCAGTCAAGTTTCTTCTGATTTAGATTCACG 301
|||||
Qy 609 CCCTTCCTGGCCCAATTCATTAAGGCAACAATATACCTTCATGACACACAC 668
|||||
Db 300 CCCTTCCTGGCCCAATTCATTAAGGCAACAATATACCTTCATGACACACAC 241
|||||
Qy 669 AGACTTTTGAAGCAAGCAATGACTGTTGATTTAGAGCCCTTGAAGAAATGAGCTTGG 728
|||||
Db 240 AGACTTTTGAAGCAAGCAATGACTGTTGATTTAGAGCCCTTGAAGAAATGAGCTTGG 181
|||||
Qy 729 AAGGAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCATGTTAACAACCTGC 788
|||||
Db 180 AAGGAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCATGTTAACAACCTGC 121
|||||
Qy 789 CTTCCTGACCTTGAGCAGCAGGTGACTGATTAATGATTTAGAAATGATTTTA 848
|||||
Db 120 CTTCCTGACCTTGAGCAGCAGGTGACTGATTAATGATTTAGAAATGATTTTA 61
|||||
Qy 849 GAGTTCTGATGTTCAAGAGATGATTAATATATCAATTTCT 890
|||||
Db 60 GAGTTCTGATGTTCAAGAGATGATTAATATATCAATTTCT 19
|||||

RESULT 9
CA426580/c
LOCUS CA426580 660 bp mRNA linear EST 07-NOV-2002
DEFINITION UI-H-FBI-beh-p-14-0-UI.s1 NCI CGAP FBI Homo sapiens cDNA clone
CA426580
ACCESSION UI-H-FBI-beh-p-14-0-UI 3', mRNA sequence.
VERSION CA426580.1 GI:24789306
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 660)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
AUTHORS
TITLE
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, Bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..660
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FBI-beh-p-14-0-UI"
/issue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="NCI CGAP_FBI"
/note="Organ: Chondrosarcoma; Vector: pT73-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI CGAP FBI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines

from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-CAT vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCTACCGAC. The cell lines were provided by Dr James Martin from the University of Iowa.

TAG TISSUE=human grade 2 chondrosarcoma cell line pool
TAG_LIB=UT-H-FEI
TAG_SEQ=CGCTACCGAC"

Db 439 GAATGCGCTGATGGATTTATCTTCAGCTGTGTGAGCTTATAGTTCTTCCCTTCATTC 380
QY 530 TACCTGCAAGCAAGTTCTGTAAAGAAATGCTGTGTTCTAGTCTTCTTCTACT 589
Db 379 TACCCTGCAAGCAAGTTCTGTAAAGAAATGCTGTGTTCTAGTCTTCTTCTACT 320
QY 590 CTGAATTTAGATCTCCAGACCCCTTCTGCGCACATTCATTAAGGCAACAAATATA 649
Db 319 CTGAATTTAGATCTCCAGACCCCTTCTGCGCACATTCATTAAGGCAACAAATATA 260
QY 650 CCTTCATGAGACACACAGACTTTTGAAGACGACATGACTGCTGAATTGAGGC 709
Db 259 CCTTCATGAGACACACAGACTTTTGAAGACGACATGACTGCTGAATTGAGGC 200
QY 710 CTGAGGAATGAGCTTTGAAGAAAGAAATGCTTGTCCAGCCCTTCCACACTC 769
Db 199 CTGAGGAATGAGCTTTGAAGAAAGAAATGCTTGTTCAGCCCTTCCACACTC 140
QY 770 TTGATGTGTAAACACTGCTTCTGAGACCTTGGAGCAGGTGATGTTATTCATGTTG 829
Db 139 TTGATGTGTAAACACTGCTTCTGAGACCTTGGAGCAGGTGATGTTATTCATGTTG 80
QY 830 TTATAGAAAATGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCC 889
Db 79 TTATAGAAAATGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCC 20
QY 890 T 890
Db 19 T 19

RESULT 11
CA503188/c 594 bp mRNA linear EST 14-NOV-2002

DEFINITION UI-CF-FNO-afp-D-10-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
ACCESSION CA503188
VERSION CA503188
KEYWORDS CA503188.1 GI:24994142

SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 594)
AUTHORS Ronaldo M.F., Lennon G. and Soares M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source 1..594
Location/Qualifiers
1..594
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-afp-D-10-0-UI"
/issue_type="Human Lung Epithelial cells"

/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DU1). The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

ORIGIN
Query Match 63.8%; Score 568; DB 6; Length 594;
Best local similarity 99.1%; Pred. No. 3e-158;
Matches 571; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 315 AAGAGGGGAGCCAAATCTGTCCTTCCATTAAGTATGCAAAATTAACATT 374
Db 594 AAGAGGGGAGCCAAATCTGTCCTTCCATTAAGTATGCAAAATTAACATT 535
QY 375 CTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAACTATGCGGACAGAGATA 434
Db 534 CTGCTCAATGCTGCTGCTCAGACAGAGAGCCAACTATGCGGACAGAGATA 475
QY 435 CATCTCTAGTGAAACAGAGTTGCAAGGCTATGGAAATGCTGATGGATTAATCTCA 494
Db 474 CATCTCTAGTGAAACAGAGTTGCAAGGCTATGGAAATGCTGATGGATTAATCTCA 415
QY 495 GCTTGTGAGCTTCAAGTTCTTCCCTCACTTCAAGCTGAAAGCTTCTGTAAG 554
Db 414 GCTTGTGAGCTTCAAGTTCTTCCCTCACTTCAAGCTGAAAGCTTCTGTAAG 355
QY 555 AGAATAGCTGAGTTTACCTCAGTTTCTTACCTGATTTAGATTCACAGACCTTC 614
Db 354 AGAATAGCTGAGTTTACCTCAGTTTCTTACCTGATTTAGATTCACAGACCTTC 295
QY 615 CTGGCCAAATTCAAATTAAGGCAACAAATATACCTTCATGAAGACACAGACTT 674
Db 294 CTGGCCAAATTCAAATTAAGGCAACAAATATACCTTCATGAAGACACAGACTT 235
QY 675 TTGAAGCAAGACATGATGCTGTAATTTAGAGGCTTGAAGAAATGAAGTTGAAGAA 734
Db 234 TTGAAGCAAGACATGATGCTGTAATTTAGAGGCTTGAAGAAATGAAGTTGAAGAA 175
QY 735 AAGATATCTTTGTTTCCAGCCCTTCCCACTCTTCACTGTTTAAACACTGCTTCT 794
Db 174 AAGATATCTTTGTTTCCAGCCCTTCCCACTCTTCACTGTTTAAACACTGCTTCT 115
QY 795 GGAAGCTTGAAGCCAGGTGATGATTAATGATGTTTAAAGAAATGAAGTTGAAGTT 854
Db 114 GGAAGCTTGAAGCCAGGTGATGATTAATGATGTTTAAAGAAATGAAGTTGAAGTT 55
QY 855 TGATGCTTCAAGAGATGATTAATTAATTAATTTCT 890
Db 54 TGATGCTTCAAGAGATGATTAATTAATTAATTTCT 19

RESULT 12
A1684143/c 556 bp mRNA linear EST 16-DEC-1999

DEFINITION UI-CF-FNO-UI1 Homo sapiens cDNA clone IMAGE:2275830 3',
mRNA sequence.
ACCESSION A1684143
VERSION A1684143
KEYWORDS A1684143.1 GI:4895437

SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 556)

| | |
|---------|--------------------------------------------------------------------------------------------------|
| AUTHORS | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . |
| TITLE | National Cancer Institute, Cancer Genome Anatomy Project (CGAP) |
| JOURNAL | Tumor Gene Index |
| COMMENT | Unpublished (1997) Contact: Robert Strausberg, Ph.D. |

ORIGIN

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 62.0%; | Score 552; | DB 1; | Length 556; |
| Best Local Similarity | 100.0%; | Pred. No. 1.8e-153; | | |
| Matches 552; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---------------------------------------------------------------|-----|
| Qy | 339 | TTGCTTCTCTCAATTAGTCATTGGGAATTAAGCAATTCGTCTGCTTGGCTGCTGCTCAG | 398 |
| Db | 556 | CTGCTCTCTCAATTAGTCATTGGGAATTAAGCAATTCGTCTGCTTGGCTGCTGCTCAG | 497 |
| Qy | 399 | CACAGAGCCGAGAACTCTATCGGGGCAACGAGATTAACATCTCTCAGTGAACAGAGTTGAC | 458 |
| Db | 496 | CACAGAGCCGAGAACTCTATCGGGGCAACGAGATTAACATCTCTCAGTGAACAGAGTTGAC | 437 |
| Qy | 459 | AAGGCTTATGGGAAATGCTGATGGGATTAATCTCAGCTTGTGAGCTTTGAATTTCTT | 518 |
| Db | 436 | AAGGCTTATGGGAAATGCTGATGGGATTAATCTCAGCTTGTGAGCTTTGAATTTCTT | 377 |
| Qy | 519 | TCCCTTCAATTCTACCTTCGACGACCAAGTTCTGTAAAGAAATGCTGAGTTTACTGACG | 578 |
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| Db | 316 | GTTTTCTACTCTGAAATTTAGATCTCCAGACCTTCCTGGGCACAATTCAAATTAAGGCA | 257 |
| Qy | 639 | ACAAACATATACCTTCCATGGAAGCACACACAAGCTTTGAAAGCAAGCAATGACTGCT | 698 |
| Db | 256 | ACAAACATATACCTTCCATGGAAGCACACACAAGCTTTGAAAGCAAGCAATGACTGCT | 197 |
| Qy | 699 | TGAATTGAGGCTTGAAGATGAGCTTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCC | 758 |
| Db | 196 | TGAATTGAGGCTTGAAGATGAGCTTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCC | 137 |
| Qy | 759 | TTCCCACTCTTCAATGTTTAAACAAGCTGCTTCTGGAACCTTGAAGCCAGGTTGACTGT | 818 |
| Db | 136 | TTCCCACTCTTCAATGTTTAAACAAGCTGCTTCTGGAACCTTGAAGCCAGGTTGACTGT | 77 |
| Qy | 819 | ATTACATGTTGTTAAGAAAATGATTTTAGGTTCTGATGTTCAAGAAATGATTAAT | 878 |
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| QY | 879 | TATACATTTTCCT | 890 |
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| ACCESSION | AA040425 |
| VERSION | AA040425.1 GI:2058967 |
| KEYWORDS | EST. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |

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| TITLE | Generation and analysis of 280,000 human expressed sequence tags |
| JOURNAL | Genome Res. 6 (9), 807-828 (1996) |
| MEDLINE | 97044478 |
| PUBMED | 8889549 |
| COMMENT | Contact: Wilson RK |

FEATURES

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strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAAGTGGGAGCGCGCGGCTTTTTTTTTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTR73 vector
(pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. "

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DEFINITION 5608407J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD632169
VERSION CD632169.1 GI:40280436
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
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QY 455 TCAGCAGAGCCATAGGGAATAGCCCTGATGGATTAATCTTCAAGCTTGTAGCTTCAAGT 514
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QY 515 TCCTTCCCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 574
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DEFINITION 5608407J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD632170
VERSION CD632170.1 GI:40280437
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
source 1..560
/organism="Homo sapiens"
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Query Match 61.1%; Score 544.2; DB 6; Length 560;
Best Local Similarity 99.5%; Pred. No. 3,9e-151;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 335 CTGTGCTTCTCAGATTAAGTGAAGCAATTAAGATTCGTCTTCTTCTGCTGCTGCC 394
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Db 549 CAGTGTGCTTCTCAGATTAAGTGAAGCAATTAAGATTCGTCTTCTTCTGCTGCTGCC 490
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OY 395 TCAGACAGAGAGCCGAGACTCTATCGGCGCACAGGATTAACATCTCTCAGTGAACAGAGT 454
DB 489 TCAGACAGAGAGCCGAGACTCTATCGGCGCACAGGATTAACATCTCTCAGTGAACAGAGT 430
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DB 429 TCAGACAGGCGCTATGGGAAATGCCCTGATGGGATTAATCTCAGCTTGTGAGCTTCTAAGTT 370
OY 515 TCTTTCCCTTCATTCGACCCGCAAGCTTCGTAGAGAAATGCCGAGTTCTAGC 574
DB 369 TCTTTCCCTTCATTCGACCCGCAAGCTTCGTAGAGAAATGCCGAGTTCTAGC 310
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OY 635 GGCACAAACATATACCTTCCATGAAGCACACACAGACTTTGAAAGCAAGACAATGAC 694
DB 249 GGCACAAACATATACCTTCCATGAAGCACACACAGACTTTGAAAGCAAGACAATGAC 190
OY 695 TGCCTGAATTGAGGCGCTTGAGGAATGAGCTTTGAGGAAAGAAATACCTTGTTCAGC 754
DB 189 TGCCTGAATTGAGGCGCTTGAGGAATGAGCTTTGAGGAAAGAAATACCTTGTTCAGC 130
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DB 129 CCCCTTCCCACTCTTCATGTGTCAACACAGCTGCTTCTTGACCTTGAGCCACGCTGA 70
OY 815 CTGATTTACATGTGTTATAGAAAACCTGATTTTGAAGTTCTGATGTTCAAGAGAAATGAT 874
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DB 9 TAAATATAC 1
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Job time : 3464.52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 07:16:54 ; Search time 1873.08 Seconds
(without alignments)
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Title: US-09-763-978B-12

Perfect score: 406
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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1: gb_ba: *
2: gb_btg: *
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4: gb_om: *
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6: gb_pat: *
7: gb_ph: *
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12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 403 | 916 | 9 | BC074729 | BC074729 Homo sapi |
| 3 | 403 | 1065 | 6 | AX375858 | AX375858 Sequence |
| 4 | 403 | 99.3 | 1070 | AY346100 | AY346100 Homo sapi |
| 5 | 403 | 99.3 | 1190 | BC065717 | BC065717 Homo sapi |
| 6 | 403 | 99.3 | 1658 | C0875680 | C0875680 Sequence |
| 7 | 403 | 99.3 | 1658 | AR252569 | AR252569 Sequence |
| 8 | 403 | 99.3 | 1658 | AX092328 | AX092328 Sequence |
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| 10 | 403 | 99.3 | 1658 | AX395215 | AX395215 Sequence |
| 11 | 403 | 99.3 | 1658 | AX403403 | AX403403 Sequence |
| 12 | 403 | 99.3 | 1658 | AX468680 | AX468680 Sequence |
| 13 | 403 | 99.3 | 1658 | AY358352 | AY358352 Homo sapi |
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| 15 | 403 | 99.3 | 2587 | BD235830 | BD235830 A novel m |
| 16 | 403 | 99.3 | 2603 | AX403048 | AX403048 Sequence |
| 17 | 403 | 99.3 | 2626 | AX375860 | AX375860 Sequence |
| 18 | 403 | 99.3 | 2627 | BD265002 | BD265002 Compositi |
| 19 | 403 | 99.3 | 2627 | AR238405 | AR238405 Sequence |

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| 20 | 403 | 99.3 | 2627 | 6 | AR478744 | AR478744 Sequence |
| 21 | 403 | 99.3 | 2627 | 6 | AX156350 | AX156350 Sequence |
| 22 | 403 | 99.3 | 2627 | 6 | AX366624 | AX366624 Sequence |
| 23 | 401.4 | 98.9 | 1811 | 9 | AK026071 | AK026071 Homo sapi |
| 24 | 398.2 | 98.1 | 2671 | 9 | HSM808167 | BX648021 Homo sapi |
| 25 | 384 | 94.6 | 849 | 9 | AY280972 | AY280972 Homo sapi |
| 26 | 344.6 | 84.9 | 94664 | 9 | HSJ1025A1 | AL080312 Human DNA |
| 27 | 296.2 | 73.0 | 1343 | 10 | BC032925 | BC032925 Mus muscu |
| 28 | 289.8 | 71.4 | 1382 | 10 | AY346059 | AY346059 Mus muscu |
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| 30 | 278.8 | 68.7 | 852 | 10 | AY280973 | AY280973 Mus muscu |
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| 33 | 258.4 | 63.6 | 805 | 6 | CO430390 | CO430390 Sequence |
| 34 | 257.4 | 59.2 | 412 | 6 | CO414027 | CO414027 Sequence |
| 35 | 240.4 | 59.2 | 579 | 6 | AX375859 | AX375859 Sequence |
| 36 | 219 | 53.9 | 199673 | 10 | AL669872 | AL669872 Mouse DNA |
| 37 | 215.8 | 53.2 | 218776 | 2 | AC134291 | AC134291 Rattus no |
| 38 | 215.8 | 53.2 | 286029 | 2 | AC110845 | AC110845 Rattus no |
| 39 | 208.4 | 51.3 | 418 | 6 | CO409778 | CO409778 Sequence |
| 40 | 194 | 47.8 | 336 | 6 | AX375856 | AX375856 Sequence |
| 41 | 189.4 | 46.7 | 364 | 6 | CQ397088 | CQ397088 Sequence |
| 42 | 189.4 | 46.7 | 364 | 6 | CO403394 | CO403394 Sequence |
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ALIGNMENTS

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A novel method of diagnosing, monitoring, staging, imaging and treating various cancers.
ACCESSION
BD235841
VERSION
BD235841.1 GI:33045611
KEYWORDS
JP 2002523760-A/12.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 406)
Salceda,S., Sun,Y., Recipon,H. and Cafferkey,R.
A novel method of diagnosing, monitoring, staging, imaging and treating various cancers
JOURNAL
Patent: JP 2002523760-A 12 30-JUL-2002;
DIADEXUS INC

COMMENT
OS Homo sapiens (human)
PN JP 2002523760-A/12
PD 30-JUL-2002
PR 01-SEP-1999 JP 2000567741
PR 02-SEP-1998 US 60/098880

PI SUSANA SALCEDA YONGMING SUN, HERVE RECIPON ROBERT CAFFERKEY PC
G01N33/574,A61K39/395,A61K39/395,A61K39/395 PC
,A61K49/00,A61K49/00,
PC A61K51/00,C07K16/32,C12N15/09,C12Q1/68,C12N15/00,A61K49/02 CC
A novel method of diagnosing, monitoring,
staging, imaging and
treating
CC various cancers
FH Key
FT unsure (30)
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FT unsure (383)
Location/Qualifiers

FEATURES
source
Location/Qualifiers

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 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 CTCAGCCCTTACTGATGCTATANAATATGCTTGGCCCAAAAA 406
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RESULT 2
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 DEFINITION MGCL103801 IMAGE:30915182), complete cds.
 ACCESSION BC074729
 VERSION BC074729.2 GI:50959545
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 916)
 Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheaffer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, J., Wang, J., Heish, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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 Fahy, J., Hellon, E., Kettman, M., Madan, A.C., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A.C., Shevchenko, Y.,
 Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL PUMED 12477932
 TITLE 2 (bases 1 to 916)
 AUTHORS Director MGC Project.
 DIRECTOR Direct Substation
 SUBMITTED (25-JUN-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK
 COMMENT
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 On Aug 4, 2004 this sequence version replaced gi:49901510.
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
 Center
 CDNA Library Preparation: British Columbia Cancer Research Center
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
 Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Amara Maeson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabh, P
 Parvaneh Saeedi, JR Santos, Angeliq Scherch, Ursula Skalska,
 Duane Smalls, Jeff Stott, Miranda Teal, George Yang, Jacque
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNW at: <http://image.llnl.gov>
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ORIGIN
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 Best Local Similarity 99.3%; Pred. No. 2,2e-109;
 Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATTAATGCGAGCTCAGANACCTTCGGGTGAGGCTCCCGATGTTTC 60
 1 GTGAATGTGACTATTAATGCGAGCTCAGANACCTTCGGGTGAGGCTCCCGATGTTTC 60

DB 494 GTGAATGTGACTATTAATGCGAGCTCAGANACCTTCGGGTGAGGCTCCCGATGTTTC 553
 494 GTGAATGTGACTATTAATGCGAGCTCAGANACCTTCGGGTGAGGCTCCCGATGTTTC 553

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 61 CCCGAGCCCAAGTGTCTGGGCGATCCCAAGTTGACCAAGGAGGCAACTTCTCGGAAGTC 120

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 554 CCCGAGCCCAAGTGTCTGGGCGATCCCAAGTTGACCAAGGAGGCAACTTCTCGGAAGTC 613

QY 121 TCCAAATACAGCTTTGAGCTGAAGCTCTGAGATGATGACCATGAGGTTGTGTGCTC 180
 121 TCCAAATACAGCTTTGAGCTGAAGCTCTGAGATGATGACCATGAGGTTGTGTGCTC 180

DB 614 TCCAAATACAGCTTTGAGCTGAAGCTCTGAGATGATGACCATGAGGTTGTGTGCTC 673
 614 TCCAAATACAGCTTTGAGCTGAAGCTCTGAGATGATGACCATGAGGTTGTGTGCTC 673

QY 181 TACAAATGTTACGATCAACAACACATATCTCTGTATGATTAATAATGACATTGCCAAGCA 240
 181 TACAAATGTTACGATCAACAACACATATCTCTGTATGATTAATAATGACATTGCCAAGCA 240

Db 674 TACATTTAGATGATCAACAAACACTACTCCTGTATGATTAATAATGACATTGCCAAAGCA 733
Qy 241 ACAGGGGATATCAAAAGTGAAGAAATCGAGATCAAAAGCGGAGTCACTTACAGCTGCTA 300
Db 734 ACAGGGGATATCAAAAGTGAAGAAATCGAGATCAAAAGCGGAGTCACTTACAGCTGCTA 793
Qy 301 AACCTAAAGGCTTCTGTGTGTCTCTTCTTCTTCCATGACGTGGGACCTTCTGCT 360
Db 794 AACCTAAAGGCTTCTGTGTGTCTCTTCTTCTTCCATGACGTGGGACCTTCTGCT 853
Qy 361 CTCAGCCCTTACCTGATGCTAANATAATGTCCTTGCCCAAAAA 406
Db 854 CTCAGCCCTTACCTGATGCTAANATAATGTCCTTGCCCAAAAA 899

RESULT 3
LOCUS AX375858 1065 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 5 from Patent WO0194641.
ACCESSION AX375858
VERSION AX375858.1 GI:19170330
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Ople, E., McLachlan, K. and Heard, C.
TITLE Gene targets and ligands that bind thereto for treatment and
JOURNAL diagnosis of ovarian carcinomas
Patent: WO 0194641-A 5 13-DEC-2001;
Idex Pharmaceuticals Corporation (US)
FEATURES
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ORIGIN

Query Match 99.3%; Score 403; DB 6; Length 1065;
Best local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 654 TCCAAATACCAAGCTTGAAGTGAATGACATGAAAGTTGTGTCTGTC 713
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Db 834 AACCTAAAGGCTTCTGTGTGTCTCTTCTTCTTCCATGACGTGGGACCTTCTGCT 893
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Db 894 CTCAGCCCTTACCTGATGCTAANATAATGTCCTTGCCCAAAAA 939

RESULT 4
LOCUS AY346100 1070 bp mRNA linear PRI 09-SEP-2003
DEFINITION Homo sapiens T cell costimulatory molecule B7x mRNA, complete cds.
ACCESSION AY346100
VERSION AY346100.1 GI:33638210
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1070)
AUTHORS Zang, X., Locke, P., Kim, J., Murphy, K., Waite, R. and Allison, J.P.
TITLE B7x: A widely expressed B7 family member that inhibits T cell
activation
Proc. Natl. Acad. Sci. U.S.A. 100 (18), 10388-10392 (2003)

JOURNAL MEDLINE
PUBMED 22833980
12920180
2 (bases 1 to 1070)
Zang, X. and Allison, J.P.
Direct Submission
Submitted (19-JUN-2003) Howard Hughes Medical Institute, Department
of Molecular and Cell Biology, Cancer Research Laboratory,
University of California at Berkeley, LS4415, Berkeley, CA 94720,
USA

FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 99.3%; Score 403; DB 9; Length 1070;
Best local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGAATGTGACTATTAATGCGCAAGCTTCAGANACCTTGGGTGTGAGGCTCCCGATGGTTC 60
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RESULT 5
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DEFINITION BC065717 1190 bp mRNA linear PRI 03-FEB-2004
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MGC:71941 IMAGE:4295775), complete cds.
ACCESSION BC065717
VERSION BC065717.1 GI:41350861
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1190)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schlier, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapelton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Utsdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulys, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shcherchenko, Y.,
Boutfair, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.B.,
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL PubMed 12477932
REFERENCE 2 (bases 1 to 1190)
AUTHORS Straussberg, R.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@gscc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao,
Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Telia Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabh, P
Paraneh Saeedi, JR Santos, Angeliqne Scherch, Ursula Skalska,
Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
Series: IRAL Plate: 51 Row: f Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13375849.
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1. 1190

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500. 871
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This family consists of several mammalian T-cell surface
antigen CD2 proteins as well as homologous African swine
fever virus sequences. CD2 mediates T cell adhesion via
its ectodomain and signal transduction utilising its
117-amino acid cytoplasmic tail. The structural and
functional similarities of the African swine fever virus
(ASFV) LMWH-DR to CD2, a protein that is involved in
cell-cell adhesion and immune response modulation, suggest
a possible role in the pathogenesis of ASFV infection"
/db_xref="CDD:pfam05790"

misc_feature
Query Match 99.3%; Score 403; DB 9; Length 1190;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 629 GTGAATGGAGTAAATTAATGCGAGCTCAGANACCTTGGGGTGGAGCCCGGATGCTC 688
QY 61 CCCGAGCCCAAGTGGTGGGATCCCAAGTTGACGAGGAGGCCAAGCTTCGGAAGTTC 120
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QY 121 TCCAAATACCAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 180
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QY 181 TCAATGTTACAGTAAACAACAATCAATCTGTATGATTTGAAATGACATTTGCCAACA 240
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QY 241 ACAGGGATATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
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QY 361 CTCAGCCCTTACCTGATGCTAATATATGCTTGGCCACAAAA 406
Db 989 CTCAGCCCTTACCTGATGCTAATATATGCTTGGCCACAAAA 1034

RESULT 6
CO875680
LOCUS CO875680 1658 bp DNA linear PAT 27-SEP-2004
DEFINITION Sequence 3 from Patent EP145317.
ACCESSION CO875680
VERSION CO875680.1 GI:52748533
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Goddard, A., Godowski, P. J., Gurney, A. L., Hillan, K. J., Polakis, P., Smith, V., Wood, W. I., Wu, T. D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: EP 145317-A 3 11-AUG-2004;
Genentech Inc. (US)
FEATURES
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Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 61 CCCAGGCCACAGTGTGCTGGGCACTCCCAATTTGACCGAGGAGCACTTTCGGAAGTC 120
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DB 883 CTCAGCCCTTACCTGATGCTAANAATAATGTCCTTGGCCACAAAAA 928
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LOCUS AR252569 1658 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 290 from patent US 6478825.
ACCESSION AR252569
VERSION AR252569.1 GI:27300477
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1658)
TITLE Unclassified.
AUTHORS Winterbottom, J. M., Shimp, L., Boyce, T. M. and Kees, D.
JOURNAL Patent: US 6478825-A 290 12-NOV-2002;
FEATURES location/Qualifiers

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ORIGIN
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Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 523 GTGAATGTGACTATTAATGCGAGCTCAGAGACCTTGGGTGTGAGGCTCCCGATGGTTC 582
QY 61 CCCAGGCCACAGTGTGCTGGGCACTCCCAATTTGACCGAGGAGCACTTTCGGAAGTC 120
DB 583 CCCAGGCCACAGTGTGCTGGGCACTCCCAATTTGACCGAGGAGCACTTTCGGAAGTC 642
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DB 763 ACAGGGGATATCAAAAGTACAGAAATCGAGATCAAAAAGGCGAGTCACTTACAGCTGTA 822
QY 301 AACTCAAAAGGCTTCTGTGTGTCTCTTTCTTTGCAATCAGCTGGGCACTTCTGCT 360
DB 823 AACTCAAAAGGCTTCTGTGTGTCTCTTTCTTTGCAATCAGCTGGGCACTTCTGCT 882
QY 361 CTCAGCCCTTACCTGATGCTAANAATAATGTCCTTGGCCACAAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAANAATAATGTCCTTGGCCACAAAAA 928
RESULT 8
AX092328
LOCUS AX092328 1658 bp DNA linear PAT 23-MAR-2001
DEFINITION Sequence 59 from Patent WO0116318.
ACCESSION AX092328
VERSION AX092328.1 GI:13444478
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eaton, D. L., Filvaroff, E., Gerritsen, M. E., Goddard, A., Godowski, P. J., Grimaldi, C. J., Gurney, A. L., Watanabe, C. K. and Wood, W. I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0116318-A 59 08-MAR-2001;
Genentech, Inc. (US)
FEATURES location/Qualifiers
1..1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 99.3%; Score 403; DB 6; Length 1658;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGAATGTGACTATTAATGCGAGCTCAGANACCTTGGGTGTGAGGCTCCCGATGGTTC 60
DB 523 GTGAATGTGACTATTAATGCGAGCTCAGAGACCTTGGGTGTGAGGCTCCCGATGGTTC 582
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Db CCCACCCCAAGTGTCTGGGCATCCCAAGTTGACACAGGAGCCAACTTCTCGAAGTC 642
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LOCUS Sequence 217 from Patent WO0168848.
DEFINITION AX376150
ACCESSION AX376150
VERSION AX376150.1 GI:19170467
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.

TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: WO 0168848-A 217 20-SEP-2001;
Genentech, Inc. (US)

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1. 1658
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ORIGIN

Query Match 99.3%; Score 403; DB 6; Length 1658;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATATATATGCTGACCTCAGANACCTTGCCTGTGAGGCTCCCGATGTTTC 60
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QY 241 ACAGGGGNTATCAAAAGTACAGAAATGAGATCAAAAAGCGAGTCACTACAGCTGCTA 300
Db 763 ACAGGGGNTATCAAAAGTACAGAAATGAGATCAAAAAGCGAGTCACTACAGCTGCTA 822

QY 301 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTTGGCCATCACTGGGCACTTGCGCT 360
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QY 361 CTCAGCCCTTACTGATGCTAANAATATGTGCTTGGCCACAAAAA 406
Db 883 CTCAGCCCTTACTGATGCTAANAATATGTGCTTGGCCACAAAAA 928

RESULT 10
AX395215 1658 bp DNA linear PAT 18-MAY-2002
LOCUS Sequence 3 from Patent WO0216429.
DEFINITION AX395215
ACCESSION AX395215
VERSION AX395215.1 GI:21066246
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,
Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
Compositions and methods for the diagnosis and treatment of tumor
Patent: WO 0216429-A 3 28-FEB-2002;
Genentech, Inc. (US)

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1. 1658
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Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 883 CTCAGCCCTTACTGATGCTAANAATATGTGCTTGGCCACAAAAA 928

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AX403403 1658 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 290 from Patent WO0073454.
DEFINITION AX403403
ACCESSION AX403403
VERSION AX403403.1 GI:21436923

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS 1 Aghkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D., Ferrara, N., Gerber, H., Gertsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napiet, M.A., Pan, J., Proulx, N.F., Roy, M., Stewart, T.A., Thomas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.
TITLE The secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0073454-A 290 07-DEC-2000;
Genentech Inc. (US)
FEATURES
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Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 643 TCCAAATACAGCTTTGAGTGAAGTCAATGATGACATGAAGTGTGTCTGTCTC 702
QY 181 TACAAATGTTACGATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 240
DB 703 TACAAATGTTACGATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 762
QY 241 ACAGGGGATATCAAAGTGAAGATCGAGATCAAAAGGCGAGTCACTACAGTCTCTA 300
DB 763 ACAGGGGATATCAAAGTGAAGATCGAGATCAAAAGGCGAGTCACTACAGTCTCTA 822
QY 301 AACTCAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAAGCTGGGCACTTCTGCTT 360
DB 823 AACTCAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAAGCTGGGCACTTCTGCTT 882
QY 361 CTCAGCCCTTACCTGATGCTAATTAATATGTCCTTGGCCCAAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAATTAATATGTCCTTGGCCCAAAAA 928
RESULT 12
AX468680 1658 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 4 from Patent WO0216581.
DEFINITION AX468680
ACCESSION AX468680.1 GI:21901458
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS 1 Gao, W.Q., Polakis, P., Shou, J., Smith, V., Soriano, R., Williams, P.M., Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216581-A 4 28-FEB-2002;
Genentech, Inc. (US)
FEATURES
Source Location/Qualifiers

source 1.1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGAATGTGACATTAATGCGAGTCAAGAACCTTGGGGTGTGAGGCTCCCGATGTTT 60
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QY 181 TACAAATGTTACGATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 240
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QY 241 ACAGGGGATATCAAAGTGAAGATCGAGATCAAAAGGCGAGTCACTACAGTCTCTA 300
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QY 301 AACTCAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAAGCTGGGCACTTCTGCTT 360
DB 823 AACTCAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAAGCTGGGCACTTCTGCTT 882
QY 361 CTCAGCCCTTACCTGATGCTAATTAATATGTCCTTGGCCCAAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAATTAATATGTCCTTGGCCCAAAAA 928
RESULT 13
AY358352 1658 bp mRNA linear PRI 03-OCT-2003
LOCUS Homo sapiens clone DNA59610 B7h.5 (UNG659) mRNA, complete cds.
DEFINITION AY358352
ACCESSION AY358352
VERSION AY358352.1 GI:37181828
KEYWORDS
SOURCE FLI_CDNA.
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS 1 Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Denel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Sehnagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.
TITLE The Secreted Protein Discovery Initiative (SPDI): a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
JOURNAL A Bioinformatics Assessment
PUBMED Genome Res. 13 (10), 2265-2270 (2003)
REFERENCE 2 (bases 1 to 1658)
AUTHORS Clark, H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
Source Location/Qualifiers
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Query Match      99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATTAATGCGACCTGAGANACCTTCGGGTGTGAGGCTCCCGATGTTTC 60
DB 523 GTGAATGTGACTATTAATGCGACCTGAGANACCTTCGGGTGTGAGGCTCCCGATGTTTC 582
QY 61 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACAGGAGGCCAACTTCTCGAAGTC 120
DB 583 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACAGGAGGCCAACTTCTCGAAGTC 642
QY 121 TCCAAATACAGCTTTGAGTGAATCTGAGAAATGTGACCAATGAAGTTGTCTGTGCTC 180
DB 643 TCCAAATACAGCTTTGAGTGAATCTGAGAAATGTGACCAATGAAGTTGTCTGTGCTC 702
QY 181 TACAATGTTACGATCAACAACACATACCTCTGTATGATTGAANAATGACATTGCCAAGA 240
DB 703 TACAATGTTACGATCAACAACACATACCTCTGTATGATTGAANAATGACATTGCCAAGA 762
QY 241 ACAAGGGATNTCAAATGACAGAAATGGAGATCAAAAAGCGAGTCACTTACAGCTGCTA 300
DB 763 ACAAGGGATNTCAAATGACAGAAATGGAGATCAAAAAGCGAGTCACTTACAGCTGCTA 822
QY 301 AACTCAAGGCTTCTGTGTGTCTCTCTCTTTCTTTGCCATCAGCTGACATTTGACCT 360
DB 823 AACTCAAGGCTTCTGTGTGTCTCTCTCTTTCTTTGCCATCAGCTGACATTTGACCT 882
QY 361 CTCAGCCCTTACCTGATGTCTAANATATGTGCTTGGCCACAAAA 406
DB 883 CTCAGCCCTTACCTGATGTCTAANATATGTGCTTGGCCACAAAA 928

RESULT 14
CO412191      1965 bp      DNA      linear      PAT 23-JUN-2004
LOCUS      CO412191
DEFINITION      Sequence 19262 from Patent WO0170979.
ACCESSION      CO412191
VERSION      CO412191.1 GI:41319972
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 Lee, J. and Lillie, J.
  Genes, compositions, kits, and method for identification,
  assessment, prevention, and therapy of ovarian cancer
  Patent: WO 0170979-A 19262 27-SEP-2001;
  Millennium Pharmaceuticals, Inc. (US)
FEATURES
source      Location/Qualifiers
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ORIGIN
Query Match      99.3%; Score 403; DB 6; Length 1965;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 602 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACAGGAGGCCAACTTCTCGAAGTC 661
QY 121 TCCAAATACAGCTTTGAGTGAATCTGAGAAATGTGACCAATGAAGTTGTCTGTGCTC 180
DB 662 TCCAAATACAGCTTTGAGTGAATCTGAGAAATGTGACCAATGAAGTTGTCTGTGCTC 721
QY 181 TACAATGTTACGATCAACAACACATACCTCTGTATGATTGAANAATGACATTGCCAAGA 240
DB 722 TACAATGTTACGATCAACAACACATACCTCTGTATGATTGAANAATGACATTGCCAAGA 781
QY 241 ACAAGGGATNTCAAATGACAGAAATGGAGATCAAAAAGCGAGTCACTTACAGCTGCTA 300
DB 782 ACAAGGGATNTCAAATGACAGAAATGGAGATCAAAAAGCGAGTCACTTACAGCTGCTA 841
QY 301 AACTCAAGGCTTCTGTGTGTCTCTCTCTTTCTTTGCCATCAGCTGAGCACTTGCTC 360
DB 842 AACTCAAGGCTTCTGTGTGTCTCTCTCTTTCTTTGCCATCAGCTGAGCACTTGCTC 901
QY 361 CTCAGCCCTTACCTGATGTCTAANATATGTGCTTGGCCACAAAA 406
DB 902 CTCAGCCCTTACCTGATGTCTAANATATGTGCTTGGCCACAAAA 947

RESULT 15
BD235830      2587 bp      DNA      linear      PAT 17-JUL-2003
LOCUS      BD235830
DEFINITION      A novel method of diagnosing, monitoring, staging, imaging and
ACCESSION      BD235830.1 GI:33045600
VERSION      JP 2002523760-A/1.
KEYWORDS      A novel method of diagnosing, monitoring, staging, imaging and
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 (bases 1 to 2587)
Salceda, S., Sun, Y., Recipon, H. and Cafferty, R.
A novel method of diagnosing, monitoring, staging, imaging and
treating various cancers
Patent: JP 2002523760-A 1 30-JUL-2002;
JOURNAL
DIADEXUS INC
OS      Homo sapiens (human)
PN      JP 2002523760-A/1
PD      30-JUL-2002
PR      02-SEP-1999 JP 2000567741
PF      02-SEP-1998 US 60/098880
PI      SUSANA SALCEDA, YONGMING SUN, HERVE RECIPON, ROBERT CAFFERTY PC
GOINJ3/574,A6IK39/395,A6IK39/395,A6IK39/395,A6IK39/395 PC
PC      A6IK51/00,C07K16/32,C12N15/09,C12Q1/68,C12N15/00,A6IK49/02 CC
A novel method of diagnosing, monitoring,
staging, imaging and
treating
CC      various cancers
CC      Key
FT      source      Location/Qualifiers
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FEATURES
source      Location/Qualifiers
            1..2587
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

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Query Match      99.3%; Score 403; DB 6; Length 2587;
Best Local Similarity 99.3%; Pred. No. 2.1e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTTAATGCGCAAGCTTGGGGTGTGAGGCTCCCGATGTTTC 60
Db 524 GTGAATGTGACTTAATGCGCAAGCTTGGGGTGTGAGGCTCCCGATGTTTC 583
QY 61 CCCAGGCCACAGTGTGTGGGCAATCCCAAGTTGACCAAGGAGCCACTTCTGGAAAGTC 120
Db 584 CCCAGGCCACAGTGTGTGGGCAATCCCAAGTTGACCAAGGAGCCACTTCTGGAAAGTC 643
QY 121 TCGAATACCAAGCTTTGAGCTGAACCTGAGAAATGTGACCAATGAAGTTGTGTCTGTCTC 180
Db 644 TCGAATACCAAGCTTTGAGCTGAACCTGAGAAATGTGACCAATGAAGTTGTGTCTGTCTC 703
QY 181 TACAAATGTTCGATCAACCAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 240
Db 704 TACAAATGTTCGATCAACCAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 763
QY 241 ACAGGGGATTCAAAGTGACAGAAATGGAGATCAAAAGGCGAGTCACTACAGCTGTCTA 300
Db 764 ACAGGGGATTCAAAGTGACAGAAATGGAGATCAAAAGGCGAGTCACTACAGCTGTCTA 823
QY 301 AACTCAAAGGCTTCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 824 AACTCAAAGGCTTCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 883
QY 361 CTCAGCCCTTACCTGATGCTTAATATATGTCCTTGCCCAAAAA 406
Db 884 CTCAGCCCTTACCTGATGCTTAATATATGTCCTTGCCCAAAAA 929
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Job time : 1875.08 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 05:15:03 ; Search time 249.008 Seconds
(without alignments)
9651.969 Million cell updates/sec

Title: US-09-763-978B-12

Perfect score: 406
Sequence: 1 gtcgactgtgacataatgc.....atgtgcttgcgcacacaaa 406

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 403 | 99.3 | 406 | 3 | AAZ90481 |
| 2 | 403 | 99.3 | 1046 | 6 | ABZ11450 |
| 3 | 403 | 99.3 | 1046 | 12 | ADMA3968 |
| 4 | 403 | 99.3 | 1065 | 6 | ABL56580 |
| 5 | 403 | 99.3 | 1657 | 3 | AAZ65059 |
| 6 | 403 | 99.3 | 1657 | 10 | ADB90935 |
| 7 | 403 | 99.3 | 1658 | 4 | AA546033 |
| 8 | 403 | 99.3 | 1658 | 4 | AAF92087 |
| 9 | 403 | 99.3 | 1658 | 5 | AAF44205 |
| 10 | 403 | 99.3 | 1658 | 6 | ABK11744 |
| 11 | 403 | 99.3 | 1658 | 6 | AB574407 |
| 12 | 403 | 99.3 | 1658 | 6 | ABK11091 |
| 13 | 403 | 99.3 | 1658 | 8 | ACA89483 |
| 14 | 403 | 99.3 | 1658 | 8 | ACA73493 |
| 15 | 403 | 99.3 | 1658 | 8 | ACA05808 |
| 16 | 403 | 99.3 | 1658 | 8 | ACA66642 |
| 17 | 403 | 99.3 | 1658 | 8 | ACA64352 |
| 18 | 403 | 99.3 | 1658 | 8 | ACA91193 |
| 19 | 403 | 99.3 | 1658 | 8 | ACD81570 |
| 20 | 403 | 99.3 | 1658 | 8 | ACF20217 |

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| 22 | 403 | 99.3 | 1658 | 8 | ACD21891 |
| 23 | 403 | 99.3 | 1658 | 8 | ACF13056 |
| 24 | 403 | 99.3 | 1658 | 8 | ACD25159 |
| 25 | 403 | 99.3 | 1658 | 8 | ACF00208 |
| 26 | 403 | 99.3 | 1658 | 8 | ACA60392 |
| 27 | 403 | 99.3 | 1658 | 8 | ACA72265 |
| 28 | 403 | 99.3 | 1658 | 8 | ACD04789 |
| 29 | 403 | 99.3 | 1658 | 8 | ACD18250 |
| 30 | 403 | 99.3 | 1658 | 8 | ACD08257 |
| 31 | 403 | 99.3 | 1658 | 8 | ACA88691 |
| 32 | 403 | 99.3 | 1658 | 8 | ACA70133 |
| 33 | 403 | 99.3 | 1658 | 8 | ACD12355 |
| 34 | 403 | 99.3 | 1658 | 8 | ACG74270 |
| 35 | 403 | 99.3 | 1658 | 8 | ACD15898 |
| 36 | 403 | 99.3 | 1658 | 8 | ACD25466 |
| 37 | 403 | 99.3 | 1658 | 8 | ACD17943 |
| 38 | 403 | 99.3 | 1658 | 8 | ACC88230 |
| 39 | 403 | 99.3 | 1658 | 8 | ACD21584 |
| 40 | 403 | 99.3 | 1658 | 8 | ACD18651 |
| 41 | 403 | 99.3 | 1658 | 8 | ACA58839 |
| 42 | 403 | 99.3 | 1658 | 8 | ABX98261 |
| 43 | 403 | 99.3 | 1658 | 8 | ACD14012 |
| 44 | 403 | 99.3 | 1658 | 8 | ACD09792 |
| 45 | 403 | 99.3 | 1658 | 8 | ACC88537 |

ALIGNMENTS

RESULT 1
AAZ90481
ID AAZ90481 standard; cDNA; 406 BP.
XX
AC AAZ90481;
DT 06-JUN-2000 (first entry)
DB
XX "Cancer specific gene (clone ID 16656542) fragment #12.
--XX
KW CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
KW endometrial; uterine; lung; cytotoxic; ss.
XX
OS Homo sapiens.
XX
FN W0200012758-A1.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WC-US019655.
XX
PR 02-SEP-1998; 98US-0098860P.
XX
PA (DIAD-) DIADEXUS LLC.
XX
PI Salceda S, Sun Y, Recipon H, Cafferty R;
XX
DR WPI; 2000-256657/22.
XX
PT Diagnosing, staging, monitoring, imaging and treating cancer especially
PT gynecological cancers e.g. breast, ovarian cancer and lung cancer.
PT involves measuring cancer specific gene levels in cells and body fluids.
XX
PS Claim 9; Page 51-52; 58pp; English.
XX
CC The invention relates to detecting, diagnosing metastasis and staging
CC cancer by measuring levels of cancer specific genes (CSG) in cells,
CC tissues or body fluids. Their remission and progression, decreases and
CC increases in CSG levels, is also monitored, by periodic sample analysis.
CC The methods are useful for detecting cancers, especially gynecologic
CC cancers which include ovarian, breast, endometrial and uterine cancer and
CC lung cancer. Antibodies against the CSGs labeled with paramagnetic ions
CC or a radioisotope is useful for imaging cancer and when conjugated with a

CC cytotoxic agent are useful for treating cancer. The present sequence
 CC represents a CSG (clone ID: 16656542 and gene ID: 234617) fragment
 XX
 SQ Sequence 406 BP; 106 A; 104 C; 92 G; 101 T; 0 U; 3 Other;

Query Match 99.3%; Score 403; DB 3; Length 406;
 Best Local Similarity 100.0%; Pred. No. 2.5e-121;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGAATGTGACATTAATATGCGAGCTGAGANACCTTGCGGTGAGGCTCCCGATGCTTC 60
 DB 1 GTGAATGTGACATTAATATGCGAGCTGAGANACCTTGCGGTGAGGCTCCCGATGCTTC 60
 QY 61 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACCCAGGAGCCCACTTCTCGAAGTC 120
 DB 61 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACCCAGGAGCCCACTTCTCGAAGTC 120
 QY 121 TCCAAATACCAAGCTTTGAGCTGAACTGTGAATGTGACCAATGAGTTGTCTGTCTC 180
 DB 121 TCCAAATACCAAGCTTTGAGCTGAACTGTGAATGTGACCAATGAGTTGTCTGTCTC 180
 QY 181 TCAATGTATGACATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 240
 DB 181 TCAATGTATGACATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 240
 QY 241 ACAGGGGNTATCAAAAGTGAAGATCGAGATCAAAAAGGCGAGTCACTACAGCTGCTA 300
 DB 241 ACAGGGGNTATCAAAAGTGAAGATCGAGATCAAAAAGGCGAGTCACTACAGCTGCTA 300
 QY 301 AACTCAAAAGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCTC 360
 DB 301 AACTCAAAAGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCTC 360
 QY 361 CTCAGCCCTTACCTGATGCTAANATATGATGCTTGGCCACAAAAA 406
 DB 361 CTCAGCCCTTACCTGATGCTAANATATGATGCTTGGCCACAAAAA 406

RESULT 2
 AB211450
 ID AB211450 standard; cDNA; 1046 BP.
 XX
 AC AB211450;
 XX
 DT 20-JUN-2003 (first entry)
 XX

DE Human polynucleotide SEQ ID NO 332.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; neurotopic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vlnnerary; fungicide; antibacterial; vlnnuide; protozoacide;
 KW antiarthritic; gene; ss.

OS Homo sapiens.
 XX
 PN WO200270539-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 05-MAR-2002; 2002WO-US005095.
 XX
 PR 05-MAR-2001; 2001US-00799451.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX

DR WPI; 2002-759812/82.
 DR P-PsDB; ABP69233.
 XX

PT New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX
 PS Claim 1; SEQ ID NO 332; 1012bp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (1) comprising a
 CC nucleotide sequence selected from any of 948 sequences (AB211119-
 CC AB212066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from Wipo at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1046 BP; 306 A; 223 C; 250 G; 267 T; 0 U; 0 Other;

Query Match 99.3%; Score 403; DB 6; Length 1046;
 Best Local Similarity 99.3%; Pred. No. 4e-121;
 Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACATTAATATGCGAGCTGAGANACCTTGCGGTGAGGCTCCCGATGCTTC 60
 DB 505 GTGAATGTGACATTAATATGCGAGCTGAGANACCTTGCGGTGAGGCTCCCGATGCTTC 564
 QY 61 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCCCACTTCTCGAAGTC 120
 DB 565 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCCCACTTCTCGAAGTC 624
 QY 121 TCCAAATACCAAGCTTTGAGCTGAACTGTGAATGTGACCAATGAGTTGTCTGTCTC 180
 DB 625 TCCAAATACCAAGCTTTGAGCTGAACTGTGAATGTGACCAATGAGTTGTCTGTCTC 684
 QY 181 TCAATGTATGACATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 240
 DB 685 TCAATGTATGACATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 744
 QY 241 ACAGGGGNTATCAAAAGTGAAGATCGAGATCAAAAAGGCGAGTCACTACAGCTGCTA 300
 DB 745 ACAGGGGNTATCAAAAGTGAAGATCGAGATCAAAAAGGCGAGTCACTACAGCTGCTA 804
 QY 301 AACTCAAAAGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCTC 360
 DB 805 AACTCAAAAGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCTC 864
 QY 361 CTCAGCCCTTACCTGATGCTAANATATGATGCTTGGCCACAAAAA 406
 DB 865 CTCAGCCCTTACCTGATGCTAANATATGATGCTTGGCCACAAAAA 910

RESULT 3
 ADM43968
 ID ADM43968 standard; cDNA; 1046 BP.
 XX
 AC ADM43968;
 XX
 DT 03-JUN-2004 (first entry)
 XX

DE Novel human arginine-rich protein cDNA #332.

XX ss; gene; human; arginine-rich protein; cancer; inflammation;
 KW

KM genetic disorder.
 XX Homo sapiens.
 OS US2004053250-A1.
 XX
 XX 18-MAR-2004.
 PD
 XX 21-NOV-2002; 2002US-00302172.
 PF
 XX 05-MAR-2001; 2001US-00799451.
 PR 05-MAR-2002; 2002MO-US005095.
 PR 20-AUG-2002; 2002US-00225251.
 XX
 XX (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRMA/) DRMANAC R T.
 XX
 PI Tang YT, Xue A, Drmanac RT;
 XX
 DR WPI; 2004-238579/22.
 XX
 XX New isolated arginine-rich protein-like polynucleotides and polypeptides,
 PT useful for diagnosing and/or treating conditions associated with aberrant
 PT activity of the arginine-rich polypeptides, such as cancer and
 PT inflammation.
 XX
 XX Disclosure, SEQ ID NO 332; sipp; English.
 PS
 XX The invention relates to an isolated polynucleotide. The methods and
 CC compositions of the present invention are useful for the diagnosis and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the arginine-rich protein-like polypeptides, such as
 CC cancer and inflammation. They can also be used in forensics, gene
 CC mapping, identification of mutations responsible for genetic disorders,
 CC and in assessing biodiversity. The present sequence represents a novel
 CC human arginine-rich protein cDNA.
 XX
 XX Sequence 1046 BP; 306 A; 223 C; 250 G; 267 T; 0 U; 0 Other;
 SQ
 Query Match 99.3%; Score 403; DB 12; Length 1046;
 Best Local Similarity 99.3%; Pred. No. 4e-121;
 Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTGAATGTGACTATTAATGCCAGCTCAGANACCTTGGGTGTGAGCTCCCGATGTTTC 60
 DB 505 GTGAATGTGACTATTAATGCCAGCTCAGAGACCTTGGGTGTGAGCTCCCGATGTTTC 564
 QY 61 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACCGAGGAGCACTTCTGGGAAGTC 120
 DB 565 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACCGAGGAGCACTTCTGGGAAGTC 624
 QY 121 TCCAAATACAGCTTTGAGTGAACCTCTGAGAAATGTGACCATGAAGTTGTGTCTGTC 180
 DB 625 TCCAAATACAGCTTTGAGTGAACCTCTGAGAAATGTGACCATGAAGTTGTGTCTGTC 684
 QY 181 TACAATGTTACGATCAACAACACATCTCTGTATGATTTGAAATGACATTGCCAAGCA 240
 DB 685 TACAATGTTACGATCAACAACACATCTCTGTATGATTTGAAATGACATTGCCAAGCA 744
 QY 241 ACAGGGGATATCAAGTGAAGAGATGGAGATCAAAAGGGGAGTCACTTACAGCTGCTA 300
 DB 745 ACAGGGGATATCAAGTGAAGAGATGGAGATCAAAAGGGGAGTCACTTACAGCTGCTA 804
 QY 301 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTCTTTGGCATCAAGCTGGGAGCACTTGTGCT 360
 DB 805 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTCTTTGGCATCAAGCTGGGAGCACTTGTGCT 864
 QY 361 CTGAGCCCTTACCTGATGCTAANAATATATGTCCTTGGCCCAAAAA 406
 DB 865 CTGAGCCCTTACCTGATGCTAANAATATATGTCCTTGGCCCAAAAA 910

RESULT 4
 ABL56580
 ID ABL56580 standard; cDNA; 1065 BP.
 XX
 XX ABL56580;
 AC
 XX 30-JUL-2002 (first entry)
 DT
 XX
 XX Nucleotide sequence of expressed sequence tag (EST) A1799522.
 DE
 XX Human; gene A; ovarian tumour; gene B; OREO; ovarian cancer;
 KM expressed sequence tag; EST; A1799522; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200194641-A2.
 PN
 XX 13-DEC-2001.
 PD
 XX 11-JUN-2001; 2001MO-US018700.
 PF
 XX 09-JUN-2000; 2000US-0210451P.
 PR
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX Ople B, McIachlan K, Heard C;
 PI
 XX WPI; 2002-404365/43.
 DR
 XX
 XX New polynucleotide and corresponding antigens from human ovarian cancer
 PT cells, useful for treatment and diagnosis of ovarian cancer.
 PT
 XX
 XX Example 4; Fig 4c; 71pp; English.
 PS
 XX The present sequence represents expressed sequence tag (EST) A1799522.
 CC This EST was identified as a match to the novel gene B by database
 CC analysis. Gene B was identified by representational difference analysis
 CC (RDA) screening, and is selectively expressed by certain human ovarian
 CC tumours. The specification also describes gene A, identified by the same
 CC method. Gene B is named OREO (Ople RDA of Epithelial Tissue vs. Ovary
 CC tumour). Gene A and B polynucleotides are useful for detecting ovarian
 CC cancer. Their polypeptides are useful for treating ovarian cancer
 CC
 XX
 XX Sequence 1065 BP; 293 A; 252 C; 257 G; 263 T; 0 U; 0 Other;
 SQ
 Query Match 99.3%; Score 403; DB 6; Length 1065;
 Best Local Similarity 99.3%; Pred. No. 4.1e-121;
 Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTGAATGTGACTATTAATGCCAGCTCAGANACCTTGGGTGTGAGCTCCCGATGTTTC 60
 DB 534 GTGAATGTGACTATTAATGCCAGCTCAGAGACCTTGGGTGTGAGCTCCCGATGTTTC 593
 QY 61 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACCGAGGAGCACTTCTGGGAAGTC 120
 DB 594 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACCGAGGAGCACTTCTGGGAAGTC 653
 QY 121 TCCAAATACAGCTTTGAGTGAACCTCTGAGAAATGTGACCATGAAGTTGTGTCTGTC 180
 DB 654 TCCAAATACAGCTTTGAGTGAACCTCTGAGAAATGTGACCATGAAGTTGTGTCTGTC 713
 QY 181 TACAATGTTACGATCAACAACACATCTCTGTATGATTTGAAATGACATTGCCAAGCA 240
 DB 714 TACAATGTTACGATCAACAACACATCTCTGTATGATTTGAAATGACATTGCCAAGCA 773
 QY 241 ACAGGGGATATCAAGTGAAGAGATGGAGATCAAAAGGGGAGTCACTTACAGCTGCTA 300
 DB 774 ACAGGGGATATCAAGTGAAGAGATGGAGATCAAAAGGGGAGTCACTTACAGCTGCTA 833
 QY 301 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTCTTTGGCATCAAGCTGGGAGCACTTGTGCT 360
 DB 834 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTCTTTGGCATCAAGCTGGGAGCACTTGTGCT 893

| Chr | Start (kb) | End (kb) | Gene | Transcript | Accession | Length (bp) | GC Content (%) | GC Skew | GC Bias | GC Bias2 | GC Bias3 | GC Bias4 | GC Bias5 | GC Bias6 | GC Bias7 | GC Bias8 | GC Bias9 | GC Bias10 | GC Bias11 | GC Bias12 | GC Bias13 | GC Bias14 | GC Bias15 | GC Bias16 | GC Bias17 | GC Bias18 | GC Bias19 | GC Bias20 | GC Bias21 | GC Bias22 | GC Bias23 | GC Bias24 | GC Bias25 | GC Bias26 | GC Bias27 | GC Bias28 | GC Bias29 | GC Bias30 | GC Bias31 | GC Bias32 | GC Bias33 | GC Bias34 | GC Bias35 | GC Bias36 | GC Bias37 | GC Bias38 | GC Bias39 | GC Bias40 | GC Bias41 | GC Bias42 | GC Bias43 | GC Bias44 | GC Bias45 | GC Bias46 | GC Bias47 | GC Bias48 | GC Bias49 | GC Bias50 | GC Bias51 | GC Bias52 | GC Bias53 | GC Bias54 | GC Bias55 | GC Bias56 | GC Bias57 | GC Bias58 | GC Bias59 | GC Bias60 | GC Bias61 | GC Bias62 | GC Bias63 | GC Bias64 | GC Bias65 | GC Bias66 | GC Bias67 | GC Bias68 | GC Bias69 | GC Bias70 | GC Bias71 | GC Bias72 | GC Bias73 | GC Bias74 | GC Bias75 | GC Bias76 | GC Bias77 | GC Bias78 | GC Bias79 | GC Bias80 | GC Bias81 | GC Bias82 | GC Bias83 | GC Bias84 | GC Bias85 | GC Bias86 | GC Bias87 | GC Bias88 | GC Bias89 | GC Bias90 | GC Bias91 | GC Bias92 | GC Bias93 | GC Bias94 | GC Bias95 | GC Bias96 | GC Bias97 | GC Bias98 | GC Bias99 | GC Bias100 | GC Bias101 | GC Bias102 | GC Bias103 | GC Bias104 | GC Bias105 | GC Bias106 | GC Bias107 | GC Bias108 | GC Bias109 | GC Bias110 | GC Bias111 | GC Bias112 | GC Bias113 | GC Bias114 | GC Bias115 | GC Bias116 | GC Bias117 | GC Bias118 | GC Bias119 | GC Bias120 | GC Bias121 | GC Bias122 | GC Bias123 | GC Bias124 | GC Bias125 | GC Bias126 | GC Bias127 | GC Bias128 | GC Bias129 | GC Bias130 | GC Bias131 | GC Bias132 | GC Bias133 | GC Bias134 | GC Bias135 | GC Bias136 | GC Bias137 | GC Bias138 | GC Bias139 | GC Bias140 | GC Bias141 | GC Bias142 | GC Bias143 | GC Bias144 | GC Bias145 | GC Bias146 | GC Bias147 | GC Bias148 | GC Bias149 | GC Bias150 | GC Bias151 | GC Bias152 | GC Bias153 | GC Bias154 | GC Bias155 | GC Bias156 | GC Bias157 | GC Bias158 | GC Bias159 | GC Bias160 | GC Bias161 | GC Bias162 | GC Bias163 | GC Bias164 | GC Bias165 | GC Bias166 | GC Bias167 | GC Bias168 | GC Bias169 | GC Bias170 | GC Bias171 | GC Bias172 | GC Bias173 | GC Bias174 | GC Bias175 | GC Bias176 | GC Bias177 | GC Bias178 | GC Bias179 | GC Bias180 | GC Bias181 | GC Bias182 | GC Bias183 | GC Bias184 | GC Bias185 | GC Bias186 | GC Bias187 | GC Bias188 | GC Bias189 | GC Bias190 | GC Bias191 | GC Bias192 | GC Bias193 | GC Bias194 | GC Bias195 | GC Bias196 | GC Bias197 | GC Bias198 | GC Bias199 | GC Bias200 | GC Bias201 | GC Bias202 | GC Bias203 | GC Bias204 | GC Bias205 | GC Bias206 | GC Bias207 | GC Bias208 | GC Bias209 | GC Bias210 | GC Bias211 | GC Bias212 | GC Bias213 | GC Bias214 | GC Bias215 | GC Bias216 | GC Bias217 | GC Bias218 | GC Bias219 | GC Bias220 | GC Bias221 | GC Bias222 | GC Bias223 | GC Bias224 | GC Bias225 | GC Bias226 | GC Bias227 | GC Bias228 | GC Bias229 | GC Bias230 | GC Bias231 | GC Bias232 | GC Bias233 | GC Bias234 | GC Bias235 | GC Bias236 | GC Bias237 | GC Bias238 | GC Bias239 | GC Bias240 | GC Bias241 | GC Bias242 | GC Bias243 | GC Bias244 | GC Bias245 | GC Bias246 | GC Bias247 | GC Bias248 | GC Bias249 | GC Bias250 | GC Bias251 | GC Bias252 | GC Bias253 | GC Bias254 | GC Bias255 | GC Bias256 | GC Bias257 | GC Bias258 | GC Bias259 | GC Bias260 | GC Bias261 | GC Bias262 | GC Bias263 | GC Bias264 | GC Bias265 | GC Bias266 | GC Bias267 | GC Bias268 | GC Bias269 | GC Bias270 | GC Bias271 | GC Bias272 | GC Bias273 | GC Bias274 | GC Bias275 | GC Bias276 | GC Bias277 | GC Bias278 | GC Bias279 | GC Bias280 | GC Bias281 | GC Bias282 | GC Bias283 | GC Bias284 | GC Bias285 | GC Bias286 | GC Bias287 | GC Bias288 | GC Bias289 | GC Bias290 | GC Bias291 | GC Bias292 | GC Bias293 | GC Bias294 | GC Bias295 | GC Bias296 | GC Bias297 | GC Bias298 | GC Bias299 | GC Bias300 | GC Bias301 | GC Bias302 | GC Bias303 | GC Bias304 | GC Bias305 | GC Bias306 | GC Bias307 | GC Bias308 | GC Bias309 | GC Bias310 | GC Bias311 | GC Bias312 | GC Bias313 | GC Bias314 | GC Bias315 | GC Bias316 | GC Bias317 | GC Bias318 | GC Bias319 | GC Bias320 | GC Bias321 | GC Bias322 | GC Bias323 | GC Bias324 | GC Bias325 | GC Bias326 | GC Bias327 | GC Bias328 | GC Bias329 | GC Bias330 | GC Bias331 | GC Bias332 | GC Bias333 | GC Bias334 | GC Bias335 | GC Bias336 | GC Bias337 | GC Bias338 | GC Bias339 | GC Bias340 | GC Bias341 | GC Bias342 | GC Bias343 | GC Bias344 | GC Bias345 | GC Bias346 | GC Bias347 | GC Bias348 | GC Bias349 | GC Bias350 | GC Bias351 | GC Bias352 | GC Bias353 | GC Bias354 | GC Bias355 | GC Bias356 | GC Bias357 | GC Bias358 | GC Bias359 | GC Bias360 | GC Bias361 | GC Bias362 | GC Bias363 | GC Bias364 | GC Bias365 | GC Bias366 | GC Bias367 | GC Bias368 | GC Bias369 | GC Bias370 | GC Bias371 | GC Bias372 | GC Bias373 | GC Bias374 | GC Bias375 | GC Bias376 | GC Bias377 | GC Bias378 | GC Bias379 | GC Bias380 | GC Bias381 | GC Bias382 | GC Bias383 | GC Bias384 | GC Bias385 | GC Bias386 | GC Bias387 | GC Bias388 | GC Bias389 | GC Bias390 | GC Bias391 | GC Bias392 | GC Bias393 | GC Bias394 | GC Bias395 | GC Bias396 | GC Bias397 | GC Bias398 | GC Bias399 | GC Bias400 | GC Bias401 | GC Bias402 | GC Bias403 | GC Bias404 | GC Bias405 | GC Bias406 | GC Bias407 | GC Bias408 | GC Bias409 | GC Bias410 | GC Bias411 | GC Bias412 | GC Bias413 |
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| PR | 19-JUN-1998 | 98US-00899486 |
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| PR | 22-JUN-1998 | 98US-00902522 |
| PR | 22-JUN-1998 | 98US-00902549 |
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| PR | 20-JUL-1998 | 98US-00933392 |
| PR | 30-JUL-1998 | 98US-00946512 |
| PR | 04-AUG-1998 | 98US-00952822 |
| PR | 04-AUG-1998 | 98US-00952852 |
| PR | 04-AUG-1998 | 98US-00953012 |
| PR | 04-AUG-1998 | 98US-00953022 |
| PR | 04-AUG-1998 | 98US-00953182 |
| PR | 04-AUG-1998 | 98US-00953212 |
| PR | 04-AUG-1998 | 98US-00953252 |
| PR | 10-AUG-1998 | 98US-00959162 |
| PR | 10-AUG-1998 | 98US-00959292 |
| PR | 11-AUG-1998 | 98US-00960122 |
| PR | 11-AUG-1998 | 98US-00961432 |
| PR | 11-AUG-1998 | 98US-00961462 |
| PR | 12-AUG-1998 | 98US-00963292 |
| PR | 17-AUG-1998 | 98US-00967572 |
| PR | 17-AUG-1998 | 98US-00968812 |
| PR | 17-AUG-1998 | 98US-00968892 |
| PR | 17-AUG-1998 | 98US-00968952 |
| PR | 17-AUG-1998 | 98US-00968972 |
| PR | 18-AUG-1998 | 98US-00969492 |
| PR | 18-AUG-1998 | 98US-00969502 |
| PR | 18-AUG-1998 | 98US-00969532 |
| PR | 18-AUG-1998 | 98US-00969602 |
| PR | 18-AUG-1998 | 98US-00970222 |

PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
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PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
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PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI, 2000-072883/06.
DR P-PSDB; AAY66719.
XX
XX Membrane-bound proteins and related nucleotide sequences.
PT
XX
XX Claim 2, Fig 207; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
XX
SQ Sequence 1657 BP; 521 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
Query Match 99.3%; Score 403; DB 3; Length 1657;
Best Local Similarity 99.3%; Pred. No. 5.1e-121;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGAATGTGACTATATATGCGAGTCCAGNAACCTTGGGTGTGAGGCTCCCGATGTTTC 60
DB 523 GTGAATGTGACTATATATGCGAGTCCAGNAACCTTGGGTGTGAGGCTCCCGATGTTTC 582
QY 61 CCCAGGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCAACTTCTGGAAGTC 120
DB 583 CCCAGGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCAACTTCTGGAAGTC 642
QY 121 TCCAAATACAGAGCTTTGAGTGAACCTTGAGAAATGTGACATGAAGTTGTGTGCTC 180
DB 643 TCCAAATACAGAGCTTTGAGTGAACCTTGAGAAATGTGACATGAAGTTGTGTGCTC 702
QY 181 TACAATGTTCATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 240
DB 703 TACAATGTTCATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 762
QY 241 ACAGGGATATCAAGTGAAGATGAGATCAAAAGGCGAGTCACTTCCAGAGTGTGTA 300
DB 763 ACAGGGATATCAAGTGAAGATGAGATCAAAAGGCGAGTCACTTCCAGAGTGTGTA 822
QY 301 AACTCAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAAGTGGGCACTTCTGCGCT 360
DB 823 AACTCAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAAGTGGGCACTTCTGCGCT 882

QY 361 CTCAGCCCTTACTGATGCTAATATATGTCCTTGGCCACCAAAA 406
DB 883 CTCAGCCCTTACTGATGCTAATATATGTCCTTGGCCACCAAAA 928
RESULT 6
ADB90935
ID ADB90935 standard; cDNA, 1657 BP.
XX
XX ADB90935;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Novel human secreted and transmembrane protein PRO1291 cDNA.
DE
XX
XX ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
XX Homo sapiens.
OS
XX
XX US2003083473-A1.
PN
XX
XX 01-MAY-2003.
PD
XX
XX 03-MAY-2002; 2002US-00063595.
PF
XX
XX 06-DEC-2001; 2001US-00006867.
PR
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-786922/74.
DR P-PSDB; ADB90936.
XX
XX
PT New antibody that binds a secreted and transmembrane polypeptide (PRO)
PT for treating cancer and for diagnostic assays and affinity purification
PT of PRO.
XX
XX
PS Disclosure; Fig 59; 408pp; English.
XX
XX The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides,
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide.
XX
XX
SQ Sequence 1657 BP; 522 A; 357 C; 366 G; 412 T; 0 U; 0 Other;
Query Match 99.3%; Score 403; DB 10; Length 1657;
Best Local Similarity 99.3%; Pred. No. 5.1e-121;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGAATGTGACTATATATGCGAGTCCAGNAACCTTGGGTGTGAGGCTCCCGATGTTTC 60
DB 522 GTGAATGTGACTATATATGCGAGTCCAGNAACCTTGGGTGTGAGGCTCCCGATGTTTC 581
QY 61 CCCAGGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCAACTTCTGGAAGTC 120
DB 582 CCCAGGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCAACTTCTGGAAGTC 641
QY 121 TCCAAATACAGAGCTTTGAGTGAACCTTGAGAAATGTGACATGAAGTTGTGTGCTC 180
DB 642 TCCAAATACAGAGCTTTGAGTGAACCTTGAGAAATGTGACATGAAGTTGTGTGCTC 701

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QY 181 TACAAATGTTACGATCAACAACACATATCTCTGTATGATGAAATGACATTGCCAAAGCA 240
    |||
Db 702 TCAATGTTACGATCAACAACACATATCTCTGTATGATGAAATGACATTGCCAAAGCA 761
QY 241 ACAGGGGATATCAAAATGACAGAAATGGAGATCAAAAAGCGAGTACCTTACAGCTGCTA 300
    |||
Db 762 ACAGGGGATATCAAAATGACAGAAATGGAGATCAAAAAGCGAGTACCTTACAGCTGCTA 821
QY 301 AACTCAAAAGCTTCTGTGTGTCTCTTCTTTCCATGACATGAGCTGGGACCTTGCT 360
    |||
Db 822 AACTCAAAAGCTTCTGTGTGTCTCTTCTTTCCATGACATGAGCTGGGACCTTGCT 881
QY 361 CTCAGCCCTTACCTGATGCTAATATATATGCTTGCCCAAAA 406
    |||
Db 882 CTCAGCCCTTACCTGATGCTAATATATATGCTTGCCCAAAA 927

RESULT 7
AAS46033
ID AAS46033 standard; cDNA; 1658 BP.
AC AAS46033;
XX
XX 18-DEC-2001 (first entry)
DT
XX
DE Human DNA encoding PRO polypeptide sequence #109.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN MO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
XX 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 15-MAR-2000; 2000US-0189328P.
PR 21-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192555P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199377P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199554P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.

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PR 22-AUG-2000; 2000US-00644848.
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PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
XX (GENTH ) GENENTECH INC.
XX
XX PA
XX PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
DR WPI; 2001-602746/68.
DR P-PSDB; AAU29132.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 2; Fig 217; 774pp; English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
SQ
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Best Local Similarity 99.3%; Pred. No. 5,1e-12;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 583 CCCAGCCCAAGTGTGTGGGATCCCAAGTTGACAGGAGCCCACTTCTCGGAATGTC 642
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Db 643 TCCATATACAGCTTGGAGCTGAACCTGAGATGACATGAGAGTGTGTGCTGCTC 702
QY 181 TCAATGTTACGATCAACAACACATATCTCTGTATGATGAAATGACATTGCCAAAGCA 240
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Db 763 ACAGGGGATATCAAAATGACAGAAATGGAGATCAAAAAGCGAGTACCTTACAGCTGCTA 822
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Db 823 AACTCAAAAGCTTCTGTGTGTCTCTTCTTTCCATGACATGAGCTGGGACCTTGCT 882
QY 361 CTCAGCCCTTACCTGATGCTAATATATATGCTTGCCCAAAA 406
Db 883 CTCAGCCCTTACCTGATGCTAATATATATGCTTGCCCAAAA 928

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PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoletti NF;
PI Roy MA, Stewart TA, Tumas D, Matanabe CK, Williams PM, Wood WI;
PI Zhang Z;

XX WPI; 2001-032160/04.
XX P-PSDB; AAB65242.

PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.

PS Claim 2; Fig 207; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX AAF44470 represent PCR primers and hybridisation probes used in the
XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
XX AAB65300 represent human PRO polynucleotide and protein sequences given
XX in the exemplification of the present invention

SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 99.3%; Score 403; DB 5; Length 1658;

Best Local Similarity 99.3%; Pred. No. 5,1e-121;

Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 CCCGAGCCCAAGTGTGTGGGATCCCAAGTTGACAGAGGCCAATCTTCGGAAAGTC 120

DB 583 CCCGAGCCCAAGTGTGTGGGATCCCAAGTTGACAGAGGCCAATCTTCGGAAAGTC 642

QY 121 TCCATATACAGCTTTGAGCTGAAGCTGAGAAATGTGAGCATGAAGGTTGTCTGTGCTC 180

DB 643 TCCATATACAGCTTTGAGCTGAAGCTGAGAAATGTGAGCATGAAGGTTGTCTGTGCTC 702

QY 181 TACAATGTTAGCATCAACAACATATCTCTGTATGATTGAATAATGACATTGCCAAGA 240

DB 703 TACAATGTTAGCATCAACAACATATCTCTGTATGATTGAATAATGACATTGCCAAGA 762

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DB 763 ACAAGGGGATTCAAAGTGAAGATGGAGATCAAAAAGCGAGTCACTTACAGCTGCTA 822

QY 301 AACTCAAGAGCTCTCTGTGTGTCTCTCTTTCTTTTGGCATGAGTGGGCACTTCTGCT 360

DB 823 AACTCAAGAGCTCTCTGTGTGTCTCTCTTTCTTTTGGCATGAGTGGGCACTTCTGCT 882

QY 361 CTCAGCCCTTACCTGATGCTAANATATGTCCTTG3CCCAAAAA 406

DB 883 CTCAGCCCTTACCTGATGCTAANATATGTCCTTG3CCCAAAAA 928

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QY

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QY

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QY

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QY

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QY

XX Tumour associated antigenic target polypeptide; TAT; cancer;
XX breast cancer; colorectal cancer; lung cancer; ovarian cancer;
XX central nervous system cancer; liver cancer; bladder cancer;
XX pancreatic cancer; cervical cancer; melanoma; leukaemia; TAT136; gene;
XX ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 61..909

XX FT /tag= b

XX FT /product= "TAT136"

XX FT /note= "Tumour associated antigenic target polypeptide"

XX FT sig_peptide 61..144

XX FT /tag= a

XX FT mat_peptide 145..906

XX FT /tag= c

XX FT /label= Mature_TAT136

XX PN WO200216581-A2.

XX PD 28-FEB-2002.

XX PF 14-AUG-2001; 2001WO-US025464.

XX PF 24-AUG-2000; 2000WO-US023328.

XX PR 28-FEB-2001; 2001WO-US006520.

XX PR 22-JUN-2001; 2001US-00888257.

XX PR 22-JUN-2001; 2001WO-US020118.

XX PA (GENENTECH INC.

XX PI Gao W, Polakis P, Shou J, Smith V, Soriano R, Williams PM;

XX PI Wu TD, Zhang Z;

XX PI WPI; 2002-280928/32.

XX DR P-PSDB; AAU77766.

XX DR

XX PT Novel isolated antibody which binds to tumor-associated antigenic target

PT polypeptide useful for killing cancer cells expressing the polypeptide

PT and for treating tumor comprising cells that expresses the polypeptide.

PS Claim 2; Fig 4; 123pp; English.

XX The invention describes an isolated antibody which binds to a tumour-
XX associated antigenic target (TAT) polypeptide. The antibody is useful
XX for: killing a cancer cell (such as a breast, colorectal, lung, ovarian,
XX central nervous system, liver, bladder, pancreatic, cervical, melanoma or
XX leukaemia cell) that expresses a polypeptide with at least 80% identity
XX to the TAT polypeptide sequence; treating a tumour comprising cells that
XX express a polypeptide with at least 80% identity to the TAT polypeptide
XX sequence; determining the presence of a polypeptide having at least 80 %
XX identity to the TAT polypeptide sequence in a sample suspected of
XX containing the polypeptide; diagnosing the presence of a tumour in a
XX mammal, and for antibody dependent enzyme mediated prodrug therapy
XX (ADPPT). This sequence encodes the tumour associated antigenic target
XX polypeptide (TAT) 136, described in the invention

SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 99.3%; Score 403; DB 6; Length 1658;

Best Local Similarity 99.3%; Pred. No. 5,1e-121;

Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGAGCTATTAATGCGAGCTCAGANACCTTGGGTGAGGCTCCCGAGTGTTC 60

DB 523 GTGAATGTGAGCTATTAATGCGAGCTCAGAGACCTTGGGTGAGGCTCCCGAGTGTTC 582

QY 61 CCCGAGCCCAAGTGTGTGGGATCCCAAGTTGACAGAGGCCAATCTTCGGAAAGTC 120

DB 583 CCCGAGCCCAAGTGTGTGGGATCCCAAGTTGACAGAGGCCAATCTTCGGAAAGTC 642

QY

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DB 823 AACTCAAAAGCTTCTCTGTGTCTCTCTTCTTTGTCATGAGCTGGGCACTTCTGCTCT 882
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KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
OS Homo sapiens.
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07-OCT-1998; 98MO-US021141.
PR 06-NOV-1998; 98US-00187368.
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PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99MO-US005028.
PR 14-MAY-1999; 99US-00311832.
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PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
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PR 18-OCT-1999; 99US-00403397.
PR 12-NOV-1999; 99US-00423844.
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PR 15-MAR-2000; 2000MO-US006884.
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PR 02-JUN-2000; 2000MO-US015264.
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PR 22-AUG-2000; 2000US-00644848.
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PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
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PR 08-NOV-2000; 2000MO-US030952.
PR 01-DEC-2000; 2000MO-US032678.
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PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001MO-US006520.
PR 22-MAR-2001; 2001US-00816744.
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PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001MO-US017800.
PR 05-JUN-2001; 2001US-00874503.
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PR 29-JUN-2001; 2001MO-US021066.
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PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
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PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001MO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2003-332034/31.
DR P-PSDB; ABUS6301.
XX
PT Three hundred and five nucleic acids encoding PRO polypeptides, useful in
gene therapy, chromosome identification, tissue typing, and for detecting

PT the presence of tumor in a mammal.
XX
XX Claim 2; Fig 217; 707bp; English.
PS

CC The invention relates to three hundred and five nucleic acids encoding
CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to
CC them, or encoding a PRO polypeptide lacking its associated signal peptide
CC or an extracellular domain of the PRO polypeptide, with or lacking its
CC associated signal peptide. Also included are the encoded PRO proteins,
CC PRO expression vectors, host cells transformed with the vector (used to
CC produce PRO proteins), a chimeric molecule comprising the PRO
CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, a method for stimulating the release of tumor necrosis factor
CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
CC PRO827, PRO791, PRO131, PRO316, PRO183, PRO143, PRO1760, PRO1567 or
CC PRO4333), a method for stimulating the proliferation or differentiation
CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
CC a method for detecting the presence of tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in a binding reaction, to generate transgenic animals or knockout
CC animals, which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful for detecting the presence of a tumour in a mammal, stimulating the
CC proliferation or differentiation of chondrocyte cells, stimulating the
CC release of tumour necrosis factor-alpha from human blood, in gene
CC therapy, or as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. The present sequence is a CDNA encoding a PRO
CC protein
XX
SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 99.3%; Score 403; DB 8; Length 1658;
Best Local Similarity 99.3%; Pred. No. 5,1e-121;

Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATATATGCTGAGTCAAGTTCGCTGAGGCTCCCGATGCTT 60
DB 523 GTGAATGTGACTATATATGCTGAGTCAAGTTCGCTGAGGCTCCCGATGCTT 582
QY 61 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACAGGAGCCAACTTCTGGAAGTC 120
DB 583 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACAGGAGCCAACTTCTGGAAGTC 642
QY 121 TCCATATACAGCTTTGAGCTGGAATGTGAGATGTCACATGAGGTTGTGTGCTC 180
DB 643 TCCATATACAGCTTTGAGCTGGAATGTGAGATGTCACATGAGGTTGTGTGCTC 702
QY 181 TACATGTTACGATCAACAACATATCTCTGTATGATTGAANAATGACATTGGCAAGCA 240
DB 703 TACATGTTACGATCAACAACATATCTCTGTATGATTGAANAATGACATTGGCAAGCA 762
QY 241 ACAGGGGATATCAAGATGACAGATGGAGATCAAAAGGAGGATACCTACAGCTGCTA 300
DB 763 ACAGGGGATATCAAGATGACAGATGGAGATCAAAAGGAGGATACCTACAGCTGCTA 822
QY 301 AACTCAAGGCTTCTGTGTGTGCTCTTCTTTTCCATCAGTGGGACATTCGCT 360
DB 823 AACTCAAGGCTTCTGTGTGTGCTCTTCTTTTCCATCAGTGGGACATTCGCT 882
QY 361 CTCAGCCCTTACTGATGCTAANAATATATGCTTGGCCACCAAAAA 406
DB 883 CTCAGCCCTTACTGATGCTAANAATATATGCTTGGCCACCAAAAA 928

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RESULT 15
ACAO5808
ID ACAA05808 standard; cDNA; 1658 BP.
XX
AC ACAA05808;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #109.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194423.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-0031832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 01-SEP-1999; 99US-00280142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028531.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2000WO-US034956.
PR 22-MAR-2001; 2001US-00815744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.

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PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR MPI: 2003-332039/31.
DR P-PsDB; ABU67514.
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
PT in tissue typing, and in chromosome identification.
XX
XX Claim 2; Fig 217; 706pp; English.
XX
XX The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of the
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ACAA05700-ACAA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention
XX
SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
XX
Query Match 99.3%; Score 403; DB 8; Length 1658;
Best Local Similarity 99.3%; Pred. No. 5,1e-121;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGAATGTGAGTATTAATGACGCTCAGANACCTTGCGGTGTGAGGCTCCCGATGGTTG 60
DB |||||||
DB 523 GTGAATGTGAGTATTAATGACGCTCAGAGACCTTGCGGTGTGAGGCTCCCGATGGTTG 582
QY 61 CCCGAGCCACAGTGTGCTGGGCGATCCCAAGTTGACAGGAGCCCACTTCTCGGAAGTC 120
DB |||||||
DB 583 CCCGAGCCACAGTGTGCTGGGCGATCCCAAGTTGACAGGAGCCCACTTCTCGGAAGTC 642
QY 121 TCCCAATACCAAGTTTGAGCTGAACCTTGAGATGTGACCAATCAAGGTTGTGTGCTGTC 180
DB |||||||
DB 643 TCCCAATACCAAGTTTGAGCTGAACCTTGAGATGTGACCAATCAAGGTTGTGTGCTGTC 702
QY 181 TACAATGTTACGATCAACAACATACCTCTGTATGATTTGAAATGACATTTGCCAAGA 240
DB |||||||
DB 703 TACAATGTTACGATCAACAACATACCTCTGTATGATTTGAAATGACATTTGCCAAGA 762
QY 241 ACAGGGGNTATCAAAAGTGAAGATCGAATCAAAAGCGGAGTACCTTACGCTGCTA 300

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| Qy | 301 | AACTCAAAGGCTTCTCTGTGTGTCTCTTTCTTTTGGCAATCAAGTGGGCACTTCTGCT | 360 |
| Db | 823 | AACTCAAAGGCTTCTCTGTGTGTCTCTTTCTTTTGGCAATCAAGTGGGCACTTCTGCT | 882 |
| Qy | 361 | CTGAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAAA | 406 |
| Db | 883 | CTGAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAAA | 928 |

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Job time : 251.008 secs

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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:54:34 ; Search time 75.2473 Seconds

(without alignments)
8828.602 Million cell updates/sec

Title: US-09-763-978B-12

Perfect score: 406
Sequence: 1 ggaagatgctgactataatgc.....atgtgccttgcccaaaaa 406

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5B COMB. seq: *
3: /cgn2_6/ptodata/1/ina/6A COMB. seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB. seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS COMB. seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 403 | 99.3 | 1046 | 4 US-09-799-451-332 | Sequence 332, App |
| 2 | 403 | 99.3 | 2627 | 3 US-09-404-879A-391 | Sequence 391, App |
| 3 | 403 | 99.3 | 2627 | 4 US-09-667-857-391 | Sequence 391, App |
| 4 | 38 | 9.4 | 69813 | 4 US-09-949-016-12455 | Sequence 12455, A |
| 5 | 38 | 9.4 | 69813 | 4 US-09-949-016-13905 | Sequence 13905, A |
| 6 | 38 | 9.4 | 69813 | 4 US-09-949-016-13906 | Sequence 13906, A |
| 7 | 38 | 9.4 | 69813 | 4 US-09-949-016-12861 | Sequence 12861, A |
| 8 | 34.8 | 8.6 | 1141 | 4 US-09-806-708B-22 | Sequence 22, Appl |
| 9 | 34.6 | 8.5 | 13204 | 4 US-09-054-372-49 | Sequence 49, Appl |
| 10 | 32.4 | 8.0 | 3364 | 4 US-09-621-976-17202 | Sequence 17202, A |
| 11 | 32.2 | 7.9 | 38564 | 3 US-09-734-673-3 | Sequence 3, Appl1 |
| 12 | 32 | 7.9 | 6749 | 3 US-08-961-527-84 | Sequence 84, Appl |
| 13 | 32 | 7.9 | 9062 | 4 US-08-956-171B-85 | Sequence 85, Appl |
| 14 | 32 | 7.9 | 9062 | 4 US-08-781-986A-85 | Sequence 85, Appl |
| 15 | 32 | 7.9 | 36611 | 4 US-09-949-016-17287 | Sequence 17287, A |
| 16 | 32 | 7.9 | 144362 | 4 US-09-949-016-16066 | Sequence 16066, A |
| 17 | 31.8 | 7.8 | 94156 | 4 US-09-949-016-12388 | Sequence 12388, A |
| 18 | 31.8 | 7.8 | 102406 | 4 US-09-949-016-14673 | Sequence 14673, A |
| 19 | 31.4 | 7.7 | 61777 | 4 US-09-949-016-17278 | Sequence 17278, A |
| 20 | 31.4 | 7.7 | 89716 | 4 US-09-949-016-11900 | Sequence 11900, A |
| 21 | 30.8 | 7.6 | 809 | 4 US-09-248-796A-6226 | Sequence 6226, Ap |
| 22 | 30.8 | 7.6 | 809 | 1 US-08-441-629-1 | Sequence 1, Appl1 |
| 23 | 30.8 | 7.6 | 809 | 3 US-08-776-207-1 | Sequence 1, Appl1 |
| 24 | 30.8 | 7.6 | 809 | 3 US-09-507-773-1 | Sequence 1, Appl1 |
| 25 | 30.8 | 7.5 | 809 | 5 PCT-US95-09172-1 | Sequence 1, Appl1 |
| 26 | 30.6 | 7.5 | 601 | 4 US-09-949-016-25615 | Sequence 25615, A |
| 27 | 30.6 | 7.5 | 601 | 4 US-09-949-016-25616 | Sequence 25616, A |

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| C | 28 | 30.6 | 7.5 | 601 | 4 US-09-949-016-52403 | Sequence 52403, A |
| C | 29 | 30.6 | 7.5 | 601 | 4 US-09-949-016-52404 | Sequence 52404, A |
| C | 30 | 30.6 | 7.5 | 654 | 4 US-09-252-991A-3291 | Sequence 3291, Ap |
| C | 31 | 30.6 | 7.5 | 1623 | 4 US-09-252-991A-3226 | Sequence 3226, Ap |
| C | 32 | 30.6 | 7.5 | 2024 | 4 US-09-799-451-813 | Sequence 813, App |
| C | 33 | 30.6 | 7.5 | 2322 | 4 US-09-252-991A-3345 | Sequence 3345, Ap |
| C | 34 | 30.6 | 7.5 | 2364 | 4 US-09-252-991A-3420 | Sequence 3420, Ap |
| C | 35 | 30.6 | 7.5 | 4159 | 4 US-09-614-912-139 | Sequence 139, App |
| C | 36 | 30.6 | 7.5 | 36156 | 4 US-09-949-016-12128 | Sequence 12128, A |
| C | 37 | 30.6 | 7.5 | 36156 | 4 US-09-949-016-13261 | Sequence 13261, A |
| C | 38 | 30.6 | 7.5 | 91831 | 4 US-09-949-016-13694 | Sequence 13694, A |
| C | 39 | 30.4 | 7.5 | 252 | 4 US-09-328-352-2876 | Sequence 2876, Ap |
| C | 40 | 30.4 | 7.5 | 601 | 4 US-09-949-016-79104 | Sequence 79104, A |
| C | 41 | 30.4 | 7.5 | 2166 | 4 US-09-134-000C-2061 | Sequence 2061, Ap |
| C | 42 | 30.4 | 7.5 | 98567 | 4 US-09-949-016-11750 | Sequence 11750, A |
| C | 43 | 30.4 | 7.5 | 107140 | 4 US-09-949-016-14834 | Sequence 14834, A |
| C | 44 | 30.4 | 7.5 | 784019 | 4 US-09-949-016-14033 | Sequence 14033, A |
| C | 45 | 30.4 | 7.5 | 828152 | 4 US-09-949-016-12777 | Sequence 12777, A |

ALIGNMENTS

RESULT 1
US-09-799-451-332
; Sequence 332, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryje
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aifeng J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Keena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 332
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(888)
US-09-799-451-332
Query Match 99.3%; Score 403; DB 4; Length 1046;
Best Local Similarity 99.3%; Pred. No. 3,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 1 GTGAATGACATATATGACAGTCCAGAACCTTGAGGTGAGGCTCCCATGATTC 60
DB 505 GTGAATGACATATATGACAGTCCAGAACCTTGAGGTGAGGCTCCCATGATTC 564
DB 61 CCCAGGCCACAGTGTCTGTGGGATCCCAAGTTGACCGAGGACCACTTCTCGAAGTC 120
DB 565 CCCAGGCCACAGTGTCTGTGGGATCCCAAGTTGACCGAGGACCACTTCTCGAAGTC 624

Db 27730 AACAAATTTAGATGGAGAGATATGATTTCTTGAAGAAATGATGTCTCTTAAAC 27671
Qy 187 GTTAGATTAACAACACATCTCTCTGTATGATTTGAAAAATGACATTTGCCAACAACAGG 246
Db 27670 GGGACATTCATAAGAAATTAAGAGCCCTTGAAAAATTTAAAAATGATGATCTAGAAAG 27611
Qy 247 GATATCAAGTAGACAGATCGAGATCAAAAGCGGAGTCACTACA 293
Db 27610 CCATTCAAAGGATGAAAAATTAAGTTAATCTCCCAAGAAATGACA 27564

RESULT 8

US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match 8.6%; Score 34.8; DB 4; Length 1141;
Best Local Similarity 10.4%; Pred. No. 0.38;
Matches 34; Conservative 150; Mismatches 141; Indels 2; Gaps 1;

Qy 4 AATGGAGCTATTAATCCAGCTCAGANACCTTGGGTGAGGCTCCCGAGTGTCC 63
Db 415 WWTWTKYMKAAACNNNNBRAMVRYVAMMYSRDTTDMMMTSDMBWMTYVDYTMKA 356
Qy 64 CAGCCACAGGTGCTGGGATCCCAAGTTGACACGACCACTTCGGAAGTCTCC 123
Db 355 WNNNNNNNRBCKTTSWMMMDHMTHTCTYGNNTWSAYBMAASWMAAGASNBVTYMC 296
Qy 124 AATACCACTTTGAGCTGAAGTCTGAGAAATGTCACCATGAGGTGTGTCTGTCTAC 183
Db 295 WHTWTGKTMTNNNNNNKAMYYRTKTIVAMCNRYYDIAVMTBKRYKCYAVBMY 236
Qy 184 AATGTTACATCAACACATCTCTCTGTATGATTTGAAAAATGACATTTGCCAAGACA 243
Db 235 M--GKHMMWMBRABHRSNNMMWVKCRNXYMSWHTAMRYBMAVAVGNNWMDRMAH 178
Qy 244 GGGGATATCAAGTAGACAGATCGAGATCAAAAGCGGAGTCACTACA 303
Db 177 HHWCATNNNNMMWVAIYMHMHKGAIAWNTKABRDBAHVKTYYWRIDYMCAMCW 118
Qy 304 TCAAGGCTTCTCTGTGTCTCTCTCT 330
Db 117 NNAKAKVRTAMKHMWYTTDRYVSANNT 91

RESULT 9

US-09-054-272-49
; Sequence 49, Application US/09054272
; Patent No. 6692909
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George O.
; APPLICANT: Caregill, Michele

APPLICANT: Ireland, James S.
APPLICANT: Rozen, Steven G.
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,272
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI98-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 13204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-054-272-49

Query Match 8.5%; Score 34.6; DB 4; Length 13204;
Best Local Similarity 49.2%; Pred. No. 1.8;
Matches 117; Conservative 0; Mismatches 120; Indels 1; Gaps 1;

Qy 129 CAGCTTTGAGCTGAAGTCTGAGAAATGACATGAAGGTGTGTCTCTTACATGT 188
Db 8817 CATCTGTATTCAGAAAGAGATGAGACCGAGGTGTGTCTGTGAGCTGGCAACC 8876
Qy 189 TAGATCAACAACACATCTCTCTGTATGATTTGAAAAATGACATTTGCCAAGCAACGGG 248
Db 8877 CATGAAGAAAGACGCCAGGTGAGGCTGTGGTGTGATACCGGGTCTCCACAGGGG 8936
Qy 249 TATCAAGTAGACAGATGCG-GAGATCAAAAGCGGAGTCACTTACGTGTCTAACTCA 307
Db 8937 TCATGAATTAACCAATTTTAAAGGGTGAAGTTTAAAGCCACATAGTTCTTGCGCGCAATC 8996
Qy 308 AGGCTTCTGTGTCTCTCTCTCTTCTTTCATGATGAGCTGGGCACTTCTGCTCTAG 365
Db 8997 TTGTGCTCACACTCCCTTTTGCAACATTTGCTTGGGTGATGACTTTCCTCTCTG 9054

RESULT 10

US-09-621-976-17202/c
; Sequence 17202, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976

```

      TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
      NUMBER OF SEQUENCES: 391
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Human Genome Sciences, Inc.
      STREET: 9410 Key West Avenue
      CITY: Rockville
      STATE: Maryland
      COUNTRY: USA
      ZIP: 20850

      COMPUTER READABLE FORM:
      MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
      COMPUTER: HP Vectra 486/33
      OPERATING SYSTEM: MSDOS version 6.2
      SOFTWARE: ASCII Text
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/961,527
      FILING DATE:
      CLASSIFICATION: 424
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER:
      FILING DATE:
      ATTORNEY/AGENT INFORMATION:
      NAME: Brookes, A. Anders
      REGISTRATION NUMBER: 36,373
      REFERENCE/DOCKET NUMBER: PB340P1
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (301) 309-8504
      TELEFAX: (301) 309-8512
      INFORMATION FOR SEQ. ID NO: 84:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 6749 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      US-08-961-527-84

      Query Match      7.9%; Score 32; DB 3; Length 6749;
      Best Local Similarity 53.1%; Pred. No. 9.3;
      Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

      QY      102 AGGCAACTCTGTGGAAAGTCTCCAAATGACACGCTTTGAGCTGAACTCGAAGATGACCAT 161
      Db      4344 AACCAATTGACGAGGCAAGCTCTTACTTAGAGTTGGCGGTAAATGTTGAAAGATTTCCAC 4285
      QY      162 GAAGTTGTGTCTGTGCTCTACAAATGTTACGATCAACAACACATCTCTCTATGATTGA 221
      Db      4284 GCGCTCGGTGCTCTCTCTGTTATGAACTGACACAAACAAATCAAGCTTGCAGAAATTG 4225
      QY      222 AATGACA 229
      Db      4224 AAAAGACA 4217

      RESULT 13
      US-08-956-171E-85/c
      ; Sequence 85, Application US/08956171E
      ; Patent No. 6593114
      ; GENERAL INFORMATION:
      ; APPLICANT: Charles Kunech
      ;           Gil H. Choi
      ;           Patrick S. Dillon
      ;           Craig A. Rosen
      ;           Steven C. Barash
      ;           Michael R. Fannon
      ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
      ; NUMBER OF SEQUENCES: 5256
      ; CORRESPONDENCE ADDRESS:
      ; ADDRESSEE: Human Genome Sciences, Inc.
      ; STREET: 9410 Key West Avenue
      ; CITY: Rockville
      ; STATE: Maryland
      ; COUNTRY: USA
      ; ZIP: 20850

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 9062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-08-956-171E-85

Query Match
Best Local Similarity 49.1%; Score 32; DB 4; Length 9062;
Matches 83; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 106 AACTTCGGAAGTCTCCATATACAGCTTTGAGCTGAAGTGAAGTGAAGTGAAG 165
DB 7443 AACTGTGTAAATAGCTCCAGCAATTTCTTTAACCGCATATATCAAGTCACTTTTAA 7384
QY 166 GTTGTCGTCTGTCTTACATATGTTACATCAACACATCACTCTGTATGATTAAT 225
DB 7383 TTTCGATTTTATCTGCGGTATGTCACACATGATATATCTGCTCTTTGACCA 7324
QY 226 GACATTGCCAAGCAACAGGGGNTATCAAAAGTGACGAATCGAGATCA 274
DB 7323 ATCTTTGTTACTAAACAGCGTTACCAACTGCATGACATGACATCA 7275

RESULT 14
US-08-781-986A-85/C
Sequence 85, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kneuch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 9062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-85

Query Match
Best Local Similarity 49.1%; Score 32; DB 4; Length 9062;
Matches 83; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 106 AACTTCGGAAGTCTCCATATACAGCTTTGAGCTGAAGTGAAGTGAAGTGAAG 165
DB 7443 AACTGTGTAAATAGCTCCAGCAATTTCTTTAACCGCATATATCAAGTCACTTTTAA 7384
QY 166 GTTGTCGTCTGTCTTACATATGTTACATCAACACATCACTCTGTATGATTAAT 225
DB 7383 TTTCGATTTTATCTGCGGTATGTCACACATGATATATCTGCTCTTTGACCA 7324
QY 226 GACATTGCCAAGCAACAGGGGNTATCAAAAGTGACGAATCGAGATCA 274
DB 7323 ATCTTTGTTACTAAACAGCGTTACCAACTGCATGACATGACATCA 7275

RESULT 15
US-09-949-016-17287
Sequence 17287, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYOMPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17287
LENGTH: 36611
TYPE: DNA
ORGANISM: Human
US-09-949-016-17287

Query Match
Best Local Similarity 50.3%; Score 32; DB 4; Length 36611;
Matches 77; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 201 CACATATCTCTGTATGATTAAGTGAATGATTCACAAAGCAACAGGGGNTATCAAGTGA 260
DB 32049 CACATATCATATGACAGGTGGGAAACACCCGTCTTACAGGGGAAGTTCTATTCATTCAT 32108
QY 261 AGAATCGAGATCAAAAGCGGAGTCACTTACAGCTGCTAAACTCAAAAGGCTTCTGTG 320
DB 32109 TCCATCAGAGCAAACTGGCCAGAGAACTCAAGGATGATATGACAAAGATCACTGTG 32168
QY 321 TGTCTCTTCTTCTTTCGATCAGTGGGACT 353
DB 32169 CATGCTCTCTCTAGCCAGCTTGAGACT 32201
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 17:54:16 ; Search time 278.562 Seconds
(without alignments)
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Title: US-09-763-978B-12

Perfect score: 406
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 19: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 403 | 99.3 | 1065 | 9 | US-09-877-065-5 |
| 3 | 403 | 99.3 | 1658 | 9 | US-09-989-722-290 |
| 4 | 403 | 99.3 | 1658 | 9 | US-09-989-723-290 |
| 5 | 403 | 99.3 | 1658 | 9 | US-09-989-723-290 |
| 6 | 403 | 99.3 | 1658 | 9 | US-09-989-727-290 |
| 7 | 403 | 99.3 | 1658 | 9 | US-09-989-731-290 |
| 8 | 403 | 99.3 | 1658 | 9 | US-09-989-732-290 |
| 9 | 403 | 99.3 | 1658 | 9 | US-09-991-073-290 |
| 10 | 403 | 99.3 | 1658 | 9 | US-09-990-442-290 |
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| 12 | 403 | 99.3 | 1658 | 9 | US-09-993-604-290 | Sequence 290, App |
| 13 | 403 | 99.3 | 1658 | 9 | US-09-990-456-290 | Sequence 290, App |
| 14 | 403 | 99.3 | 1658 | 9 | US-09-989-721-290 | Sequence 290, App |
| 15 | 403 | 99.3 | 1658 | 9 | US-09-992-598-290 | Sequence 290, App |
| 16 | 403 | 99.3 | 1658 | 9 | US-09-989-293A-290 | Sequence 290, App |
| 17 | 403 | 99.3 | 1658 | 9 | US-09-989-735-290 | Sequence 290, App |
| 18 | 403 | 99.3 | 1658 | 9 | US-09-990-444-290 | Sequence 290, App |
| 19 | 403 | 99.3 | 1658 | 9 | US-09-991-181-290 | Sequence 290, App |
| 20 | 403 | 99.3 | 1658 | 9 | US-09-989-730-290 | Sequence 290, App |
| 21 | 403 | 99.3 | 1658 | 9 | US-09-990-436-290 | Sequence 290, App |
| 22 | 403 | 99.3 | 1658 | 9 | US-09-993-687-290 | Sequence 290, App |
| 23 | 403 | 99.3 | 1658 | 10 | US-09-989-734-290 | Sequence 290, App |
| 24 | 403 | 99.3 | 1658 | 10 | US-09-997-653-290 | Sequence 290, App |
| 25 | 403 | 99.3 | 1658 | 10 | US-09-989-728-290 | Sequence 290, App |
| 26 | 403 | 99.3 | 1658 | 10 | US-09-989-728-290 | Sequence 290, App |
| 27 | 403 | 99.3 | 1658 | 10 | US-09-990-441-290 | Sequence 290, App |
| 28 | 403 | 99.3 | 1658 | 10 | US-09-993-667-290 | Sequence 290, App |
| 29 | 403 | 99.3 | 1658 | 10 | US-09-997-428-290 | Sequence 290, App |
| 30 | 403 | 99.3 | 1658 | 10 | US-09-997-666-290 | Sequence 290, App |
| 31 | 403 | 99.3 | 1658 | 10 | US-09-990-438-290 | Sequence 290, App |
| 32 | 403 | 99.3 | 1658 | 10 | US-09-990-562-290 | Sequence 290, App |
| 33 | 403 | 99.3 | 1658 | 10 | US-09-990-711-290 | Sequence 290, App |
| 34 | 403 | 99.3 | 1658 | 10 | US-09-989-726-290 | Sequence 290, App |
| 35 | 403 | 99.3 | 1658 | 10 | US-09-998-156-290 | Sequence 290, App |
| 36 | 403 | 99.3 | 1658 | 10 | US-09-990-437-290 | Sequence 290, App |
| 37 | 403 | 99.3 | 1658 | 10 | US-09-991-157-290 | Sequence 290, App |
| 38 | 403 | 99.3 | 1658 | 10 | US-09-997-514-290 | Sequence 290, App |
| 39 | 403 | 99.3 | 1658 | 10 | US-09-997-573-290 | Sequence 290, App |
| 40 | 403 | 99.3 | 1658 | 10 | US-09-991-172-290 | Sequence 290, App |
| 41 | 403 | 99.3 | 1658 | 10 | US-09-990-726-290 | Sequence 290, App |
| 42 | 403 | 99.3 | 1658 | 10 | US-09-997-559-290 | Sequence 290, App |
| 43 | 403 | 99.3 | 1658 | 10 | US-09-997-601-290 | Sequence 290, App |
| 44 | 403 | 99.3 | 1658 | 10 | US-09-990-443-290 | Sequence 290, App |
| 45 | 403 | 99.3 | 1658 | 10 | US-09-929-769-4 | Sequence 4, App11 |

ALIGNMENTS

RESULT 1
US-10-302-172-332
Sequence 332, Application US/10302172
Publication No. US20040053250A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids a
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803_1CNDP
CURRENT APPLICATION NUMBER: US/10/302,172
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pt_Fl_genes Version 2.0
SEQ ID NO 332
LENGTH: 1046
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (4) ..(886)
US-10-302-172-332
Query Match 99.3% ; Score 403; DB 17; Length 1046;
Best local Similarity 99.3% ; Pred. No. 1.1e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATTAATGCGAGCTGAGANACCTTGCGGTGTGAGGCTCCCGATGTTTC 60
DB 505 GTGAATGTGACTATTAATGCGAGCTGAGANACCTTGCGGTGTGAGGCTCCCGATGTTTC 564
QY 61 CCCCAGCCCAAGTGTCTGGGGATGCCAAGTTGACAGGAGGCCAACTTTCCGAAATC 120
DB 565 CCCCAGCCCAAGTGTCTGGGGATGCCAAGTTGACAGGAGGCCAACTTTCCGAAATC 624
QY 121 TCCAAATACAGCTTTGAGCTGAACTCTGAGAAATGTGACCATGAAAGTTGTGTGCTC 180
DB 625 TCCAAATACAGCTTTGAGCTGAACTCTGAGAAATGTGACCATGAAAGTTGTGTGCTC 684
QY 181 TACAAATGTTACGATCAACAACATATCTCTGTATGATTTGAAATGACATTTGCCAAAGA 240
DB 685 TACAAATGTTACGATCAACAACATATCTCTGTATGATTTGAAATGACATTTGCCAAAGA 744
QY 241 ACAGGGGATNTCAAATGACAGAAATGGAGATCAAAAGCCGAGTACCTTACAGCTGCTA 300
DB 745 ACAGGGGATNTCAAATGACAGAAATGGAGATCAAAAGCCGAGTACCTTACAGCTGCTA 804
QY 301 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATGACGTGGGCACTTGTGCT 360
DB 805 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATGACGTGGGCACTTGTGCT 864
QY 361 CTCAGCCCTTACCTGATGCTTANANATATGTCCTTGCCCAAAAA 406
DB 865 CTCAGCCCTTACCTGATGCTTANANATATGTCCTTGCCCAAAAA 910

RESULT 2

US-09-877-065-5
; Sequence 5, Application US/09877065
; Patent No. US20020051990A1
; GENERAL INFORMATION:
; APPLICANT: OPLE, ERIC
; APPLICANT: MCLACHLAN, KAREN
; APPLICANT: HEARD, CHERYL J.
; TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR
; FILE REFERENCE: 037003-0280631
; CURRENT APPLICATION NUMBER: US/09/877,065
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,451
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-065-5

Query Match 99.3%; Score 403; DB 9; Length 1065;
Best Local Similarity 99.3%; Pred. No. 1,1e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATTAATGCGAGCTGAGANACCTTGCGGTGTGAGGCTCCCGATGTTTC 60
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DB 594 CCCCAGCCCAAGTGTCTGGGGATGCCAAGTTGACAGGAGGCCAACTTTCCGAAATC 653
QY 121 TCCAAATACAGCTTTGAGCTGAACTCTGAGAAATGTGACCATGAAAGTTGTGTGCTC 180
DB 654 TCCAAATACAGCTTTGAGCTGAACTCTGAGAAATGTGACCATGAAAGTTGTGTGCTC 713
QY 181 TACAAATGTTACGATCAACAACATATCTCTGTATGATTTGAAATGACATTTGCCAAAGA 240
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QY 241 ACAGGGGATNTCAAATGACAGAAATGGAGATCAAAAGCCGAGTACCTTACAGCTGCTA 300

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DB 834 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATGACGTGGGCACTTGTGCT 893
QY 361 CTCAGCCCTTACCTGATGCTTANANATATGTCCTTGCCCAAAAA 406
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RESULT 3

US-09-989-722-290
; Sequence 290, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerdler, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/087759
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; PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090349
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACATTAATATCCAGCTCAGANACCTTGCGGTGTGAGGCTCCCGATGTTTC 60
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DB 583 CCCCGCCCAAGTGTGTGCGGATGCCAAGTTGACACAGGAGCCAACTTTCGGAAATC 642
QY 121 TCCAAATACAGCTTTGAGCTGAACTCTGAAATGTGACCATGAAAGTTGTGTGCTC 180
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DB 763 ACAGGGGATATCAAAATGTGACAGATGTGAGATCAAAAAGCGAGTACCTACAGCTGCTA 822
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DB 763 ACAGGGGATATCAAAATGTGACAGATGTGAGATCAAAAAGCGAGTACCTACAGCTGCTA 822
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DB 823 AACTCAAGGCTTCTGTGTGCTCTTCTTTTCCCATCAGCTGGGCACTTGTGCT 882
QY 361 CTCAGCCTTACCTGATGCTAANAATATGTGCTTGCCCAAAAA 406
DB 883 CTCAGCCTTACCTGATGCTAANAATATGTGCTTGCCCAAAAA 928

RESULT 4

US-09-989-723-290
Sequence 290, Application US/09989723
Patent No. US20020072092A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1.4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; Sequence 290, Application US/09989279
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 99.3%; Score 403; DB 9; Length 1658;

Best Local Similarity 99.3%; Pred. No. 1,4e-125; Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 361 CTCAGCCCTTACCTGATGATTAANATATGCTTGGCCCAAAAA 406
DB 883 CTCAGCCCTTACCTGATGATTAANATATGCTTGGCCCAAAAA 928

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RESULT 6
US-09-989-727-290

; Sequence 290, Application US/09989727
; Patent No. US20020072497A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

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; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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523 GGAATGAGGACTAATAAGCCAGCTCAGAGACTTGCGGTGAGGCTCCCGATGCTTC 582
61 CCCAGCCCAAGTGTGAGGATCCCAAGTTGACAGGAGGCCAAGCTTCGGAGTGC 120
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121 TCCAAATGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 180
643 TCCAAATGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 702
181 TCCAAATGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240
703 TCCAAATGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 762
241 ACAGGGATATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
763 ACAGGGATATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 822
301 AACTGAAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360

Db 823 AACTCAAGGCTTCTGTGTGTCTCTTCTTTCTTGCCATCAGCTGGGCACTTCTGCT 882
Qy 361 CTGAGCCCTTACCGATGATTAATATATGCGCTTGGCCCAAAA 406
Db 883 CTCAGCCCTTACCGATGATTAATATATGCGCTTGGCCCAAAA 928

RESULT 7

US-09-989-731-290
Sequence 290, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyere, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: p2730p1c70
CURRENT APPLICATION NUMBER: US/09/989,731
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGAGCTATTAATGCTCAGANACCTTGCGGTGTGAGGCTCCCGATGATGTC 60
DB 523 GTGAATGTGAGCTATTAATGCTCAGANACCTTGCGGTGTGAGGCTCCCGATGATGTC 582
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583 CCCAGCCCAAGTGTCTGTGGGATCCCAAGTTGACAGGAGCCCAACTTCTCGAAGTC 642
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DB 643 TCCATATACAGCTTTAGACTGAACCTGAGATGAGCCATGAGAGGTGTGTGTGCTC 702
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DB 703 TACATGTATGAGATCAACACATACCTCTGTATGATTGAAAAATGACATTGCCAAGCA 762
QY 241 ACAGGGGATATCAAAAGTACAGATCGAGATCAAAAGGCGGAGTCACTTACAGTGTCTA 300
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DB 823 AACTCAAAAGGCTCTGTGTGTCTCTCTTCTTGTGCATCAGCTGGGCACTTGTGCT 882
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Sequence 290, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC57
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/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 523 GTGAATGTGACTAATATATCCAGCTCAGAGACTTTCGCGGTGAGGCTCCCGAGTGTTC 582
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QY 121 TCCAAATACAGCTTTGAGCTGAATCTGTGAATGTGAGCAAGTTGTGTGTCTC 180
DB 643 TCCAAATACAGCTTTGAGCTGAATCTGTGAATGTGAGCAAGTTGTGTGTCTC 702
QY 181 TACAATGTTCAGATCAACAACATATCTCTGTATGATTGAATAATGACATTCGCAAGA 240
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DB 763 ACAGGGGATATCAAGTGCAGATGAGATCAAAAGGCGAGTACCTACAGCTGCTA 822
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DB 823 AACTCAAGGCTTCTCTGTGTCTCTTCTTTCTTTCCATGACGTGGCACTTGTGCT 882
QY 361 CTCAGCCCTTACCTGATGCTTAANATATGTGCTTGCCCACAAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTTAANATATGTGCTTGCCCACAAAAA 928

RESULT 9

US-09-991-073-290
/ Sequence 290, Application US/09991073
/ Patent No. US20020127576A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerlitsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kijavini, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C15

/ CURRENT APPLICATION NUMBER: US/09/991,073
/ CURRENT FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/049787
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/065186
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGAATGTGACATATATATGACAGCTCAGANACCTTGCAGTGTGAGGCTCCCGATGATTC 60
Db 523 GTGAATGTGACATATATATGACAGCTCAGAGACTTCCGATGTGAGGCTCCCGATGATTC 582

Qy 61 CCCAGCCCAACAGTGTCTGGGATCTCCAGATTGACAGGAGCCAACTTCTCGAAGTC 120
Db 583 CCCAGCCCAACAGTGTCTGGGATCTCCAGATTGACAGGAGCCAACTTCTCGAAGTC 642

Qy 121 TCCAAATACCACTTTAGCTGAACTCTGAGAAATGACATGAAAGTTGTGTGCTC 180
Db 643 TCCAAATACCACTTTAGCTGAACTCTGAGAAATGACATGAAAGTTGTGTGCTC 702

Qy 181 TACAATGTATACATCAACAACACATCTCTGTATGTAATAATGACATTTGCCAAGCA 240
Db 703 TACAATGTATACATCAACAACACATCTCTGTATGTAATAATGACATTTGCCAAGCA 762

Qy 241 ACAGGGANTATCAAAAGTGAAGAAATCGAATCAAAAGGCGAGTCACTTACAGTGTCTA 300
Db 763 ACAGGGANTATCAAAAGTGAAGAAATCGAATCAAAAGGCGAGTCACTTACAGTGTCTA 822

Qy 301 AACTCAAAAGCTTCTGTGTGTCTTCTTTCTTTTCCATCAGCTGGGCACTTCTGCTT 360
Db 823 AACTCAAAAGCTTCTGTGTGTCTTCTTTCTTTTCCATCAGCTGGGCACTTCTGCTT 882

Qy 361 CTCAGCCCTTACCTGATGCTAANAATATATGCTTGGCCACAAA 406
Db 883 CTCAGCCCTTACCTGATGCTAANAATATATGCTTGGCCACAAA 928

RESULT 10
US-09-990-442-290
; Sequence 290, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 583 CCCGAGCCCACTGCTGCTGGGATCCCAAGTTGACCGAGGACCACTTCTCGAAGTC 642
QY 121 TCCAAATACAGCTTTGAGCTGAGACTCTGAGATGTGACCATGAAGGTTGCTGCTC 180
DB 643 TCCAAATACAGCTTTGAGCTGAGACTCTGAGATGTGACCATGAAGGTTGCTGCTC 702
QY 181 TACAAATGTATGATCAACAACACATATCTCTGTATGATGAAATGACATTTGCCAAGA 240
DB 703 TACAAATGTATGATCAACAACACATATCTCTGTATGATGAAATGACATTTGCCAAGA 762
QY 241 ACAAGGGATATCAAAATGACAGAAATGGAGATCAAAAGGCGAGTCACTTACAGCTGCTA 300
DB 763 ACAAGGGATATCAAAATGACAGAAATGGAGATCAAAAGGCGAGTCACTTACAGCTGCTA 822
QY 301 AACTCAAGGCTTCTGCTGCTCTCTTCTTTTCCCATGAGCTGGGCACTTCTGCTC 360
DB 823 AACTCAAGGCTTCTGCTGCTCTCTTCTTTTCCCATGAGCTGGGCACTTCTGCTC 882
QY 361 CTCAGCCCTTACCTGATGCTAANATATGCTCCCTGGCCACAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAANATATGCTCCCTGGCCACAAAA 928

RESULT 11
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; Sequence 290, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Rong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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Db 703 TACAAATGTTGCGATCAACAAACACATCTCTGTATGATTTGAAATGACATTTGCCAAAGCA 762
Qy 241 ACAGGGGNTTCAAGGAGCAAGATCGAGATCAAAAGGGGGAGTCACTACAGCTGCTA 300
Db 763 ACAGGGGATTCAAAGTACAGCAAGTCCGAGATCAAAAGGGGGAGTCACTACAGCTGCTA 822
Qy 301 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATCAAGCTGGGCACTTCTGCT 360
Db 823 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATCAAGCTGGGCACTTCTGCT 882
Qy 361 CTCAGCCTTACTGATGCTTAATATATGCTTGGCCACAAAA 406
Db 883 CTCAGCCTTACTGATGCTTAATATATGCTTGGCCACAAAA 928

RESULT 12
US-09-93-604-290
; Sequence 290, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC22
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 15
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Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC20
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Query Match 99.3%; Score 403; DB 9; Length 1658;
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Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 121 TCCAAATCCAGCTTTGAGTGAAGTGTGAGATGTGACATGAAGGTTGTGTGCTGCTC 180
Db 643 TCCAAATCCAGCTTTGAGTGAAGTGTGAGATGTGACATGAAGGTTGTGTGCTGCTC 702
QY 181 TACAATGTATGATCAACAAACATACCTCTGTATGATGAAATGACATTTGCCAAAGCA 240
Db 703 TACAATGTATGATCAACAAACATACCTCTGTATGATGAAATGACATTTGCCAAAGCA 762

```

```

QY 241 ACAGGGGNTATCAAGTGAACAGATGGAGATCAAAAGGCGAGTCACTAGAGTGTCTA 300
Db 763 ACAGGGGNTATCAAGTGAACAGATGGAGATCAAAAGGCGAGTCACTAGAGTGTCTA 822
QY 301 AACTCAAGGCTTCTGTGTGTCTCTTCTTTGCAATGAGTGGCACTTCTGCTT 360
Db 823 AACTCAAGGCTTCTGTGTGTCTCTTCTTTGCAATGAGTGGCACTTCTGCTT 882
QY 361 CTCAGCCCTTACTGTATGCTAANATATGTGCTTGGCCACAAA 406
Db 883 CTCAGCCCTTACTGTATGCTAANATATGTGCTTGGCCACAAA 928

```

Search completed: May 31, 2005, 10:07:39
Job time : 279.562 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:48:09 ; Search time 1579.08 Seconds
(without alignments)
9786.800 Million cell updates/sec

Title: US-09-763-978B-12

Perfect score: 406

Sequence: 1 gtcgacgtgacataatgc.....atgtgcttgccacacaaa 406

Scoring table: IDENTITY_NUC

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hnc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 403 | 99.3 | 595 | 5 | BU680630 UT-CF-DUI |
| 2 | 403 | 99.3 | 925 | 5 | BX369964 BX369964 |
| 3 | 401.4 | 98.9 | 655 | 7 | CN259811 17006000 |
| 4 | 401.4 | 98.9 | 751 | 5 | BM981657 UI-CF-EN1 |
| 5 | 401.4 | 98.9 | 2431 | 3 | CR603772 full-length |
| 6 | 384 | 94.6 | 849 | 9 | AY405846 Homo sapi |
| 7 | 379.2 | 93.4 | 849 | 9 | AY405847 Pan trogl |
| 8 | 315 | 77.6 | 443 | 1 | AI799522 tr49b02.x |
| 9 | 308.8 | 76.1 | 436 | 8 | AQ479831 RPI1-11-2 |
| 10 | 282 | 69.5 | 852 | 9 | AY405848 Mus muscu |
| 11 | 219 | 53.3 | 830 | 4 | BG172919 602337353 |
| 12 | 216.2 | 53.3 | 767 | 5 | BX358434 BX358434 |
| 13 | 215 | 52.1 | 714 | 7 | CN259813 17006000 |
| 14 | 211.6 | 52.1 | 698 | 7 | CN259812 |
| 15 | 186.8 | 46.0 | 757 | 4 | BI454643 603170538 |
| 16 | 173 | 42.6 | 324 | 6 | CB306900 UI-CF-FNO |
| 17 | 166 | 40.9 | 686 | 2 | BB551556 BB551556 |
| 18 | 164 | 40.4 | 779 | 6 | CA311913 UI-CF-FNO |
| 19 | 119.2 | 29.4 | 917 | 2 | BE573890 603331875 |
| 20 | 118 | 29.1 | 487 | 7 | CN259818 17006000 |
| 21 | 108.8 | 24.6 | 702 | 6 | BY736335 |
| 22 | 99.6 | 26.5 | 827 | 7 | CV079354 ACBNCOURT |
| 23 | 70 | 17.2 | 604 | 5 | BX499180 DKFZP779B |
| 24 | 69 | 17.0 | 670 | 2 | BB666051 BB666051 |

| | | | | | | |
|----|------|------|------|---|----------|---------------------|
| 25 | 63 | 15.5 | 681 | 2 | BE741325 | BE741325 601594166 |
| 26 | 51 | 12.6 | 584 | 5 | BP255229 | BP255229 BP255229 |
| 27 | 48 | 11.8 | 583 | 5 | BP255264 | BP255264 BP255264 |
| 28 | 47.2 | 11.6 | 639 | 2 | BE381883 | BE381883 601272421 |
| 29 | 47 | 11.6 | 712 | 5 | BU471021 | BU471021 603364509 |
| 30 | 47 | 11.6 | 792 | 5 | BU458718 | BU458718 603367659 |
| 31 | 46 | 11.3 | 172 | 1 | AI370413 | AI370413 qv77d03.x |
| 32 | 42.2 | 10.4 | 932 | 7 | CR439118 | CR439118 CR439118 |
| 33 | 41.6 | 10.2 | 689 | 7 | CR424164 | CR424164 CR424164 |
| 34 | 41.6 | 10.2 | 882 | 7 | CF238625 | CF238625 ACBNCOURT |
| 35 | 41 | 10.1 | 419 | 5 | BY217767 | BY217767 BY217767 |
| 36 | 40 | 9.9 | 1101 | 9 | CNS0178M | AL107728 Drosophila |
| 37 | 38 | 9.4 | 549 | 7 | CN288086 | CN288086 170060328 |
| 38 | 38 | 9.3 | 603 | 6 | CB928916 | CB928916 ABA1_38 C |
| 39 | 37.6 | 9.3 | 395 | 2 | BE427973 | BE427973 MTD001-I. |
| 40 | 37.6 | 9.3 | 666 | 2 | AM212469 | AM212469 u089a12.x |
| 41 | 37.2 | 9.2 | 357 | 1 | AA821479 | AA821479 v59a10.r |
| 42 | 37.2 | 9.2 | 443 | 2 | BE982875 | BE982875 UI-M-CGDP |
| 43 | 37.2 | 9.2 | 499 | 2 | BE852674 | BE852674 uw26903.x |
| 44 | 37.2 | 9.2 | 592 | 2 | AW761877 | AW761877 uq26h05.y |
| 45 | 37.2 | 9.2 | 615 | 2 | BE334708 | BE334708 u862912.y |

ALIGNMENTS

RESULT 1
BU680630/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 595)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.researchgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Source
Location/Qualifiers
1..595
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-DUI-aaz-1-18-0-UI"
/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-CF-DUI is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGGTGTAGGC.

TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368

TAG_LIB=UI-CF-DUI

TAG_SEQ=GGGTGTAGGC"

ORIGIN

Query Match 99.3%; Score 403; DB 5; Length 595;
Best Local Similarity 99.3%; Pred. No. 8.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GTGAATGTGACTATATATGCGAGTCCAGANACCTTGCGGTGAGGCTCCCGATGTTTC 60
|||||
539 GTGAATGTGACTATATATGCGAGTCCAGACTTTCGGTGTAGGCTCCCGATGTTTC 480
|||||
61 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTC 120
|||||
479 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTC 420
|||||
121 TCCAAATACCAAGCTTTGAGCTGAACCTGTGAAGATGACCAATGAGTTGTCTGTGCTC 180
|||||
419 TCCAAATACCAAGCTTTGAGCTGAACCTGTGAAGATGACCAATGAGTTGTCTGTGCTC 360
|||||
181 TCAATATGTTACGATCAACAACATATCTCTGTATGATTTGAATAATGACATGGCAAGA 240
|||||
359 TCAATATGTTACGATCAACAACATATCTCTGTATGATTTGAATAATGACATGGCAAGA 300
|||||
241 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAAGCGAGTCACTACAGCTGTCTA 300
|||||
299 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAAGCGAGTCACTACAGCTGTCTA 240
|||||
301 AACTCAAAAGCTTCTCTGTGTCTCTTTCTTTTCCATCACTGAGGCACTTGTGCT 360
|||||
239 AACTCAAAAGCTTCTCTGTGTCTCTTTCTTTTCCATCACTGAGGCACTTGTGCT 180
|||||
361 CTCAGCCCTTACCTGATGCTAATATATGAGCTTGCGGCAAAAA 406
|||||
179 CTCAGCCCTTACCTGATGCTAATATATGAGCTTGCGGCAAAAA 134
|||||

RESULT 2
BX369964 925 bp mRNA linear EST 26-APR-2004
LOCUS BX369964 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION Clone CS0D1039Y21 5-PRIME, mRNA sequence.
ACCESSION BX369964
VERSION BX369964.1 GI:30449865
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 925)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr; Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 742.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0BAG030ZA11_CS02865_1&c=742.r
Location/Qualifiers

1..925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039Y21"
/cbase="PLACENTA COT 25-NORMALIZED"
/cbase_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 99.3%; Score 403; DB 5; Length 925;
Best Local Similarity 99.3%; Pred. No. 9.3e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GTGAATGTGACTATATATGCGAGTCCAGANACCTTGCGGTGAGGCTCCCGATGTTTC 60
|||||
140 GTGAATGTGACTATATATGCGAGTCCAGACTTTCGGTGTAGGCTCCCGATGTTTC 199
|||||
61 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTC 120
|||||
200 CCCGAGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTC 259
|||||
121 TCCAAATACCAAGCTTTGAGCTGAACCTGTGAAGATGACCAATGAGTTGTCTGTGCTC 180
|||||
260 TCCAAATACCAAGCTTTGAGCTGAACCTGTGAAGATGACCAATGAGTTGTCTGTGCTC 319
|||||
181 TCAATATGTTACGATCAACAACATATCTCTGTATGATTTGAATAATGACATGGCAAGA 240
|||||
320 TCAATATGTTACGATCAACAACATATCTCTGTATGATTTGAATAATGACATGGCAAGA 379
|||||
241 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAAGCGAGTCACTACAGCTGTCTA 300
|||||
380 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAAGCGAGTCACTACAGCTGTCTA 439
|||||
301 AACTCAAAAGCTTCTCTGTGTCTCTTTCTTTTCCATCACTGAGGCACTTGTGCT 360
|||||
440 AACTCAAAAGCTTCTCTGTGTCTCTTTCTTTTCCATCACTGAGGCACTTGTGCT 499
|||||
361 CTCAGCCCTTACCTGATGCTAATATATGAGCTTGCGGCAAAAA 406
|||||
500 CTCAGCCCTTACCTGATGCTAATATATGAGCTTGCGGCAAAAA 545
|||||

RESULT 3
CN259811 655 bp mRNA linear EST 16-MAY-2004
LOCUS CN259811
DEFINITION 17000600059341 GRN_PRENUEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259811
VERSION CN259811.1 GI:47276225
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 655)
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Genon Corporation

TITLE
JOURNAL
COMMENT

230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@erogen.com
 Insert Length: 655 Std Error: 0.00.
 Location/Qualifiers

FEATURES

source

1. .655
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_id="GRN PRENEU"
 /note="oligo dt primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic and mitogens."

ORIGIN

Query Match 98.9%; Score 401.4; DB 7; Length 655;
 Best Local Similarity 99.0%; Pred. No. 2.5e-108;
 Matches 402; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATAATGCGAGCTCAGANACCTTGGCGTGTGAGGCTCCCGCATGGTTC 60
 DB 136 GTGAATGTGACTATAATGCGAGCTCAGAGACCTTGGCGTGTGAGGCTCCCGCATGGTTC 195
 QY 61 CCCGAGCCCAAGTGTGCTGGGCACTCCCAAGTTGACAGGAGCAACTCTTCGGAAGTC 120
 DB 196 CCCGAGCCCAAGTGTGCTGGGCACTCCCAAGTTGACAGGAGCAACTCTTCGGAAGTC 255
 QY 121 TCCAAATACGAGCTTTGAGTGAAGTCTGAGAAATGACCAAGGTTGTCGTGCTC 180
 DB 256 TCCAAATACGAGCTTTGAGTGAAGTCTGAGAAATGACCAAGGTTGTCGTGCTC 315
 QY 181 TACAAATGTTACGATCAACAACACACTACTCTGTATGATTAATAATGACATTGGCCAAAGCA 240
 DB 316 TACAAATGTTACGATCAACAACACACTACTCTGTATGATTAATAATGACATTGGCCAAAGCA 375
 QY 241 ACAGGGGATATCAAAAGTGAAGATCGAGATCAAAAAGCGAGTCACTTACAGTCTCTA 300
 DB 376 ACAGGGGATATCAAAAGTGAAGATCGAGATCAAAAAGCGAGTCACTTACAGTCTCTA 435
 QY 301 AACCTCAAGGCTCTCTGTGTGCTCTCTCTTTCTTTGGCCATCAGCTGGGCACTTCTGGCT 360
 DB 436 AACCTCAAGGCTCTCTGTGTGCTCTCTCTTTCTTTGGCCATCAGCTGGGCACTTCTGGCT 495
 QY 361 CTCAGCCCTTACCTGATGTATTAATATGCTTGGCCACCAAAAA 406
 DB 496 CTCAGCCCTTACCTGATGTATTAATATGCTTGGCCACCAAAAA 541

RESULT 4

BM981657/c 751 bp mRNA linear EST 21-FEB-2003
 LOCUS BM981657
 DEFINITION UI-CF-EN1-adi-m-02-0-UI s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-adi-m-02-0-UI 3', mRNA sequence.

ACCESSION BM981657.1 GI:19604370
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548

COMMENT Contact: McCray, PB
 McCray Lab

University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171

Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing Arrayed by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 Polya=yes.

FEATURES

source

1. .751
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-adi-m-02-0-UI"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial
 Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_id="UI-CF-EN1"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: Ecor I; Site_2: Not I;
 UI-CF-EN1 is a normalized cDNA library containing the
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. First strand cDNA synthesis was primed with an
 oligo-dt primer containing a Not I site. Double stranded
 cDNA was ligated to an Ecor I adaptor, digested with Not
 I, and cloned directionally into pT73-Pac vector. The
 oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CTGCTCAGGT.
 TAG_TISSUE=human Lung Epithelial Cell lines untreated LPS
 6hr to LPS 24h
 TAG_LIB=UI-CF-EN1
 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 98.9%; Score 401.4; DB 5; Length 751;
 Best Local Similarity 99.0%; Pred. No. 2.6e-108;
 Matches 402; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATAATGCGAGCTCAGANACCTTGGCGTGTGAGGCTCCCGCATGGTTC 60
 DB 549 GTGAATGTGACTATAATGCGAGCTCAGAGACCTTGGCGTGTGAGGCTCCCGCATGGTTC 490
 QY 61 CCCGAGCCCAAGTGTGCTGGGCACTCCCAAGTTGACAGGAGCAACTTCTCGGAAGTC 120
 DB 489 CCCGAGCCCAAGTGTGCTGGGCACTCCCAAGTTGACAGGAGCAACTTCTCGGAAGTC 430
 QY 121 TCCAAATACGAGCTTTGAGTGAAGTCTGAGAAATGACCAATGAAAGTTGTGTGCTC 180
 DB 429 TCCAAATACGAGCTTTGAGTGAAGTCTGAGAAATGACCAATGAAAGTTGTGTGCTC 370
 QY 181 TACAAATGTTACGATCAACAACACACTACTCTGTATGATTAATAATGACATTGGCCAAAGCA 240
 DB 369 TACAAATGTTACGATCAACAACACACTACTCTGTATGATTAATAATGACATTGGCCAAAGCA 310
 QY 241 ACAGGGGATATCAAAAGTGAAGATCGAGATCAAAAAGCGAGTCACTTACAGTCTCTA 300
 DB 309 ACAGGGGATATCAAAAGTGAAGATCGAGATCAAAAAGCGAGTCACTTACAGTCTCTA 250
 QY 301 AACCTCAAGGCTCTCTGTGTGCTCTCTCTTTCTTTGGCCATCAGCTGGGCACTTCTGGCT 360
 DB 249 AACCTCAAGGCTCTCTGTGTGCTCTCTCTTTCTTTGGCCATCAGCTGGGCACTTCTGGCT 190

QY 361 CTCAGCCCTTACTGATGCTAATAATATATATGCTTGGCCACAAAAA 406
 DB 189 CTCAGCCCTTACTGATGCTAATAATATATATGCTTGGCCACAAAAA 144

RESULT 5
 CR603772 2431 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CSODI039Yg21 of Placenta Cot 25-normalized
 DEFINITION of Homo sapiens (human).
 ACCESSION CR603772.1 GI:50484579
 VERSION CR603772.1
 KEYWORDS HTC; CNSLT; cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2431)
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 2431)
 REFERENCE 2 (bases 1 to 2431)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Direct Submission
 PUBLISHED (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 FEATURES
 source location/Qualifiers
 1..2431
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI039Yg21"
 /tissue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN
 Query Match 98.9%; Score 401.4; DB 3; Length 2431;
 Best Local Similarity 99.0%; Pred. No. 3.7e-108;
 Matches 402; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGAATGTGAGCTATATATGCTCAGAGCTTCAGAACCTTGGCTGTGAGGCTCCCGATGGTTC 60
 DB 394 GTGAATGTGAGCTATATATGCTCAGAGCTTCAGAGACCTTGGCTGTGAGGCTCCCGATGGTTC 453

QY 61 CCCGAGCCCAAGTGTCTGGGCAATCCAAAGTTGACAGGAGGCCAATCTTCGGAATGC 120
 DB 454 CCCGAGCCCAAGTGTCTGGGCAATCCAAAGTTGACAGGAGGCCAATCTTCGGAATGC 513

QY 121 TCCAAATACAGCTTGAAGTGAAGCTGTGAATGTGACATGAAGGTTGTGTGTGCTC 180
 DB 514 TCCAAATACAGCTTGAAGTGAAGCTGTGAATGTGACATGAAGGTTGTGTGTGCTC 573

QY 181 TACAAATGTAGATCAACAACATATCTCTGTATGATTTGAAATGACATTTGCCAAGA 240
 DB 574 TACAAATGTAGATCAACAACATATCTCTGTATGATTTGAAATGACATTTGCCAAGA 633

QY 241 ACAAGGAGTATCAAAAGTGAAGAGATCGAAGATCAAAAGCGAGATCACTTACAGTGTCTA 300
 DB 634 ACAAGGAGTATCAAAAGTGAAGAGATCGAAGATCAAAAGCGAGATCACTTACAGTGTCTA 693

QY 301 AACTCAAAGGCTTCTGTGTGTCTCTTCTTCTTTCATGATGAGTGGGCACTTGTGCT 360
 DB 694 AACTCAAAGGCTTCTGTGTGTCTCTTCTTCTTTCATGATGAGTGGGCACTTGTGCT 753

QY 361 CTCAGCCCTTACTGATGCTAATAATATATATGCTTGGCCACAAAAA 406
 DB 754 CTCAGCCCTTACTGATGCTAATAATATATATGCTTGGCCACAAAAA 799

RESULT 6
 AY405846 849 bp DNA linear GSS 12-DEC-2003
 LOCUS Homo sapiens HCM2360 gene, VIRTUAL TRANSCRIPT, partial sequence.
 DEFINITION genomic survey sequence.
 ACCESSION AY405846.1 GI:39761820
 VERSION AY405846.1
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 849)
 AUTHORS Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snijsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBLISHED 14671302
 REFERENCE 2 (bases 1 to 849)
 AUTHORS Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snijsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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 Best Local Similarity 99.2%; Pred. No. 4.2e-103;
 Matches 384; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGAGCTATATATGCTCAGAGCTTCAGAACCTTGGCTGTGAGGCTCCCGATGGTTC 60
 DB 463 GTGAATGTGAGCTATATATGCTCAGAGCTTCAGAGACCTTGGCTGTGAGGCTCCCGATGGTTC 522

QY 61 CCCGAGCCCAAGTGTCTGGGCAATCCAAAGTTGACAGGAGGCCAATCTTCGGAATGC 120
 DB 523 CCCGAGCCCAAGTGTCTGGGCAATCCAAAGTTGACAGGAGGCCAATCTTCGGAATGC 582

QY 121 TCCAAATACAGCTTGAAGTGAAGCTGTGAATGTGACATGAAGGTTGTGTGTGCTC 180
 DB 583 TCCAAATACAGCTTGAAGTGAAGCTGTGAATGTGACATGAAGGTTGTGTGTGCTC 642

QY 181 TACAAATGTAGATCAACAACATATCTCTGTATGATTTGAAATGACATTTGCCAAGA 240
 DB 643 TACAAATGTAGATCAACAACATATCTCTGTATGATTTGAAATGACATTTGCCAAGA 702

QY 241 ACAAGGAGTATCAAAAGTGAAGAGATCGAAGATCAAAAGCGAGATCACTTACAGTGTCTA 300
 DB 703 ACAAGGAGTATCAAAAGTGAAGAGATCGAAGATCAAAAGCGAGATCACTTACAGTGTCTA 762

QY 301 AACTCAAAGGCTTCTGTGTGTCTCTTCTTCTTTCATGATGAGTGGGCACTTGTGCT 360
 DB 763 AACTCAAAGGCTTCTGTGTGTCTCTTCTTCTTTCATGATGAGTGGGCACTTGTGCT 822

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QY      361 CTCAGCCCTTACCTGATGCTAANATAA 387
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      823 CTCAGCCCTTACCTGATGCTAANATAA 849

RESULT 7
LOCUS   AY405847
DEFINITION Pan troglodytes HCM2360 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY405847
VERSION   AY405847.1 GI:39761821
KEYWORDS GSS.
SOURCE    Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes

REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
          1 (bases 1 to 849)
          Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,
          Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
          Perrier, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, D.J.,
          Adams, M.D. and Cargill, M.
          Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene trios
          Science 302 (5652), 1960-1963 (2003)

JOURNAL
PUBMED   14671302
REFERENCE 2 (bases 1 to 849)
AUTHORS  Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,
          Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
          Perrier, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, D.J.,
          Adams, M.D. and Cargill, M.
          Direct Submission
          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
          This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
          Location/Qualifiers
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Matches 381; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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      61 CCCAGGCCACAGTGTCTGTGGCATCCCAAGTTGACAGGAGCACTTCTCGAAGTC 120
      523 CCCAGGCCACAGTGTCTGTGGCATCCCAAGTTGACAGGAGCACTTCTCGAAGTC 582
      121 TCCAAATACCAAGCTTTGAGCTGAAGTCTGAGATGTGACCATGAAGTGTGTCTGTGCTC 180
      583 TCCAAATACCAAGCTTTGAGCTGAAGTCTGAGATGTGACCATGAAGTGTGTCTGTGCTC 642
      181 TACAATGTTACGATCAACAACACATATCTCTGTATATGTAAGAAATGACATTTGCCAAGCA 240
      643 TACAATGTTACGATCAACAACACATATCTCTGTATATGTAAGAAATGACATTTGCCAAGCA 702
      241 ACAGGGGATATCAAAAGTGAAGATGAGATGAGATCAAAAGGCGAGTCACTTACAGTCTCTA 300
      703 ACAGGGGATATCAAAAGTGAAGATGAGATGAGATCAAAAGGCGAGTCACTTACAGTCTCTA 762
      301 AACTCAAAAGCTTCTGTGTGTCTCTTTCTTTTCCATCAAGCTGGGCACTTCTGCGCT 360
      763 AACTCAAAAGCTTCTGTGTGTCTCTTTCTTTTCCATCAAGCTGGGCACTTCTGCGCT 822

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QY      361 CTCAGCCCTTACCTGATGCTAANATAA 387
      |||
      823 CTCAGCCCTTACCTGATGCTAANATAA 849

RESULT 8
LOCUS   AI799522/c
DEFINITION tr49p02.x1 NCI_CGAP_Ov23 Homo sapiens cDNA IMAGE:2221611 3',
ACCESSION AI799522
VERSION   AI799522
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 443)
          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          CDNA Library Preparation: Life Technologies, Inc.
          CDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/biopr/image/image.html
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          High quality sequence stop: 418.
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                           /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1_Salt;
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                           Average insert size 1.35 kb. Tumor types include: mixed
                           Mullerian tumor, papillary serous, clear cell, spindle
                           cell. All are primary tumors, metastasis positive. Life
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Query Match      77.6%; Score 315; DB 1; Length 443;
Best Local Similarity 99.4%; Pred. No. 1.3e-82;
Matches 315; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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      443 AGTTGACCAAGGAGCAACTTCTCGGAAGTCTCCAAATACCACTTGAAGCTGAACCTCTGA 384
      150 GAATGACCAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 209
      383 GAATGACCAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 324
      210 CTGTATGATTAAGTAATGACATTTGCCAAGCAACAGGGTATCAAAAGTGAAGATCGGA 269
      323 CTGTATGATTAAGTAATGACATTTGCCAAGCAACAGGGTATCAAAAGTGAAGATCGGA 264
      270 GATCAAAAGGCGAGTCACTTACCTGTAAACTCAAAAGGCTTCTGTGTGTCTCTTC 329
      263 GATCAAAAGGCGAGTCACTTACCTGTAAACTCAAAAGGCTTCTGTGTGTCTCTTC 204
      330 TTTCTTTGGCATCAGCTGGGCACTTCTGCGCTCTCAGCCCTTACCTGATGCTAANATAATG 389

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Db      203 TTTCTTTGCCATGACGTGGGCACTTCTGCTCTGACCCCTTACCTGATGCTAAATTAATG 144
QY      390 TGCCTTGGCCACAAAAA 406
      143 TGCCTTGGCCACAAAAA 127

RESULT 9
LOCUS   AQ479831/c
DEFINITION RPCT-11-269N1.TV RPCT-11 Homo sapiens genomic clone RPCT-11-269N1,
ACCESSION AQ479831
VERSION   AQ479831
KEYWORDS  GS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 436)
AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
          Venter,J.C.
TITLE      Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready
JOURNAL   Map Building
COMMENT   Unpublished (1997)
          Contact: Shaying Zhao, William Nierman, Mark Adams
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: hbe@tigr.org
          Clones are derived from the human BAC library RPCT-11. For BAC
          library availability, please contact Pieter de Jong
          (pieter@edj.med.buffalo.edu). Clones may be purchased from
          BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
          Research Genet cs (info@resgen.com). BAC end search page:
          http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
          Seq primer: T7
          Class: BAC ends.
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Matches 336; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY      40 TGTGAGGCTCCCGAGTGTCCCGCCGACGAGTGTCTGGGCAATCCCAAGTTGACG 99
Db      435 TGTGAGGCTCCCTTAATGGGTCTCTCAGCCGACGAGTATGAAGATCCCTAGTTGACG 376

QY      100 GGAGCCAATCTTCGGAAGTCTCCAAATACAGCTTTGAGTGAATCTGAGATGTGACC 159
Db      375 GGAGCCAATCTTCGGAAGTCTCCAAATACAGCTTTGAGTGAATCTGAGATGTGACC 316

QY      160 ATGAAGTTGTGTCTGTGCTCAAAATGTTACGATCAACAACATATCTCTGATGATT 219
Db      315 ATTAAGTTGTGTGTGTGCTCTCAATGTTACGATCAACAACATATCTCTGATGATT 256

QY      220 GAAATGACATTTGCCAAGCAAGGGGATATTAAGTGACAGAAATCGAGATCAAAAG 279
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QY      280 CGAGTCACTTACAGCTGTCTAAACTCAAGGCTTCTGTGTGCTCTTTCTTTTGGC 339
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QY      340 ATCAGCTGGGCACTTTCCTCTCAGCCCTTACCTGATGCTAANAATATGCGCTGGCC 399
Db      136 ATCAGCTGGGCACTTTCCTCTTGTGCCCTTACCTGATGCTAANAATATGACTGGCC 77

QY      400 ACAAAA 405
Db      76 ACAAAA 71

RESULT 10
LOCUS   AY405848
DEFINITION Mus musculus HCM2360 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY405848
VERSION   AY405848
KEYWORDS  GS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 852)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
          Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene trios
          Science 302 (5652), 1960-1963 (2003)
          14671302
JOURNAL   PUBMED
REFERENCE 2 (bases 1 to 852)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
          Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Direct Submission
          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
          This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
FEATURES
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Matches 328; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

QY      2 TGAATGTGACATATATGCGACGCTCAGANACCTTGCAGTGAAGCTCCCGATGTTCC 61
Db      464 TAAATGTGACATATATGCGACGCTCAGAGAGTTTACGCTCGAGGCTCTCGGTGTTCC 523

QY      62 CCAGCCCAAGTGTCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTCT 121
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QY      122 CCAATACAGCTTTGAGCTGAACTGTGAATGTGACATGAAGTTGTGTGTGCTCT 181
Db      584 CGAACAACAGCTTTGAGTTGAATCTGGAATGTGACATGAAGTCTGATCTGTGCTCT 643

QY      182 ACAATGTACATGAACAACATATCTCTGATGATTTGAAATGACATTTGCCAAGCAA 241
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| QY | 242 | CAGGGGAGATCAAAAGTGCAGAGATCGAGATCAAAAGGCGAGTCACTACGACTGCTAA | 301 |
| DB | 704 | CCGGGACATCAAAATGCAGATTAGAGCTCAAAAGCGAGTCACTGCACTGCTCA | 763 |
| QY | 302 | ACTCAAAAGCTTCTGTGTG--TCTCTCTTTTCCATTCAGCTGGGCACTTTCG | 358 |
| DB | 764 | ACTCGGGGCTTCCCCGCTGTGTTTTCTTCTGCTTTCGGCTGGCTGGGCGCTCTAT | 823 |
| QY | 359 | CTCTCAGCCCTTACCTGATGCTAAATAA | 387 |
| DB | 824 | CTCTCTCTGTTCCTGATGCTAAGATGA | 852 |
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| ACCESSION | BG172919 | | |
| VERSION | BG172919.1 | GI:12679609 | |
| KEYWORDS | EST. | | |
| SOURCE | Mus musculus (house mouse) | | |
| ORGANISM | Mus musculus | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| AUTHORS | 1 (bases 1 to 830) | | |
| TITLE | NIH-MGC http://mgc.nci.nih.gov/ . | | |
| JOURNAL | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| COMMENT | Unpublished (1999) | | |
| | Contact: Robert Strausberg, Ph.D. | | |
| | Email: cgabbs-remail.nih.gov | | |
| | Tissue Procurement: Gilbert Smith, Ph.D. | | |
| | cDNA Library Preparation: Life Technologies, Inc. | | |
| | cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) | | |
| | DNA Sequencing by: Incyte Genomics, Inc. | | |
| | Clone distribution: MGC clone distribution information can be | | |
| | found through the I.M.A.G.E. Consortium/LNL at: | | |
| | http://image.llnl.gov | | |
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| Query Match | 53.9% | Score 219; | DB 4; Length 830; |
| Best Local Similarity | 89.7%; | Pred. No. 6.8e-54; | |
| Matches 234; | Conservative 0; | Mismatches 27; | Indels 0; Gaps 0; |
| QY | 2 | TGAATGTGACTATTAATCCAGAGTCAGANACCTTGCGGTGATGAGGCTCCCGATGGTTC | 61 |
| DB | 98 | TAAATGTGACTATTAATCCAGATTCAGAGATTTACGCTGCGAGGCTCTCGATGTTCC | 157 |
| QY | 62 | CCAGGCCCAAGTGTCTGGGCATCCCAAGTTGACCAAGGACCAATCTTCGAAAGTCT | 121 |
| DB | 158 | CCGAGCCCAAGTGGCTGGGCATCTCAAGTCGACCAAGGACCAATTTCTCAAGAGTCT | 217 |
| QY | 122 | CCAAATACAGATTTGAGCTGAATCTTGAGATATGACCAATGAAGTTGTGTCTGCTCT | 181 |
| DB | 218 | CCAAACACAGCTTTGAGTTGAATCTTGAGAAATGACATAGAAGTGTGATCTGTGCTCT | 277 |

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|-----------------------|------------------|---------------------------------------------------------------|-------------------|
| OY | 182 | ACATGTTAGATGAACAACAACATCCCGTGTATGATTGAATTAAGAATTCGCAAAAGCAA | 241 |
| Dd | 278 | ACATGTGCACATTAACAACAACATCTCTGTATGATTGAATAAAGCATTTGCCAAAAGCAA | 337 |
| OY | 242 | CAGGGGNTATCAAAAGTGACAG | 262 |
| Dd | 338 | CCGGGACATCAAAAGTGACAG | 358 |
| | | | |
| RESULT 12 | | | |
| BX358434 | | | |
| LOCUS | | | |
| DEFINITION | | | |
| ACCESSION | | | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| COMMENT | | | |
| | | | |
| FEATURES | | | |
| SOURCE | | | |
| | | | |
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| Best Local Similarity | 79.9%; | Pred. No. 4.5e-53; | |
| Matches 215; | Conservative 36; | Mismatches 17; | Indels 1; Gaps 1; |
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| Dd | 497 | KTGAAATGTGACATATATKCAACTCYWGAACCTTTTCGGTGTAGGCTCCCGATGTTCT | 556 |
| OY | 61 | CCCCAGCCCAAGTGTGCTGGGATCCCAGATTGACACAGGAGGACCACCTTCGGGAAGTC | 120 |
| Dd | 557 | CCCCAGCCCAAGTGTGCTGGGATCCCAGATTGACACAGGAGGACCACCTTTTAAAGTC | 616 |
| OY | 121 | TCCAATACGACGTTTAGAGCTGAACCTCTGAGATGTGACATGAAAGTTGTGTGTGCTC | 180 |
| Dd | 617 | YCVAATATYAGATTGAGCYKAWCTCTGAGAAAGTTACVWTGAAGGKTGTGTGTGYYY | 676 |
| OY | 181 | TACAATGTTACGATCAACAACATATCTCTGTATGATATGAATAATGACATTCGCAAAAGCA | 240 |
| Dd | 677 | TACAATGTTMYGAVCAACMACACACCCCTGYATGADTGAATAATGATATTCGCAAAAGCA | 736 |

DNA Sequencing by: Incyte Genomics, Inc
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 742.

ORIGIN

| | | | | |
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| Qy | 2 | GAAGTGTGGA | CTATATATG | CAGCTAG | AGNAA | CTTTGGG | GTGTAG | AGGCTCC | CCCAATGG | TTCC | 61 |
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| Dd | 535 | TAAATGTGACT | TAATATG | CCAGTTCA | GAGGTTT | TACGTGC | GAGGCTC | CTCGGGT | GTTC | 594 | |
| Qy | 62 | CCGAGCCCA | CAGTGTG | CTGGGCAT | CCCAAGTTG | AACAGGAG | GCACAA | CTTCTCG | GAAGTCT | 121 | |
| Dd | 595 | CCGAGCCCA | CAGTGTG | CTGGGCAT | CTCAAGT | GCA | CCAGGAG | GCACAA | TTTCTC | GAAGTCT | 654 |
| Qy | 122 | CCAAATAC | CAGCTTT | GAGCTGA | AACTCTG | GAAGATG | GAACAT | GAAGG | TGTGTCT | GTCTCT | 181 |
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| Qy | 182 | ACAATCTTA | CGATCA | ACAA | CACAT | ACTCTCT | GTATGA | TTGAAA | 224 | | |
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Search completed: May 31, 2005, 00:10:55
Job time : 1582.08 secs

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| ORIGIN | |
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Best Local Similarity 100.0%; Pred. No. 2.7e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGAAGGACGAGGAGCTCCAGCTCAGCAGTACCAGATGCGTGGGAACTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGAGATGCTCTTCTGGAGCATTAATAGCATCATTAATTTGAGCT 120
DB 61 ATGGCTTCCCTGGGAGATGCTCTTCTGGAGCATTAATAGCATCATTAATTTGAGCT 120
QY 121 GGAAGCAATTGCACTCATCTATGCTTTGTTGTTTTCAGGAGACATCTCCATCAGAGTCACT 180
DB 121 GGAAGCAATTGCACTCATCTATGCTTTGTTGTTTTCAGGAGACATCTCCATCAGAGTCACT 180
QY 181 ACTGTGCGCTCAGCTGGAACAATGTTGGGAGAGATGAAATCTGAGCTGCACTTTTGAACCT 240
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QY 241 GACATCAAACTTTCTGATATCGTATACAAATGCTGAGAAAGTTTAAAGCTTGTGTC 300
DB 241 GACATCAAACTTTCTGATATCGTATACAAATGCTGAGAAAGTTTAAAGCTTGTGTC 300
QY 301 CATGAGTTCAAGAGGCAAAAGATGAGCTGTGAGACAGAGATCAAAATGTTTCAGAGCCCG 360
DB 301 CATGAGTTCAAGAGGCAAAAGATGAGCTGTGAGACAGAGATCAAAATGTTTCAGAGCCCG 360
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DB 361 ACAGCAGTGTGTTGCTGATCAAGATGAGTGGCAATGCTCTTTGGGCTGAAAAACGTG 420
QY 421 CAACTCAGAGATGCTGGACCTTACAAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATGCTGGACCTTACAAATGTTATATCATCACT 462

RESULT 2
AX375858 1065 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 5 from Patent WO0194641.
DEFINITION AX375858
ACCESSION AX375858
VERSION AX375858.1 GI:19170330
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Ople, E., McLachlan, K. and Heard, C.
TITLES Gene targets and ligands that bind thereto for treatment and
diagnosis of ovarian carcinomas
JOURNAL Patent: WO 0194641-A 5 13-DEC-2001;
Idex Pharmaceuticals Corporation (US)
FEATURES
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ORIGIN
Query Match 100.0%; Score 462; DB 6; Length 1065;
Best Local Similarity 100.0%; Pred. No. 3e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGAGGAGCTCCAGCTCAGCAGTACCAGATGCGTGGGAACTCCCGAGCC 60
DB 12 GGAAGGACGAGGAGCTCCAGCTCAGCAGTACCAGATGCGTGGGAACTCCCGAGCC 71
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DB 72 ATGGCTTCCCTGGGAGATGCTCTTCTGGAGCATTAATAGCATCATTAATTTGAGCT 131
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DB 132 GGAAGCAATTGCACTCATCTATGCTTTGTTGTTTTCAGGAGACATCTCCATCAGAGTCACT 191
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DB 252 GACATCAAACTTTCTGATATCGTATACAAATGCTGAGAAAGTTTAAAGCTTGTGTC 311
QY 301 CATGAGTTCAAGAGGCAAAAGATGAGCTGTGAGACAGAGATCAAAATGTTTCAGAGCCCG 360
DB 312 CATGAGTTCAAGAGGCAAAAGATGAGCTGTGAGACAGAGATCAAAATGTTTCAGAGCCCG 371
QY 361 ACAGCAGTGTGTTGCTGATCAAGTGAATGTTGGCAATGCTCTTTGGGCTGAAAAACGTG 420
DB 372 ACAGCAGTGTGTTGCTGATCAAGTGAATGTTGGCAATGCTCTTTGGGCTGAAAAACGTG 431
QY 421 CAACTCAGAGATGCTGGACCTTACAAATGTTATATCATCACT 462
DB 432 CAACTCAGAGATGCTGGACCTTACAAATGTTATATCATCACT 473

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RESULT 3
AY346100 1070 bp mRNA linear PRI 09-SEP-2003
LOCUS Homo sapiens T cell costimulatory molecule B7x mRNA, complete cds.
DEFINITION AY346100
ACCESSION AY346100
VERSION AY346100.1 GI:33638210
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1070)
AUTHORS Zang, X., Locke, P., Kim, J., Murphy, K., Waltz, R. and Allison, J. P.
TITLES B7x: A widely expressed B7 family member that inhibits T cell
activation
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (18), 10388-10392 (2003)
MEDLINE 12920180
PUBMED 12920180
REFERENCE 2 (bases 1 to 1070)
AUTHORS Zang, X. and Allison, J. P.
TITLES Direct Submission
JOURNAL Submitted (19-JUN-2003) Howard Hughes Medical Institute, Department
of Molecular and Cell Biology, Cancer Research Laboratory,
University of California at Berkeley, LSA415, Berkeley, CA 94720,
USA

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FEATURES

source

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ORIGIN
Query Match 100.0%; Score 462; DB 9; Length 1070;
Best Local Similarity 100.0%; Pred. No. 3e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 ACAGCAGTGTGCTGATCAAGTATGATGGCAATGCCCTTTGGCGCTGAAGAAAGCTG 420
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DB 421 CAACTCAGAGATGCTGGACCTCAAAATGTTATATCATCACT 462

RESULT 4
LOCUS CO875680 1658 bp DNA linear PAT 27-SEP-2004
DEFINITION Sequence 3 from Patent EPI445317.
ACCESSION CO875680
VERSION CO875680.1 GI:52748533

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,
Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.

TITLE
JOURNAL Compositions and methods for the diagnosis and treatment of tumor
Patent: EP 145317-A 3 11-AUG-2004;

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"

ORIGIN
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Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGGAGATGGAAATCCGAGCTGCACCTTTGAACCT 240
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QY 241 GACATCAAACTTTCTGATATCGTATACAAATGAGCTGAGAGAGAGTGTATTTAGGCTTGCT 300
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DB 361 ACAGCAGTGTGCTGATCAAGTATGATGGCAATGCCCTTTGGCGCTGAAGAAAGCTG 420
QY 421 CAACTCAGAGATGCTGGACCTCAAAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATGCTGGACCTCAAAATGTTATATCATCACT 462

RESULT 5
LOCUS AR252569 1658 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 290 from patent US 6478825.
ACCESSION AR252569
VERSION AR252569.1 GI:27300477

KEYWORDS
SOURCE Unknown.

ORGANISM
Unclassified.

REFERENCE
1 (bases 1 to 1658)
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.

TITLE
JOURNAL Implant, method of making same and use of the implant for the
treatment of bone defects
Patent: US 6478825-A 290 12-NOV-2002;

FEATURES
Location/Qualifiers
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/organism="unknown"

ORIGIN
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Query Match 100.0%; Score 462; DB 6; Length 1658;
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Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 GGAACAATTGCACTCATCATTTGGCTTGGTATTTTCAGGGAGACATCCCATCAGTCACT 180
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QY 421 CAACCTCAGATGCTGGGACCTTAAATGTTATATCATCACT 462
Db 421 CAACCTCAGATGCTGGGACCTTAAATGTTATATCATCACT 462

RESULT 6
AX092328
LOCUS AX092328 1658 bp DNA linear PAT 23-MAR-2001
DEFINITION Sequence 59 from Patent WO0116318.
ACCESSION AX092328
VERSION AX092328.1 GI:13444478
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
Baker, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 59 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 ACAGCAGTGTGCTGATCAAGTATGATGGCAATGCTCTTTGGCGCTGAAGAAACGTG 420
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QY 421 CAACCTCAGATGCTGGGACCTTAAATGTTATATCATCACT 462
Db 421 CAACCTCAGATGCTGGGACCTTAAATGTTATATCATCACT 462

RESULT 7
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LOCUS AX376150 1658 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 217 from Patent WO0168848.
ACCESSION AX376150
VERSION AX376150.1 GI:19170467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 217 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
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Db 361 ACAGCAGTGTGCTGATCAAGTATGATGGCAATGCTCTTTGGCGCTGAAGAAACGTG 420
QY 421 CAACCTCAGATGCTGGGACCTTAAATGTTATATCATCACT 462
Db 421 CAACCTCAGATGCTGGGACCTTAAATGTTATATCATCACT 462

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LOCUS AX395215 1658 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 3 from Patent WO0216429.
ACCESSION AX395215
VERSION AX395215.1 GI:21066246
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,

Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216429-A 3 28-FEB-2002;
Genentech, Inc. (US)
FEATURES
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DB 421 CAACTCAGAGATGCTGGACCTTCAAAATGTTATATCACT 462
RESULT 9
AX403403 1658 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 290 from Patent WO0073454.
AX403403
VERSION AX403403.1 GI:21436923
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ahkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Bacon, D.,
Ferrara, N., Gerber, H., Gerltsen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kijavini, I., Napier, M.A., Pan, J.,
Peon, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
TITLE Secretd and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 290 07-DEC-2000;
Genentech Inc. (US)
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 3.1e-133;
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QY 361 ACAGCAGTGTGTTCTGATCAAGATAGTGGCAATGCTCTTGGCGGTGAAGAAACGTG 420
DB 361 ACAGCAGTGTGTTCTGATCAAGATAGTGGCAATGCTCTTGGCGGTGAAGAAACGTG 420
QY 421 CAACTCAGAGATGCTGGACCTTCAAAATGTTATATCACT 462
DB 421 CAACTCAGAGATGCTGGACCTTCAAAATGTTATATCACT 462
RESULT 10
AX468680 1658 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 4 from Patent WO0216581.
AX468680
VERSION AX468680.1 GI:21901458
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Gao, W.O., Polakis, P., Shou, J., Smith, V., Soriano, R., Williams, P.M.,
Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216581-A 4 28-FEB-2002;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GGAAGCGAGCGGCGAGCTCCACTCAGCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
QY 61 ATGGCTTCCCTGGGGGAGATCTCTTGAGGCAATATTAGCATCATTTATCTGGCT 120

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      361  ACAGCAGTGTTCCTGATCAAGTATGATTTGGCAATGCTCTTTCGCGCTGAAAAACGTG 420
      361  ACAGCAGTGTTCCTGATCAAGTATGATTTGGCAATGCTCTTTCGCGCTGAAAAACGTG 420
      421  CAACCTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462
      421  CAACCTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462

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RESULT 11
 AY358352 1658 bp mRNA linear PRI 03-OCT-2003
 LOCUS Homo sapiens clone DNAS9610 B7h.5 (UN0659) mRNA, complete cds.
 DEFINITION AY358352.1 GI:37181828
 ACCESSION AY358352.1
 VERSION FLI_CDNA.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,

TITLE
 JOURNAL PUBMED 12975309 2 (bases 1 to 1658)
 AUTHORS Clark,H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
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 1. 1658
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DNAS9610"
 1. 1658
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 61. 909
 /locus_tag="UN0659"
 /note="PRO1291"
 /codon_start=1
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 /protein_id="AA08718.1"

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/db_xref="GI:37181829"
/translation="MASLGGQLFMSIISIIILAGALILIGFGISGRHSITVTVAS
AGNIGEDILISCTEPEPDIKLSIDIVQMLKEVLGI VHEFKEXKDELSQDEMFGRFTA
VPAQDVIVGNASLRLKNVQLDADAGYKCYIITSKKGKANALEYKGAFSMEVANDYN
ASSETTRCEAPRWRPPQTVWASQVDSQKANSSEVSNFSPEINSEVMTKIVSYLVNVT
INMTYSCTIENDIAKATQDIYVTSERSHLQULNSKASLCVSSPFAISMALLPLS
PYLMK"
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Query Match 100.0%; Score 462; DB 9; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 3, 1e-133;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      1  GGAGGACGCGGACGCTCCACTCAGCAGTACCCAGATACGCTGGAACTTCCAGCC 60
      1  GGAGGACGCGGACGCTCCACTCAGCAGTACCCAGATACGCTGGAACTTCCAGCC 60
      61  ATGGCTCCCTGGGGGAGATCCCTCTTCGAGACATATTAAGATATCATTTATTCGCT 120
      61  ATGGCTCCCTGGGGGAGATCCCTCTTCGAGACATATTAAGATATCATTTATTCGCT 120
      121  GGAGCAATTCGACCTCATCTATTCGTTGATTTTCAGGAGACACTCCATCCAGTCACT 180
      121  GGAGCAATTCGACCTCATCTATTCGTTGATTTTCAGGAGACACTCCATCCAGTCACT 180
      181  ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGACCTTTGAACCT 240
      181  ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGACCTTTGAACCT 240
      241  GACATCAAACTTTCTGATATCGTATACATAGGCTGAAGAACTTTTACGCTTGGTC 300
      241  GACATCAAACTTTCTGATATCGTATACATAGGCTGAAGAACTTTTACGCTTGGTC 300
      301  CATGAGTTCAAGAAAGCAAGATGAGCTGTGGAGACAGATGAATGTTTCAGAGGCGG 360
      301  CATGAGTTCAAGAAAGCAAGATGAGCTGTGGAGACAGATGAATGTTTCAGAGGCGG 360
      361  ACAGCAGTGTTCCTGATCAAGTATGATTTGGCAATGCTCTTTCGCGCTGAAAAACGTG 420
      361  ACAGCAGTGTTCCTGATCAAGTATGATTTGGCAATGCTCTTTCGCGCTGAAAAACGTG 420

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RESULT 12
 CQ412191 1965 bp DNA linear PAT 23-JAN-2004
 LOCUS CQ412191
 DEFINITION Sequence 19262 from Patent WO0170979.
 ACCESSION CQ412191
 VERSION CQ412191.1 GI:41319972
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Lee,J. and Lillie,J.
 TITLE Agents, compositions, kits, and method for identification,
 assessment, prevention, and therapy of ovarian cancer
 Patent: WO 0170979-A 19262 27-SEP-2001;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES
 source
 1. 1965
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 462; DB 6; Length 1965;
 Best Local Similarity 100.0%; Pred. No. 3, 2e-133;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGGGAGCTCCAGTACGAGTACCCAGATAGCTGGGAACTTCCCGACGC 60
DB 20 GGAAGGACGGGAGCTCCAGTACGAGTACCCAGATAGCTGGGAACTTCCCGACGC 79
QY 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGGAGCAATAATTAGCATCATTAATTTGGCT 120
DB 80 ATGGCTTCCCTGGGGGAGATCTCTTCTGGAGCAATAATTAGCATCATTAATTTGGCT 139
QY 121 GGAAGCAATTGCACTCATCATTTGGCTTTGGATTTCAGGGAACAATCCATCAAGTCACT 180
DB 140 GGAAGCAATTGCACTCATCATTTGGCTTTGGATTTCAGGGAACAATCCATCAAGTCACT 199
QY 181 ACTGTGGCTCAGCTGGGAAATTTGGGGAGATGGAAATCTGAGCTGCACTTTTGAACCT 240
DB 200 ACTGTGGCTCAGCTGGGAAATTTGGGGAGATGGAAATCTGAGCTGCACTTTTGAACCT 259
QY 241 GACATCAAACTTTCTGATATCGTATCAAAATGCTGAAGAAAGTGTTTTAAAGCTTGGTC 300
DB 260 GACATCAAACTTTCTGATATCGTATCAAAATGCTGAAGAAAGTGTTTTAAAGCTTGGTC 319
QY 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGGAGAGATGAATGTTCAAGAGCCGG 360
DB 320 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGGAGAGATGAATGTTCAAGAGCCGG 379
QY 361 ACAGAGTGTGTTGCTGATCAAGATAGTGTGGCAATGCTCTTTGGCGCTGAAAACGTC 420
DB 380 ACAGAGTGTGTTGCTGATCAAGATAGTGTGGCAATGCTCTTTGGCGCTGAAAACGTC 439
QY 421 CAACTCAGAGATGCTGGCACTTAATGTTATATCATCACT 462
DB 440 CAACTCAGAGATGCTGGCACTTAATGTTATATCATCACT 481

RESULT 13
AX375860 2626 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 7 from Patent WO0194641.
DEFINITION AX375860
ACCESSION AX375860.1 GI:19170332
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ople,E., McIachlan,K. and Heard,C.
TITLE Gene targets and ligands that bind thereto for treatment and
diagnosis of ovarian carcinomas
JOURNAL Patent: WO 0194641-A 7 13-DEC-2001;
Idex Pharmaceuticals Corporation (US)
FEATURES
source 1. .2626
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 462; DB 6; Length 2626;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGGGAGCTCCAGTACGAGTACCCAGATAGCTGGGAACTTCCCGACGC 60
DB 1 GGAAGGACGGGAGCTCCAGTACGAGTACCCAGATAGCTGGGAACTTCCCGACGC 60
QY 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGGAGCAATAATTAGCATCATTAATTTGGCT 120
DB 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGGAGCAATAATTAGCATCATTAATTTGGCT 120
QY 121 GGAAGCAATTGCACTCATCATTTGGCTTTGGATTTCAGGGAACAATCCATCAAGTCACT 180
DB 121 GGAAGCAATTGCACTCATCATTTGGCTTTGGATTTCAGGGAACAATCCATCAAGTCACT 180

QY 181 ACTGTGGCTCAGCTGGGAAATTTGGGGAGATGGAAATCTGAGCTGCACTTTGAACCT 240
DB 181 ACTGTGGCTCAGCTGGGAAATTTGGGGAGATGGAAATCTGAGCTGCACTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATCAAAATGCTGAAGAAAGTGTTTTAAAGCTTGGTC 300
DB 241 GACATCAAACTTTCTGATATCGTATCAAAATGCTGAAGAAAGTGTTTTAAAGCTTGGTC 300
QY 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGGAGAGATGAATGTTCAAGAGCCGG 360
DB 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGGAGAGATGAATGTTCAAGAGCCGG 360
QY 361 ACAGAGTGTGTTGCTGATCAAGATAGTGTGGCAATGCTCTTTGGCGCTGAAAACGTC 420
DB 361 ACAGAGTGTGTTGCTGATCAAGATAGTGTGGCAATGCTCTTTGGCGCTGAAAACGTC 420
QY 421 CAACTCAGAGATGCTGGCACTTAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATGCTGGCACTTAATGTTATATCATCACT 462

RESULT 14
BD265002 2627 bp DNA linear PAT 17-JUL-2003
LOCUS Compositions and methods for the therapy and diagnosis of ovarian
DEFINITION cancer.
ACCESSION BD265002.1 GI:33074770
VERSION BD265002.1
KEYWORDS JP 2002532093-A/387.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A. and Prudakis,T.N.
TITLE 1 (bases 1 to 2627)
JOURNAL Compositions and methods for the therapy and diagnosis of ovarian
Patent: JP 2002532093-A 387 02-OCT-2002;
CORIXA CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002532093-A/387
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588356
PR 17-DEC-1998 US 09/215681,17-DEC-1998 US 09/215603 PR
23-JUN-1999 US 09/338933,24-SEP-1999 US 09/404879 PI
JENNIFER L MITCHAM,GORDON E KING,PAUL A ALGATE,TONY N PRUDAKIS PC
C12N15/09,A61K31/7115,A61K35/14,A61K35/76,A61K39/00,A61K39/395, PC
A61K39/395,
PC A61K48/00,A61P35/00,A61P37/04,C07K14/82,C07K19/00,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/06,C12N5/10,C12O1/68,G01N33/53,G01N33/53,G01N33/ PC
566,
PC G01N33/574,G01N33/577,C12N15/00,C12N5/00,C12N5/00 CC
Compositions and methods for the therapy and diagnosis of CC
ovarian cancer
FH Key Location/Qualifiers
FT source 1. .2627
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 462; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGACGGGAGCTCCAGTACGAGTACCCAGATAGCTGGGAACTTCCCGACGC 60
DB 23 GGAAGGACGGGAGCTCCAGTACGAGTACCCAGATAGCTGGGAACTTCCCGACGC 82

| | | | |
|----|-----|-----------------------------------------------------------------|-----|
| QY | 6 | ATGGCTTCCCTGGGGGACAATCCTCTCTTGGAGCAATAATTAGCATATCATATTAATTCGGCT | 120 |
| Db | 83 | ATGGCTTCCCTGGGGGACAATCCTCTCTTGGAGCAATAATTAGCATATTAATTCGGCT | 142 |
| QY | 121 | GGAGCAATTGGACCTCATCATTTGGCTTTTGGTATTTTCAGGGAGACATCTCATCAAGTCACT | 180 |
| Db | 143 | GGAGCAATTGGACCTCATCATTTGGCTTTTGGTATTTTCAGGGAGACATCTCATCAAGTCACT | 202 |
| QY | 181 | ACTGTGCGCTCAAGCTGGGAACTTTGGGGAGCATGGAAATCTGAGCTGCACTTTGAACCT | 240 |
| Db | 203 | ACTGTGCGCTCAAGCTGGGAACTTTGGGGAGCATGGAAATCTGAGCTGCACTTTGAACCT | 262 |
| QY | 241 | GACATCAAACTTTCGATATCGTGAATACAATGCGTGAAGGAAAGTGTTTAGGCTTGCTC | 300 |
| Db | 263 | GACATCAAACTTTCGATATCGTGAATACAATGCGTGAAGGAAAGTGTTTAGGCTTGCTC | 322 |
| QY | 301 | CATGAGTTTCAAGGAAGGACAAGATAGCTGTGAGAGCAGATGAATGTTTCAGAGGCCGG | 360 |
| Db | 323 | CATGAGTTTCAAGGAAGGACAAGATAGCTGTGAGAGCAGATGAATGTTTCAGAGGCCGG | 382 |
| QY | 361 | ACAGCAGTGTTCGTGATCAAGTGAATGTTGGCAATGCTCTTTGCGGCTGAAAAACGTG | 420 |
| Db | 383 | ACAGCAGTGTTCGTGATCAAGTGAATGTTGGCAATGCTCTTTGCGGCTGAAAAACGTG | 442 |
| QY | 421 | CAACTCAGAGATGCTGGACCTACAAATGTTATATCACTACT | 462 |
| Db | 443 | CAACTCAGAGATGCTGGACCTACAAATGTTATATCACTACT | 484 |

| | | | |
|------------|--------------------------------------|-----|-----------------|
| RESULT 15 | | | |
| AR238405 | | | |
| LOCUS | 2627 bp | DNA | linear |
| DEFINITION | AR238405 | | |
| | Sequence 391 from patent US 6468546. | | PAT 20-DEC-2007 |

| | |
|-----------|-------------|
| ACCESSION | AR238405 |
| VERSION | AR238405.1 |
| | GI:27283369 |

| | |
|----------|----------|
| KEYWORDS | . |
| SOURCE | Unknown. |

| | |
|----------|---------------------------|
| ORGANISM | Unknown. Unclassified. |
|----------|---------------------------|

| REFERENCE | 1 (bases 1 to 2627) |
|-----------|-------------------------|
| AUTHORS | Mitcham, J.L., King, C. |

TITLE compositions and methods for therapy and diagnosis of ovarian cancer

| JOURNAL | Patent: | US 6468546-A 391 22-OCT-2002; |
|----------|---------------------|-------------------------------|
| FEATURES | Location/Qualifiers | |

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source      1. .2627
            /organism="unknown"
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/mol_type="genomic DNA

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| Query Match | Score | DB | Length |
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| 100.0% | 462 | 6 | 2627 |

Best Local Similarity 100.0%; Pred. NO. 3.3e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGCGGCGAGCTTCACTGCGCAGTACCGAGATACGCTGGAACTTCCCCAGCC 60

db 23 GGAAGGCAGCGCAGCTTCACTCAGCCAGTACCAGATACGCTGGAACTTCCCCAGCC 82

61 ATGCGTTCCTGGGGCAGATCCTCTCTTGAGCATAAATTAGCATCATTAATTCTGGCT 120

Db 83 ATGGCTTCCCTGGGGCAGATCCTTCTTGAGCATAAATTAGCATCATTAATTCTGGCT 142

121 GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGAGACACTCCATCATCAGTCACT 180

Db 143 GGAGCAATTGCACTCAATCATTTGGCTTTGGTATTTCAGGAGACACTCCATCATCAGTACT 202

181 ACTGTGCGCTCAGCTGGGAACTTTGGGAGATGGAATCTGAGCTGCACTTTGAACCT 240

Db 203 ACTGTGCGCTCAGCTGGGACATTGGGGAGATGGAATCCTGAGCTGCATTTTGAAGCT 262

241 GACATCAAACTTTCTGATATCGTATACAAATGGCTGAAGGAGGCTTTTAAAGCTTGGTC 300

| | | | |
|----|-----|----------------------------------------------------------------|-----|
| Db | 265 | GACATCAAACTTTCTGATATCGTATGATACAAAGCGCTGAAGAAAGGTTTATAGCGTTGGTC | 322 |
| Qy | 301 | CATGAGTTCAAAAGAGGCAAAAGATAGCTGTGCGAGCAGATGAAATGTTCAAGAGCGCGG | 366 |
| Db | 323 | CATGAGTTCAAAAGAGGCAAAAGATAGCGTGTGCGAGCAGAGTGAATGTTCAAGAGCGCGG | 382 |
| Qy | 361 | ACGCGAGTGTTCGTGATCAAGTGATGTGGCAATGCTCTTTGGCGGCTGAATAAAGCTG | 420 |
| Db | 383 | ACGCGAGTGTTCGTGATCAAGTGATGTGGCAATGCTCTTTGGCGGCTGAATAAAGCTG | 442 |
| Qy | 421 | CAACTCACAAGATCTGGCACTACACAAATGTTATCATCACT | 462 |
| Db | 443 | CAACTCACAAGATCTGGCACTACACAAATGTTATCATCACT | 484 |

Search completed: May 30, 2005, 17:54:08
Job time : 2132.43 secs

CC cytotoxic agent are useful for treating cancer. The present sequence
 CC represents a CSG (clone ID: 16656542 and gene ID: 234617) fragment
 XX
 SQ Sequence 462 BP; 119 A; 108 C; 119 G; 116 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 3; Length 462;
 Best Local Similarity 100.0%; Pred. No. 7,2e-136; Indels 0; Gaps 0;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGAGGAGCTCCAGCTCAGCCAGTACCCAGATCGCTGGAACTTCCCGAGCC 60
 DB 1 GGAAGGACGAGGAGCTCCAGCTCAGCCAGTACCCAGATCGCTGGAACTTCCCGAGCC 60
 QY 61 ATGGCTTCCCTGGGCGAGATCCTCTTCTGAGCATTAATGACATCATTAATTCGCT 120
 DB 61 ATGGCTTCCCTGGGCGAGATCCTCTTCTGAGCATTAATGACATCATTAATTCGCT 120
 QY 121 GGAGCAATTGCACTCATTAATGGCTTTGATTTTCAGGGAGACCTCCATCAGTCACT 180
 DB 121 GGAGCAATTGCACTCATTAATGGCTTTGATTTTCAGGGAGACCTCCATCAGTCACT 180
 QY 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 DB 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 QY 241 GACATCAAACTTTCGATATCGTATATCAATGAGCTGGAAGAGTGTGTTAGGCTTGGTC 300
 DB 241 GACATCAAACTTTCGATATCGTATATCAATGAGCTGGAAGAGTGTGTTAGGCTTGGTC 300
 QY 301 CATGAGTTCAAGAAGAGCAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGG 360
 DB 301 CATGAGTTCAAGAAGAGCAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGG 360
 QY 361 ACAGCAGTGTGTTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAACGTG 420
 DB 361 ACAGCAGTGTGTTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAACGTG 420
 QY 421 CAACTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462
 DB 421 CAACTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462

RESULT 2
 ABL56580
 ID ABL56580 standard; cDNA; 1065 BP.
 XX
 AC ABL56580;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Nucleotide sequence of expressed sequence tag (EST) A1799522.
 XX
 KW Human; gene A: ovarian tumour; gene B: ORO; ovarian cancer;
 KW expressed sequence tag; EST; A1799522; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200194641-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 11-JUN-2001; 2001WO-US018700.
 XX
 PR 09-JUN-2000; 2000US-0210451P.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Ople E, McLachlan K, Heard C;
 XX
 DR WPI; 2002-404365/43.
 XX
 PT New polynucleotide and corresponding antigens from human ovarian cancer
 cells, useful for treatment and diagnosis of ovarian cancer.

XX Example 4; Fig 4c; 71bp; English.

PS The present sequence represents expressed sequence tag (EST) A1799522.
 XX
 CC This EST was identified as a match to the novel gene B by database
 CC analysis. Gene B was identified by representational difference analysis
 CC (RDA) screening, and is selectively expressed by certain human ovarian
 CC tumours. The specification also describes gene A, identified by the same
 CC method. Gene A is named ORO (Ople RDA of Epithelial Tissue vs. Ovary
 CC tumour). Gene B and B polynucleotides are useful for detecting ovarian
 CC cancer. Their polypeptides are useful for treating ovarian cancer

SQ Sequence 1065 BP; 293 A; 252 C; 257 G; 263 T; 0 U; 0 Other;
 Query Match 100.0%; Score 462; DB 6; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 1.1e-135; Indels 0; Gaps 0;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGAGGAGCTCCAGCTCAGCCAGTACCCAGATCGCTGGAACTTCCCGAGCC 60
 DB 12 GGAAGGACGAGGAGCTCCAGCTCAGCCAGTACCCAGATCGCTGGAACTTCCCGAGCC 71
 QY 61 ATGGCTTCCCTGGGCGAGATCCTCTTCTGAGCATTAATGACATCATTAATTCGCT 120
 DB 72 ATGGCTTCCCTGGGCGAGATCCTCTTCTGAGCATTAATGACATCATTAATTCGCT 131
 QY 121 GGAGCAATTGCACTCATTAATGGCTTTGATTTTCAGGGAGACACTCCATCAGTCACT 180
 DB 132 GGAGCAATTGCACTCATTAATGGCTTTGATTTTCAGGGAGACACTCCATCAGTCACT 191
 QY 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 DB 192 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 251
 QY 241 GACATCAAACTTTCGATATCGTATATCAATGAGCTGGAAGAGTGTGTTAGGCTTGGTC 300
 DB 252 GACATCAAACTTTCGATATCGTATATCAATGAGCTGGAAGAGTGTGTTAGGCTTGGTC 311
 QY 301 CATGAGTTCAAGAAGAGCAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGG 360
 DB 312 CATGAGTTCAAGAAGAGCAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGG 371
 QY 361 ACAGCAGTGTGTTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAACGTG 420
 DB 372 ACAGCAGTGTGTTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAACGTG 431
 QY 421 CAACTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462
 DB 432 CAACTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 473

RESULT 3
 AA265059
 ID AA265059 standard; cDNA; 1657 BP.
 XX
 AC AA265059;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO1291 encoding cDNA.
 XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9963088-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 02-JUN-1999; 99WO-US012252.
 XX
 PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088722P.
 PR 10-JUN-1998; 98US-0088730P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088741P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088811P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089090P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089410P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 17-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089588P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 19-JUN-1998; 98US-0089947P.
 PR 19-JUN-1998; 98US-0089948P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090252P.
 PR 22-JUN-1998; 98US-0090254P.
 PR 23-JUN-1998; 98US-0090349P.
 PR 23-JUN-1998; 98US-0090355P.
 PR 24-JUN-1998; 98US-0090429P.
 PR 24-JUN-1998; 98US-0090431P.
 PR 24-JUN-1998; 98US-0090435P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 24-JUN-1998; 98US-0090445P.
 PR 24-JUN-1998; 98US-0090461P.
 PR 24-JUN-1998; 98US-0090472P.
 PR 24-JUN-1998; 98US-0090535P.
 PR 24-JUN-1998; 98US-0090538P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 24-JUN-1998; 98US-0090557P.
 PR 25-JUN-1998; 98US-0090676P.
 PR 25-JUN-1998; 98US-0090678P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090689P.
 PR 25-JUN-1998; 98US-0090681P.
 PR 25-JUN-1998; 98US-0090694P.
 PR 25-JUN-1998; 98US-0090695P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090662P.

PR 26-JUN-1998; 98US-0090863P.
 PR 01-JUL-1998; 98US-0091358P.
 PR 01-JUL-1998; 98US-0091360P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091519P.
 PR 02-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091566P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 02-JUL-1998; 98US-0091633P.
 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 07-JUL-1998; 98US-0091982P.
 PR 09-JUL-1998; 98US-0092182P.
 PR 10-JUL-1998; 98US-0092472P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 04-AUG-1998; 98US-0095285P.
 PR 04-AUG-1998; 98US-0095301P.
 PR 04-AUG-1998; 98US-0095302P.
 PR 04-AUG-1998; 98US-0095318P.
 PR 04-AUG-1998; 98US-0095321P.
 PR 10-AUG-1998; 98US-0095325P.
 PR 10-AUG-1998; 98US-0095316P.
 PR 10-AUG-1998; 98US-0095329P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 11-AUG-1998; 98US-0096143P.
 PR 11-AUG-1998; 98US-0096146P.
 PR 12-AUG-1998; 98US-0096329P.
 PR 17-AUG-1998; 98US-0096757P.
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 PR 17-AUG-1998; 98US-0096768P.
 PR 17-AUG-1998; 98US-0096773P.
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 PR 17-AUG-1998; 98US-0096867P.
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 PR 17-AUG-1998; 98US-0096894P.
 PR 17-AUG-1998; 98US-0096895P.
 PR 18-AUG-1998; 98US-0096897P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096950P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0096960P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 19-AUG-1998; 98US-0097022P.
 PR 20-AUG-1998; 98US-0097141P.
 PR 24-AUG-1998; 98US-0097218P.
 PR 26-AUG-1998; 98US-0097561P.
 PR 26-AUG-1998; 98US-0097551P.
 PR 26-AUG-1998; 98US-0097552P.
 PR 26-AUG-1998; 98US-0097554P.
 PR 26-AUG-1998; 98US-0097555P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 26-AUG-1998; 98US-0097978P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 26-AUG-1998; 98US-0097986P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 31-AUG-1998; 98US-0098525P.
 PR 16-SEP-1998; 98US-0100634P.
 PR 12-JAN-1999; 99US-0115565P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX WPI, 2000-072883/06.
 DR P-PSDB; AAY66719.
 XX
 PT Membrane-bound proteins and related nucleotide sequences.
 XX

PS Claim 2; Fig 207; 822bp; English.

XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques

SQ Sequence 1657 BP; 521 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 3; Length 1657;
Best Local Similarity 100.0%; Pred. No. 1,4e-135;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGCGAGCGAGCTCCAGCTCAGCCAGTACCCAGATACGCTGGAACTTCCCGAGCC 60
DB 1 GGAAGGCGAGCGAGCTCCAGCTCAGCCAGTACCCAGATACGCTGGAACTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGGAGATCCCTCTTCTGAGAGATTAATAGATCATCATTAATCTGGGCT 120
DB 61 ATGGCTTCCCTGGGGAGATCCCTCTTCTGAGAGATTAATAGATCATCATTAATCTGGGCT 120
QY 121 GGAGCAATTCGACTCATCATTCGCTTGGTATTTTCAGGAGACACTCCATCAGTCACT 180
DB 121 GGAGCAATTCGACTCATCATTCGCTTGGTATTTTCAGGAGACACTCCATCAGTCACT 180
QY 181 ACTGTCGCTCAGCTGGGAAACATTTGGGGAGAGATGAAATCTTGAGCTGCACTTTGAACCT 240
DB 181 ACTGTCGCTCAGCTGGGAAACATTTGGGGAGAGATGAAATCTTGAGCTGCACTTTGAACCT 240
QY 241 GACATCAAACTTTCGATATTCGATATCAATATGCTGTAAGAAAGTCTTTAGGCTTGGTC 300
DB 241 GACATCAAACTTTCGATATTCGATATCAATATGCTGTAAGAAAGTCTTTAGGCTTGGTC 300
QY 301 CATGATCAAAAGAAAGGCAAGATGAGCTGTCGAGCAGAGATGAATGTTTCAGAGGCCGG 360
DB 301 CATGATCAAAAGAAAGGCAAGATGAGCTGTCGAGCAGAGATGAATGTTTCAGAGGCCGG 360
QY 361 ACAGCAGTGTTCGATCAAGTATGATTTGGCAATGCTCTTTCGGCTGAAAAACGTG 420
DB 361 ACAGCAGTGTTCGATCAAGTATGATTTGGCAATGCTCTTTCGGCTGAAAAACGTG 420
QY 421 CAACCTCAGATGCTGGACCTTAACAATGTTATATCATCACT 462
DB 421 CAACCTCAGATGCTGGACCTTAACAATGTTATATCATCACT 462

RESULT 4

AA546033 standard; cDNA; 1658 BP.

AA546033;

18-DEC-2001 (first entry)

Human DNA encoding PRO polypeptide sequence #109.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.

OS Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

PF 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 06-MAR-2000; 2000US-0186968P.
XX 14-MAR-2000; 2000US-0189320P.
XX 14-MAR-2000; 2000US-0189328P.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000US-0190828P.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000US-0191048P.
XX 21-MAR-2000; 2000US-0191314P.
XX 28-MAR-2000; 2000US-0192655P.
XX 29-MAR-2000; 2000US-0193032P.
XX 29-MAR-2000; 2000US-0193053P.
XX 30-MAR-2000; 2000WO-US008439.
XX 04-APR-2000; 2000US-0194449P.
XX 04-APR-2000; 2000US-0194647P.
XX 11-APR-2000; 2000US-0195975P.
XX 11-APR-2000; 2000US-0196000P.
XX 11-APR-2000; 2000US-0196187P.
XX 11-APR-2000; 2000US-0196690P.
XX 11-APR-2000; 2000US-0196820P.
XX 18-APR-2000; 2000US-0198121P.
XX 18-APR-2000; 2000US-0198585P.
XX 25-APR-2000; 2000US-0199397P.
XX 25-APR-2000; 2000US-0199550P.
XX 25-APR-2000; 2000US-0199654P.
XX 03-MAY-2000; 2000US-0201515P.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 05-JUN-2000; 2000US-0209832P.
XX 28-JUL-2000; 2000WO-US020710.
XX 22-AUG-2000; 2000US-00644848.
XX 24-AUG-2000; 2000WO-US023328.
XX 08-NOV-2000; 2000WO-US030952.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000WO-US034956.

XX (GENTH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI: 2001-602746/68.

XX P-PSDB; AAU29132.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.

XX Claim 2; Fig 217; 774bp; English.

XX Sequences AA545925-AA546231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also

CC susceptibility to tumour development, particularly adrenal, lung, colon, CC breast, prostate, rectal, cervical, or liver tumours, in mammalian CC subjects. The oligonucleotide probes specific for the PRO nucleic acids CC can be used for genetic analysis of individuals with genetic disorders XX

Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 4; Length 1658;

Best Local Similarity 100.0%; Pred. No. 1.4e-135;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGCGGGGAGCTCCAGCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
 DB 1 GGAAGGCGGGGAGCTCCAGCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
 QY 61 ATGGCTTCCCTGGGGGAGATCTTCTTGAGAGCATATTAGCATCATTTATTTGGCT 120
 DB 61 ATGGCTTCCCTGGGGGAGATCTTCTTGAGAGCATATTAGCATCATTTATTTGGCT 120
 QY 121 GGAGCAATTGCACTCATCTTGGCTTGATTTTCAAGGAGACATCTCATCAGTCACT 180
 DB 121 GGAGCAATTGCACTCATCTTGGCTTGATTTTCAAGGAGACATCTCATCAGTCACT 180
 QY 181 ACTGTGCTTCAAGCTGGAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 DB 181 ACTGTGCTTCAAGCTGGAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 QY 241 GACATCAAACTTTCTGATATCGTGATCAATGCGTGAAGAGAGGTTTAAAGCTGGTC 300
 DB 241 GACATCAAACTTTCTGATATCGTGATCAATGCGTGAAGAGAGGTTTAAAGCTGGTC 300
 QY 301 CATGAGTTCAAAAGGCAAGAGATGAGCTGTCGAGAGAGATGAATGTTCAAGAGCCGG 360
 DB 301 CATGAGTTCAAAAGGCAAGAGATGAGCTGTCGAGAGAGATGAATGTTCAAGAGCCGG 360
 QY 361 ACAGCAGTGTCTGATCAAGTATGATGAGCAATGCTCTTTCGCGCTGAAAAACGTG 420
 DB 361 ACAGCAGTGTCTGATCAAGTATGATGAGCAATGCTCTTTCGCGCTGAAAAACGTG 420
 QY 421 CAACCTCAGATGCTGGCAGCTTCAAAATGTTATATCATCACT 462
 DB 421 CAACCTCAGATGCTGGCAGCTTCAAAATGTTATATCATCACT 462

RESULT 5

AAAF92087 standard; cDNA; 1658 BP.

XX AAF92087;
 XX 15-MAY-2001 (first entry)
 DE Human PRO1291 cDNA.
 XX Human; PRO protein; mapping; ss.
 XX Homo sapiens.
 OS WO200116318-A2.
 PN 08-MAR-2001.
 PD 24-AUG-2000; 2000MO-US023328.
 XX 01-SEP-1999; 99MO-US020111.
 XX 15-SEP-1999; 99MO-US021090.
 PR 07-DEC-1999; 99US-016945P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.

PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 25-APR-2000; 2000US-019397P.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.

XX (GENTH) GENENTECH INC.

PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CV, Gurney AL, Watanabe CK, Wood WI;
 PT P-PSDB; AAB87555.

DR WPI; 2001-183260/18.

XX P-PSDB; AAB87555.

PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.

PS Claim 2; Fig 59; 278pp; English.

XX The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a CC medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO CC protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping

XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 4; Length 1658;

Best Local Similarity 100.0%; Pred. No. 1.4e-135;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGCGGGGAGCTCCAGCTGAGCAATGAGTACGCTGGAACTTCCCGACCC 60
 DB 1 GGAAGGCGGGGAGCTCCAGCTGAGCAATGAGTACGCTGGAACTTCCCGACCC 60
 QY 61 ATGGCTTCCCTGGGGGAGATCTTCTTGAGAGCATATTAGCATCATTTATTTGGCT 120
 DB 61 ATGGCTTCCCTGGGGGAGATCTTCTTGAGAGCATATTAGCATCATTTATTTGGCT 120
 QY 121 GGAGCAATTGCACTCATCTTGGCTTGATTTTCAAGGAGACATCTCATCAGTCACT 180
 DB 121 GGAGCAATTGCACTCATCTTGGCTTGATTTTCAAGGAGACATCTCATCAGTCACT 180
 QY 181 ACTGTGCTTCAAGCTGGAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 DB 181 ACTGTGCTTCAAGCTGGAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 QY 241 GACATCAAACTTTCTGATATCGTGATCAATGCGTGAAGAGAGGTTTAAAGCTGGTC 300
 DB 241 GACATCAAACTTTCTGATATCGTGATCAATGCGTGAAGAGAGGTTTAAAGCTGGTC 300
 QY 301 CATGAGTTCAAAAGGCAAGAGATGAGCTGTCGAGAGAGATGAATGTTCAAGAGCCGG 360
 DB 301 CATGAGTTCAAAAGGCAAGAGATGAGCTGTCGAGAGAGATGAATGTTCAAGAGCCGG 360
 QY 361 ACAGCAGTGTCTGATCAAGTATGATGAGCAATGCTCTTTCGCGCTGAAAAACGTG 420
 DB 361 ACAGCAGTGTCTGATCAAGTATGATGAGCAATGCTCTTTCGCGCTGAAAAACGTG 420
 QY 421 CAACCTCAGATGCTGGCAGCTTCAAAATGTTATATCATCACT 462
 DB 421 CAACCTCAGATGCTGGCAGCTTCAAAATGTTATATCATCACT 462

RESULT 6

AAAF44205 standard; cDNA; 1658 BP.


```

XX AAF44205;
AC
XX
XX 02-APR-2001 (first entry)
XX
XX Human PRO1291 (UNQ659) nucleotide sequence SEQ ID NO:290.
DE
XX
XX Human; secreted and transmembrane protein; PRO; cytosolic; cell death;
XX cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay; ss.
XX
XX Homo sapiens.
XX
XX WO200073454-A1.
XX
XX 07-DEC-2000.
XX
XX
XX 30-MAR-2000; 2000WO-US008439.
XX
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 07-JUL-1999; 99US-0143048P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 17-AUG-1999; 99US-0149396P.
XX 15-SEP-1999; 99WO-US021547.
XX 15-SEP-1999; 99WO-US021547.
XX 08-OCT-1999; 99US-0158663P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000375.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
XX 20-MAR-2000; 2000WO-US007377.
XX
XX (GENTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DI;
XX Ferrara N, Fong S, Gettier H, Gerltzen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX
XX MPI; 2001-032160/04.
XX P-PSDB; AAB65242.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX molecules such as toxins, radiolabels or antibodies, to specific cells,
XX to cause targeted cell death.
XX
XX Claim 2; Fig 207; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytosolic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF4270 to
XX AAF4470 represent PCR primers and hybridisation probes used in the
XX isolation of human PRO sequences. AAF4087 to AAF44269 and AAB65154 to

```

```

CC AAB65300 represent human PRO polynucleotide and protein sequences given
XX in the exemplification of the present invention
XX
XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 462; DB 5; Length 1658;
XX Best Local Similarity 100.0%; Pred. No. 1,4e-135;
XX Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGAAGGACGGGCGAGCTCAGCTACGAGCTACGCCAGTACCGAGATGAGCTGGACCTTCCACACC 60
Db 1 GGAAGGACGGGCGAGCTCAGCTACGAGCTACGCCAGTACCGAGATGAGCTGGACCTTCCACACC 60
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Db 61 ATGGCTTCCCTGGGCGAGATCCTCTTTCGAGCATTAATTAACATCATTAATTCGTGCT 120
QY 121 GGAGCAATTGCACTCATTAATTCGCTTTGGTATTTTCAGGAGACACTCCATCACACTACT 180
Db 121 GGAGCAATTGCACTCATTAATTCGCTTTGGTATTTTCAGGAGACACTCCATCACACTACT 180
QY 181 ACTGTCGCTCAGCTGGAGCATTTGGGAGATGAGATCCTGAGCTGCATTTGAACCT 240
Db 181 ACTGTCGCTCAGCTGGAGCATTTGGGAGATGAGATCCTGAGCTGCATTTGAACCT 240
QY 241 GACATCAAACTTTCGATATGCTGATACATGCTGAGAGAGGTGTTTAAAGCTTGCTC 300
Db 241 GACATCAAACTTTCGATATGCTGATACATGCTGAGAGAGGTGTTTAAAGCTTGCTC 300
QY 301 CATGATTCAAAGAAAGCAAGATGAGTGTGCGAGCAGATGAATTTTCAGAGCCGG 360
Db 301 CATGATTCAAAGAAAGCAAGATGAGTGTGCGAGCAGATGAATTTTCAGAGCCGG 360
QY 361 ACAGCAGTGTTCGATCAAGTGAATGATGAGTGCATGCTCTTTCGCGCTGAAAAACGTG 420
Db 361 ACAGCAGTGTTCGATCAAGTGAATGATGAGTGCATGCTCTTTCGCGCTGAAAAACGTG 420
QY 421 CAACTCAGATGCTGCGACCTACCAATGTTATATCATCACT 462
Db 421 CAACTCAGATGCTGCGACCTACCAATGTTATATCATCACT 462
XX
XX RESULT 7
XX ABR11744
XX ID ABR11744 standard; cDNA; 1658 BP.
XX
XX AC ABR11744;
XX
XX DT 05-JUN-2002 (first entry)
XX
XX DE DNA encoding tumour associated antigenic target polypeptide (TAT) 136.
XX
XX Tumour associated antigenic target polypeptide; TAT; cancer;
XX breast cancer; colorectal cancer; lung cancer; ovarian cancer;
XX central nervous system cancer; liver cancer; bladder cancer;
XX pancreatic cancer; cervical cancer; melanoma; leukaemia; TAT136; gene;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 61..909
XX FT /*tag= b
XX FT /product= "TAT136"
XX FT /note= "Tumour associated antigenic target polypeptide"
XX FT sig_peptide 61..144
XX FT /*tag= a
XX FT mat_peptide 145..906
XX FT /*tag= c
XX FT /label= Mature_TAT136
XX
XX WO200216581-A2.
XX

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| Db | 421 | CNACTCAGAGATGCTGGACACTACAAATGTATATATCATCACT | 462 |
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| RESULT 8 | | | |
| AB574407 | | | |
| ID | AB574407 | standard; cDNA; 1658 BP. | |
| XX | | | |
| AC | AB574407; | | |
| XX | | | |
| DT | 10-DEC-2002 | (first entry) | |
| XX | | | |
| DE | Human cDNA encoding secreted/transmembrane protein PRO1291. | | |
| XX | | | |
| KW | Human; <i>se</i> ; gene; secreted protein; transmembrane protein; antirheumatic; | | |
| KW | antiarthritic; osteopathic; sports-related joint problem; | | |
| KW | articular cartilage defect; osteoarthritis; rheumatoid arthritis. | | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | US2002119130-A1. | | |
| XX | | | |
| PD | 29-AUG-2002. | | |
| XX | | | |
| BP | 06-DEC-2001; 2001US-00006867. | | |
| XX | | | |
| PR | 29-OCT-1997; | 97US-0063435P. | |
| PR | 29-OCT-1997; | 97US-0064215P. | |
| PR | 22-APR-1998; | 98US-0082797P. | |
| PR | 29-APR-1998; | 98US-0083495P. | |
| PR | 15-MAY-1998; | 98US-0085579P. | |
| PR | 02-JUN-1998; | 98US-0087759P. | |
| PR | 04-JUN-1998; | 98US-0088021P. | |
| PR | 04-JUN-1998; | 98US-0088029P. | |
| PR | 10-JUN-1998; | 98US-0088734P. | |
| PR | 10-JUN-1998; | 98US-0088740P. | |
| PR | 10-JUN-1998; | 98US-0088811P. | |
| PR | 10-JUN-1998; | 98US-0088824P. | |
| PR | 10-JUN-1998; | 98US-0088825P. | |
| PR | 11-JUN-1998; | 98US-0088863P. | |
| PR | 12-JUN-1998; | 98US-0089105P. | |
| PR | 16-JUN-1998; | 98US-0089514P. | |
| PR | 17-JUN-1998; | 98US-0089563P. | |
| PR | 19-JUN-1998; | 98US-0089952P. | |
| PR | 22-JUN-1998; | 98US-0090246P. | |
| PR | 24-JUN-1998; | 98US-0090444P. | |
| PR | 25-JUN-1998; | 98US-0090688P. | |
| PR | 25-JUN-1998; | 98US-0090696P. | |
| PR | 26-JUN-1998; | 98US-0090862P. | |
| PR | 02-JUL-1998; | 98US-0091628P. | |
| PR | 10-AUG-1998; | 98US-0096012P. | |
| PR | 17-AUG-1998; | 98US-0096575P. | |
| PR | 18-AUG-1998; | 98US-0096949P. | |
| PR | 18-AUG-1998; | 98US-0096959P. | |
| PR | 26-AUG-1998; | 98US-0097954P. | |
| PR | 26-AUG-1998; | 98US-0097971P. | |
| PR | 26-AUG-1998; | 98US-0097979P. | |
| PR | 01-SEP-1998; | 98US-0098479P. | |
| PR | 10-SEP-1998; | 98US-0099741P. | |
| PR | 10-SEP-1998; | 98US-0099763P. | |
| PR | 10-SEP-1998; | 98US-0099792P. | |
| PR | 10-SEP-1998; | 98US-0099812P. | |
| PR | 10-SEP-1998; | 98US-0099815P. | |
| PR | 16-SEP-1998; | 98US-0100627P. | |
| PR | 16-SEP-1998; | 98US-0100652P. | |
| PR | 16-SEP-1998; | 98WO-US019330. | |
| PR | 17-SEP-1998; | 98US-0100684P. | |
| PR | 17-SEP-1998; | 98US-0100683P. | |
| PR | 17-SEP-1998; | 98US-0100930P. | |
| PR | 22-SEP-1998; | 98US-0101279P. | |
| PR | 23-SEP-1998; | 98US-0101475P. | |
| PR | 24-SEP-1998; | 98US-0101738P. | |
| PR | 24-SEP-1998; | 98US-0101743P. | |

PR 24-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 22-DEC-1999; 99WO-US021194.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
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 PR 23-AUG-2000; 2000WO-US023522.
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 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

XX (GENTH) GENENTECH INC.

PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;

XX WPI; 2002-731348/79.
 DR P-PSDB; ABG95880.

PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 2; Fig 59; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG5851-ABG9534 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis

CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the
 CC invention

XX SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 6; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 1,4e-135;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAAGCAGCGGACGCTCACTCAAGCCAGTACCAGATACGCTGGAACTTCCCAAGCC 60
 DB 1 GGAAGGACGCGGACGCTCACTCAAGCCAGTACCAGATACGCTGGAACTTCCCAAGCC 60
 QY 61 ATGGCTTCCCTGGGCAAGATCTCTTCTGAGCATATATTACATCATATATCTGGCT 120
 DB 61 ATGGCTTCCCTGGGCAAGATCTCTTCTGAGCATATATTACATCATATATCTGGCT 120
 QY 121 GGAGCAATTGACATCATATGGCTTTGGTATTTTCAGGAGACACTCCATCAAGTCACT 180
 DB 121 GGAGCAATTGACATCATATGGCTTTGGTATTTTCAGGAGACACTCCATCAAGTCACT 180
 QY 181 ACTGTGCGCTCAGCTGGAGACATTGGGAGGAGATGGAATCTGAGCTGACATTTTGAACCT 240
 DB 181 ACTGTGCGCTCAGCTGGAGACATTGGGAGGAGATGGAATCTGAGCTGACATTTTGAACCT 240
 QY 241 GACATCAAACTTCTGATATGTGATATACAATGGCTGAAGAGATGTTTGGCTGGTC 300
 DB 241 GACATCAAACTTCTGATATGTGATATACAATGGCTGAAGAGATGTTTGGCTGGTC 300
 QY 301 CATGATCAAAAGAGGAGGAGATGAGCTGTGAGAGCAGATGAATGTTGAGAGCCGG 360
 DB 301 CATGATCAAAAGAGGAGGAGATGAGCTGTGAGAGCAGATGAATGTTGAGAGCCGG 360
 QY 361 ACAGCAGTGTTCGTGATCAAGTGAATGATGCGCAATGCTTTGCGGCTGAAAAACGTG 420
 DB 361 ACAGCAGTGTTCGTGATCAAGTGAATGATGCGCAATGCTTTGCGGCTGAAAAACGTG 420
 QY 421 CAATCAGAGATGCTGGACCTACCAAAATGTTATATCATCACT 462
 DB 421 CAATCAGAGATGCTGGACCTACCAAAATGTTATATCATCACT 462

RESULT 9

ABK11091
 ID ABK11091 standard; cDNA; 1658 BP.

AC ABK11091;

DT 05-JUN-2002 (first entry)

DE cDNA encoding tumour-associated antigenic target protein, TAT136.

XX TAT136; Tumour-associated Antigenic Target; tumour; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer;

KW central nervous system cancer; liver cancer; bladder cancer; melanoma;

XX pancreatic cancer; leukemia; gene therapy; gene; 88.

OS Homo sapiens.

FT Key Location/Qualifiers
 FT CDS 61..909
 FT /*tag= a
 FT /product= "TAT136"

/note="Tumour-associated antigenic target"

FT XX W0200216429-A2.

XX PD 28-FEB-2002.

XX PF 22-JUN-2001; 2001WO-US020118.

XX PR 24-AUG-2000; 2000WO-US023328.

PR 26-SEP-2000; 2000US-0235451P.

PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PA (GETH) GENENTECH INC.

XX Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,

PI Wood WI, Wu TD, Zhang Z;

XX WPI: 2002-280917/32.

DR P-PSDB; AAU76536.

XX Novel isolated tumor-associated antigenic target polypeptides which are

PT useful as targets for cancer therapy and diagnosis in mammals.

XX

PS Claim 1; Fig 3; 121pp; English.

XX The invention relates to an isolated tumour-associated antigenic target

CC polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the

CC polynucleotides (II) encoding them. (II) is useful for diagnosing the

CC presence of a tumour in a mammal, where the level of expression of (II)

CC is indicative on the presence of tumour in the mammal from which the test

CC sample was obtained. Antibody to (I) is useful for killing a cancer cell

CC (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,

CC an ovarian cancer cell, a central nervous system (CNS) cancer cell, a

CC liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a

CC melanoma cell or a leukemia cell) that expresses (I). Oligonucleotides

CC hybridizing to (II) are useful as diagnostic probes, antisense

CC oligonucleotide probes or for encoding fragments of full length TAT

CC polypeptide. (II) is also useful in chromosome and gene mapping and in

CC the generation of antisense RNA and DNA probes, for constructing

CC hybridisation probes for mapping the gene encoding TAT and for genetic

CC analysis of individuals with genetic disorders. (II) is also useful for

CC generating either transgenic animals or knockout animals, and in gene

CC therapy. The TAT polypeptides and nucleic acids may also be used for

CC tissue typing and the TAT polypeptides are useful for screening compounds

CC that mimic the TAT polypeptide (agonist) or prevent the effect of TAT

CC polypeptide (antagonist). The antibody is useful for staging TAT

CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT

CC polypeptide from cells, for detection and quantitation of TAT polypeptide

CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or

CC Western blot. The antibodies are also useful for treating a TAT-

CC expressing cancer or alleviating one or more symptoms of cancer in a

CC mammal. The present sequence represents the coding sequence of TAT136

XX

SO Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 6; Length 1658;

Best Local Similarity 100.0%; Pred. No. 1.4e-135;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGGGAGGCTTCACGACGATACCCAGATAGCTGGAACTTCCCGCC 60

DB 1 GGAAGGAGGGGAGGCTTCACGACGATACCCAGATAGCTGGAACTTCCCGCC 60

QY 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGGAGCATATTAATGATCATCTTATTTGGCT 120

DB 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGGAGCATATTAATGATCATCTTATTTGGCT 120

QY 121 GGAAGCATTCGACTCATCTATGCTTGGTATTTAGGAGAGACATCTCATCAAGTCACT 180

DB 121 GGAAGCATTCGACTCATCTATGCTTGGTATTTAGGAGAGACATCTCATCAAGTCACT 180

QY 181 ACTGTGCGCTCAGCTGGAGAACATTTGGGGAGAGATGAGTATCGTAGTCACTTTTGAACCT 240

DB 181 ACTGTGCGCTCAGCTGGAGAACATTTGGGGAGAGATGAGTATCGTAGTCACTTTTGAACCT 240

QY 241 GACATCAAACTTTCTGATATCGTATACATATGAGAGAGAGTGTATTAGCTTGGCT 300

DB 241 GACATCAAACTTTCTGATATCGTATACATATGAGAGAGAGTGTATTAGCTTGGCT 300

QY 301 CATGAGTTCAAGAGAGCAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGAGCCGG 360

DB 301 CATGAGTTCAAGAGAGCAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGAGCCGG 360

QY 361 ACAGAGTGTTCCTGATACAGATAGTATGGCAATGCCCTTTGGGGCTGAAAAACGTC 420

DB 361 ACAGAGTGTTCCTGATACAGATAGTATGGCAATGCCCTTTGGGGCTGAAAAACGTC 420

QY 421 CAACTCAGAGATGCTGCACTTCAAAATGTTATATCATCACT 462

DB 421 CAACTCAGAGATGCTGCACTTCAAAATGTTATATCATCACT 462

RESULT 10

ACAB9483

ID ACAB9483 standard; cDNA; 1658 BP.

XX ACAB9483;

AC ACAB9483;

DT 09-JUL-2003 (first entry)

XX

DE cDNA encoding human PRO polypeptide #109.

XX

KW Human; PRO polypeptide; secreted protein; transmembrane protein;

KW chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;

KW prostate; rectal; cervical; liver; cancer; TNF-alpha;

KW tumour necrosis factor-alpha; proliferation; differentiation;

KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;

KW arthritis; cystostatic; antiarthritic; osteopathic; gene therapy; gene;

KW 88.

OS Homo sapiens.

XX

PN US2003036141-A1.

XX

PD 20-FEB-2003.

XX

PF 01-JUL-2002; 2002US-00187597.

XX

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

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PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063564P.

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PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 20-MAR-1998; 98US-0078866P.

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PR 31-MAR-1998; 98US-0080194P.
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PR 01-APR-1998; 98US-0080333P.
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PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0083222P.
PR 28-APR-1998; 98US-0083322P.
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PR 29-APR-1998; 98US-0083559P.
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PR 09-JUN-1998; 98US-0088722P.
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PR 10-JUN-1998; 98US-0088811P.
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PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
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PR 26-JUN-1998; 98US-0105413.
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PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
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PR 02-JUL-1998; 98US-0091628P.
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PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
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PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
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PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
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PR 23-SEP-1998; 98US-0101472P.
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PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102240P.
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PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.

PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
Query Match 100.0%; Score 462; DB 8; Length 1658;
Best Local Similarity 100.0%; Pred. No. 1,4e-135;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGAGGGGCGCTCCACTGAGCGAATGACCTGGGAACCTTCCCGACC 60
DB 1 GGAAGGAGGGGCGCTCCACTGAGCGAATGACCTGGGAACCTTCCCGACC 60
QY 61 ATGGCTTCCCTGGGCGAGATCTCTTGGAGCAATTAATGATCATTAATTTGGCT 120
DB 61 ATGGCTTCCCTGGGCGAGATCTCTTGGAGCAATTAATGATCATTAATTTGGCT 120
QY 121 GGAAGCAATTCATCATTAATGCTTTGATTTCAAGGAGACATCCATCAGTCACT 180
DB 121 GGAAGCAATTCATCATTAATGCTTTGATTTCAAGGAGACATCCATCAGTCACT 180
QY 181 ACTGTCCCTCAGCTGGGAACATTGGGAGAGTGAATCTGAGCTGCATTTGAACCT 240
DB 181 ACTGTCCCTCAGCTGGGAACATTGGGAGAGTGAATCTGAGCTGCATTTGAACCT 240
QY 241 GACATCAACTTCTGATATCGATATCAATGCTGAAGAGGTGTTTAGGCTTGCTC 300
DB 241 GACATCAACTTCTGATATCGATATCAATGCTGAAGAGGTGTTTAGGCTTGCTC 300
QY 301 CATGAGTTCAAGAGCAAGATGAGCTGCGAGAGAGTGAATGTTCAAGAGCCGG 360
DB 301 CATGAGTTCAAGAGCAAGATGAGCTGCGAGAGAGTGAATGTTCAAGAGCCGG 360
QY 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTTTGGCGGTGAAGAACTGTG 420
DB 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTTTGGCGGTGAAGAACTGTG 420
QY 421 CAATCAAGATGCTGACCTCAATGTTATATCACT 462
DB 421 CAATCAAGATGCTGACCTCAATGTTATATCACT 462
RESULT 11
ID ACA73493 standard; cDNA; 1658 BP.
XX ACA73493;
AC ACA73493;
XX 01-JUL-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) cDNA #109.
DE Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KM tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003036146-A1.
PN
XX 20-FEB-2003.
PD
XX
PF 02-JUL-2002; 2002US-00187603.
XX
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98MO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98MO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98MO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99MO-US005028.

PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99MO-US010733.
PR 02-JUN-1999; 99MO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99MO-US020111.
PR 15-SEP-1999; 99MO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99MO-US028301.
PR 02-DEC-1999; 99MO-US028551.
PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US000219.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US005004.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
PR 15-MAR-2000; 2000MO-US006884.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUN-2000; 2000MO-US020710.
PR 22-AUG-2000; 2000MO-US064488.
PR 24-AUG-2000; 2000MO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000MO-US030952.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001MO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001MO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001MO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-332034/31.
DR P-PSDB; AB086301.
XX
XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in
PT gene therapy, chromosome identification, tissue typing, and for detecting
the presence of tumor in a mammal.
XX
XX Claim 2; Fig 217; 707pp; English.
PS
XX
XX The invention relates to three hundred and five nucleic acids encoding
CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to

CC them, or encoding a PRO polypeptide lacking its associated signal peptide
CC or an extracellular domain of the PRO polypeptide, with or lacking its
CC associated signal peptide. Also included are the encoded PRO proteins,
CC PRO expression vectors, host cells transformed with the vector (used to
CC produce PRO proteins), a chimeric molecule comprising the PRO
CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, a method for stimulating the release of tumor necrosis factor
CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
CC PRO827, PRO791, PRO131, PRO1316, PRO183, PRO1760, PRO1567 or
CC PRO833), a method for stimulating the proliferation or differentiation
CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
CC a method for detecting the presence of tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in a binding reaction, to generate transgenic animals or knockout
CC animals, which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful for detecting the presence of a tumour in a mammal, stimulating
CC proliferation or differentiation of chondrocyte cells, stimulating the
CC release of tumour necrosis factor-alpha from human blood, in gene
CC therapy, or as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. The present sequence is a cDNA encoding a PRO
CC protein
XX
XX
SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 8; Length 1658;
Best Local Similarity 100.0%; Pred. No. 1.4e-135;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGACAGGAGGAGCTCCAGCTCAGCAGATCCAGATCGCTGGGAACTTCCCGAGCC 60
DB 1 GGAGGACAGGAGGAGCTCCAGCTCAGCAGATCCAGATCGCTGGGAACTTCCCGAGCC 60
QY 61 ATGGCTTCCTGGGAGAGATCTCTTCTGAGAGCATATTAGCATCATTTATTTGGCT 120
DB 61 ATGGCTTCCTGGGAGAGATCTCTTCTGAGAGCATATTAGCATCATTTATTTGGCT 120
QY 121 GGAAGCAATTCATCATTCATTTGGTATTTTCAGGAGACATCCATCAGATCACT 180
DB 121 GGAAGCAATTCATCATTCATTTGGTATTTTCAGGAGACATCCATCAGATCACT 180
QY 181 ACTGTGCGCTCAGCTGGGAAATTTGGGAGAGATGAATCTGAGCTGACATTTTGAACCT 240
DB 181 ACTGTGCGCTCAGCTGGGAAATTTGGGAGAGATGAATCTGAGCTGACATTTTGAACCT 240
QY 241 GACATCAAACTTCTGATATCGTATATCAATGAGCTGAGAAAGTGTTTAGCTTGGTC 300
DB 241 GACATCAAACTTCTGATATCGTATATCAATGAGCTGAGAAAGTGTTTAGCTTGGTC 300
QY 301 CATGATTCAGAGAGAGCAAAATGAGCTGTGAGACAGATGAATTTTCAGAGCCCG 360
DB 301 CATGATTCAGAGAGAGCAAAATGAGCTGTGAGACAGATGAATTTTCAGAGCCCG 360
QY 361 ACAGAGCTGTTGCTGATCAAGATAGTTGGCAATGCCCTTTGGGCTGAAAAACGCG 420
DB 361 ACAGAGCTGTTGCTGATCAAGATAGTTGGCAATGCCCTTTGGGCTGAAAAACGCG 420
QY 421 CAACTCAGAGATGCTGGACCTTCAAAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATGCTGGACCTTCAAAATGTTATATCATCACT 462

RESULT 12
ACA05808

ID ACA05808 standard; cDNA, 1658 BP.
XX AC
XX ACA05808;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #109.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
PN US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194423.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US01252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 25-AUG-1999; 99US-00380139.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99US-00403297.
PR 18-OCT-1999; 99US-00423844.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.

20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
XX (GENTH) GENENTECH INC.
XX
PI Baker KP, Chen J, Deenyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WT, Zhang Z;
XX
XX WPI; 2003-332039/31.
DR P-PSDB; ABU67514.
XX
XX PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
PT in tissue typing, and in chromosome identification.
XX
XX Claim 2; Fig 217; 706pp; English.

The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumor necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide, a method for detecting the presence of a tumor in a mammal and an oligonucleotide probe derived from any of the PRO nucleotide sequences. The nucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes and for detecting the presence of a tumor. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in AC05700-ACA06004 are the cDNAs encoding the PRO polypeptides of the invention

XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 8; Length 1658;
Best Local Similarity 100.0%; Pred. No. 1.4e-135;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGAGGAGCTCCAGTACAGGAGTACCAAGTACGCTGGAACTTCCCGGCC 60
DB 1 GGAAGGAGGAGGAGCTCCAGTACAGGAGTACCAAGTACGCTGGAACTTCCCGGCC 60
QY 61 ATGGCTTCCCTGGGGGAGATCTCTTGAGAGCAATTAATGATCATCATTAATTCGGCT 120
DB 61 ATGGCTTCCCTGGGGGAGATCTCTTGAGAGCAATTAATGATCATCATTAATTCGGCT 120
QY 121 GGAGCAATTCATCATTCATTCGCTTGTATTCAGGAGAGCAATTCATCAAGTCACT 180
DB 121 GGAGCAATTCATCATTCATTCGCTTGTATTCAGGAGAGCAATTCATCAAGTCACT 180
QY 181 ACTGTGCGCTCAGCTGGAAATTTGGGAGAGTGAATCTCGAGCTGCACTTTTGAACCT 240
DB 181 ACTGTGCGCTCAGCTGGAAATTTGGGAGAGTGAATCTCGAGCTGCACTTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATCAATTCGCTGAGAGAGGCTGTTTAAAGCTTGCT 300
DB 241 GACATCAAACTTTCTGATATCGTATCAATTCGCTGAGAGAGGCTGTTTAAAGCTTGCT 300

QY 301 CATGAGTTCAAAGAGGCAAGATGAGCTGTGGAGAGGATGAATGCTTCAGAGCGCGG 360
DB 301 CATGAGTTCAAAGAGGCAAGATGAGCTGTGGAGAGGATGAATGCTTCAGAGCGCGG 360
QY 361 ACAGCAGTGTCTGATCATCAAGTATGATGCAATGCCCTTGGCGGCTGAATAACGTC 420
DB 361 ACAGCAGTGTCTGATCATCAAGTATGATGCAATGCCCTTGGCGGCTGAATAACGTC 420
QY 421 CAACTCAGAGATCTGGACCTTACAAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATCTGGACCTTACAAATGTTATATCATCACT 462
RESULT 13
ACA66642
ID ACA66642 standard; cDNA; 1658 BP.
XX
XX ACA66642;
AC
AC 23-JUN-2003 (first entry)
DT
XX
XX cDNA encoding human PRO protein #109.
DE
XX
XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
KW liver; PRO; gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX US2003036137-A1.
PN
XX
PD 20-FEB-2003.
XX
XX 27-JUN-2002; 2002US-00184640.
PF
XX
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98MO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98MO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98MO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99MO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99MO-US010733.
PR 02-JUN-1999; 99MO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99MO-US020111.
PR 15-SEP-1999; 99MO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99MO-US028301.
PR 02-DEC-1999; 99MO-US028351.
PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US000219.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US005004.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005884.
PR 15-MAR-2000; 2000MO-US006884.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUL-2000; 2000MO-US020710.
PR 22-AUG-2000; 2000US-00644848.

PR 24-AUG-2000; 2000MO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000MO-00747259.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941992.
 PR 29-AUG-2001; 2001MO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.
 XX
 PA (GENTH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR MPI: 2003-142038/32.
 DR P-PSDB; AB080542.

XX Three hundred and five nucleic acids encoding secreted and transmembrane
 PT PRO polypeptides, useful for the diagnosis, prevention and/or treatment
 PT of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
 PT cervical or liver tumors.

XX Claim 2; Fig 217; 708bp; English.

XX The invention relates to three hundred and five nucleic acids encoding
 CC PRO polypeptides (secreted and transmembrane). Methods and compositions
 CC of the present invention are useful for the diagnosis, prevention and/or
 CC treatment of tumors, such as adrenal, lung, colon, breast, prostate,
 CC rectal, cervical or liver tumors. The PRO polypeptides are also useful
 CC as molecular weight markers, or for chromosome identification. The PRO
 CC genes are useful as hybridisation probes, or for screening libraries of
 CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
 CC therapy, particularly for replacing a defective gene. The present
 CC sequence represents a cDNA encoding a human PRO polypeptide of the
 CC invention

XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 462; DB 8; Length 1658;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-135;
 XX Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCAGCAGCAGCTCCAGTACGAGTACCGAGATACGCTGGAACTTCCAGCC 60
 DB 1 GGAAGCAGCAGCAGCTCCAGTACGAGTACCGAGATACGCTGGAACTTCCAGCC 60
 QY 61 ATGGCTTCCCTGGGAGATCTCTTCTGAGCATATTAGCATCATCTTATTCGCT 120
 DB 61 ATGGCTTCCCTGGGAGATCTCTTCTGAGCATATTAGCATCATCTTATTCGCT 120
 QY 121 GGAGCAATGCACTATCTATTTGGTATTTTCAGGAGACATCCCAAGCACT 180
 DB 121 GGAGCAATGCACTATCTATTTGGTATTTTCAGGAGACATCCCAAGCACT 180

QY 181 ACTGTCGCTCAGCTGGGAACTTGGGAGAGTGAATCTTGAGCTGCATTTGAACT 240
 DB 181 ACTGTCGCTCAGCTGGGAACTTGGGAGAGTGAATCTTGAGCTGCATTTGAACT 240
 QY 241 GACATCAACTTTCTGTATATGTATCAATAGCTGTAAGAGGTGTTTAGGCTGTC 300
 DB 241 GACATCAACTTTCTGTATATGTATCAATAGCTGTAAGAGGTGTTTAGGCTGTC 300
 QY 301 CATGATTCAGAAAGGAGAAAGATGAGCTGCGAGCAGATGAATGTTTCAGAGCCGG 360
 DB 301 CATGATTCAGAAAGGAGAAAGATGAGCTGCGAGCAGATGAATGTTTCAGAGCCGG 360
 QY 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTGAAAAAGTG 420
 DB 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTGAAAAAGTG 420
 QY 421 CAATCAGATGCTGGCAGCTACAAATGTTATTCATCACT 462
 DB 421 CAATCAGATGCTGGCAGCTACAAATGTTATTCATCACT 462

RESULT 14

ID ACA64352 standard; cDNA; 1658 BP.

XX ACA64352;

DT 17-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO1291 cDNA.

XX Human; secreted and transmembrane protein; cytosolic; anti-HIV;
 XX virucide; hepatocytic; antiinflammatory; neuroprotective; gene therapy;
 XX PRO; pharmaceutical; diagnostic; biosensor; bioindicator; malignancy;
 XX cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukemia;
 XX lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
 XX drug screening; gene; ss.

OS Homo sapiens.

PN US2003003531-A1.

XX 02-JAN-2003.

XX 19-NOV-2001; 2001US-00389734.

XX 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97MO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087755P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 16-SEP-1998; 98MO-US019330.
 PR 16-SEP-1998; 98MO-US019437.
 PR 07-OCT-1998; 98MO-US021141.
 PR 01-DEC-1998; 98MO-US025108.
 PR 05-JAN-1999; 99MO-US000106.
 PR 08-MAR-1999; 99MO-US005028.
 PR 02-JUN-1999; 99MO-US012252.
 PR 15-SEP-1999; 99MO-US021097.
 PR 15-SEP-1999; 99MO-US021547.
 PR 30-NOV-1999; 99MO-US028313.
 PR 01-DEC-1999; 99MO-US028301.
 PR 01-DEC-1999; 99MO-US028634.
 PR 20-DEC-1999; 99MO-US030911.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 20-MAR-2000; 2000MO-US007377.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 15-MAY-2000; 2000MO-US013358.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 11-AUG-2000; 2000MO-US022031.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023528.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 XX
 XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Borstein D, Deenoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gertlsen ME, Goddard A, Godowski PJ;
 PI Glimaldi JC, Guirey AL, Kljavin JF, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;
 XX
 DR WPI, 2003-352829/33.
 DR P-PSDB; AB072533.
 XX
 PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
 PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
 PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
 PT disease.
 XX
 PS Claim 1; Fig 207; 663pp; English.
 XX
 CC The invention describes a new isolated nucleic acid molecule comprising
 CC the full length coding sequence of the DNA deposited with the American
 CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
 CC 209439, 203135, etc.) or a sequence with at least 80% identity to a DNA
 CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
 CC are particularly useful for detecting or treating e.g. malignancies or
 CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
 CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
 CC disease in mammals. The PRO polypeptides are useful in drug screening,
 CC particularly as targets for therapeutic intervention in these diseases,
 CC and in the diagnostic determination of the presence of these diseases.
 CC The PRO polypeptides are also useful as molecular weight markers, or for
 CC chromosome identification. The PRO genes are useful as hybridisation
 CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
 CC The PRO genes may also be used in gene therapy, particularly for
 CC replacing a defective gene. This sequence encodes a novel human secreted
 CC and transmembrane PRO polypeptide
 XX
 SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 8; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 1.4e-135;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGGGAGAGTCCAGCTCAGCAGTACCCAGATACGCTGGAGACCTTCCCAAGC 60
 DB 1 GGAAGGACGGGAGAGTCCAGCTCAGCAGTACCCAGATACGCTGGAGACCTTCCCAAGC 60
 QY 61 ATGGCTTCCCTGGGGAGAGATCCCTTCTGGAGAGATATTAGCATCATATTATTTGGCT 120
 DB 61 ATGGCTTCCCTGGGGAGAGATCCCTTCTGGAGAGATATTAGCATCATATTATTTGGCT 120
 QY 121 GGAGCAATTGCACTATCATATGGCTTTGGTATTTCAGGAGACATCTCCATCAGTCAC 180
 DB 121 GGAGCAATTGCACTATCATATGGCTTTGGTATTTCAGGAGACATCTCCATCAGTCAC 180
 QY 181 ACTGTGGCTCAGCTGGGAACATTTGGGGAGAGATGAATCTCAGCTGCACCTTTGAACCT 240
 DB 181 ACTGTGGCTCAGCTGGGAACATTTGGGGAGAGATGAATCTCAGCTGCACCTTTGAACCT 240
 QY 241 GACATCAAACTTTCTGATATCGATATACATGAGCTGAAGAGAGTATTGAGCTTGTC 300
 DB 241 GACATCAAACTTTCTGATATCGATATACATGAGCTGAAGAGAGTATTGAGCTTGTC 300
 QY 301 CATGAGTTCAAAAGAGCAAAAGATGAGCTGTGGAGCAGAGTAAATGTTTCAGAGCCCG 360
 DB 301 CATGAGTTCAAAAGAGCAAAAGATGAGCTGTGGAGCAGAGTAAATGTTTCAGAGCCCG 360
 QY 361 ACAGCAGTGTTCCTGATATGAGATGATGTTGGCAATGCTCTTTGGGGCTGAAAAACGTC 420
 DB 361 ACAGCAGTGTTCCTGATATGAGATGATGTTGGCAATGCTCTTTGGGGCTGAAAAACGTC 420
 QY 421 CAACTCAGAGATGCTGACCTTCAAAATGTTATATCATCACT 462
 DB 421 CAACTCAGAGATGCTGACCTTCAAAATGTTATATCATCACT 462

RESULT 15
 ACA91193
 ID ACA91193 standard; cDNA; 1658 BP.

XX ACA91193;
AC
XX
XX 11-JUL-2003 (first entry)
DT
XX Novel human secreted and transmembrane protein PRO1291 cDNA.
DE
XX Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
XX
XX Homo sapiens.
OS
XX US2003018173-A1.
XX
XX 23-JAN-2003.
XX
XX 01-MAY-2002; 2002US-00063515.
XX
XX 06-DEC-2001; 2001US-00006867.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-401702/38.
DR P-PSDB; ABU0905.
XX
XX New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.
XX
XX
XX Disclosure; Fig 59; 345pp; English.
XX
XX The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostic, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
Query Match 100.0%; Score 462; DB 8; Length 1658;
Best Local Similarity 100.0%; Pred. No. 1.4e-135;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGCGAGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCGAGCC 60
DB 1 GGAAGGCGAGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGGAGATCCCTTCTGGAGCATATATTAGCATCATTTATTCGGCT 120
DB 61 ATGGCTTCCCTGGGGAGATCCCTTCTGGAGCATATATTAGCATCATTTATTCGGCT 120
QY 121 GGAGCAATTGCACTCATCTTGGCTTTGGATTTTCAGGGAGACATCCATCAAGTCACT 180
DB 121 GGAGCAATTGCACTCATCTTGGCTTTGGATTTTCAGGGAGACATCCATCAAGTCACT 180
QY 181 ACTGTCGCTTCAGCTGGGAACATTTGGGAGATGGAATCTTGAAGTCACTTTGAACCT 240
DB 181 ACTGTCGCTTCAGCTGGGAACATTTGGGAGATGGAATCTTGAAGTCACTTTGAACCT 240
QY 241 GACATCAAACTTTCGATATCGATATACATGAGCTGAAGAAAGTGTATTAGGCTTGCTC 300
DB 241 GACATCAAACTTTCGATATCGATATACATGAGCTGAAGAAAGTGTATTAGGCTTGCTC 300

QY 301 CATGAGTTCAAAAGAAAGGCAATGAGCTGTGAGAGCAGATGAATGTTCAAGAGCCGG 360
DB 301 CATGAGTTCAAAAGAAAGGCAATGAGCTGTGAGAGCAGATGAATGTTCAAGAGCCGG 360
QY 361 ACAGCAGTGTTCCTGATCAAGTGAATGTTGGCAATGCTCTTTCGGGCTGAAAAAGCTG 420
DB 361 ACAGCAGTGTTCCTGATCAAGTGAATGTTGGCAATGCTCTTTCGGGCTGAAAAAGCTG 420
QY 421 CAACTCAGATGCTGCACTTACAAATGTTATATCATCACT 462
DB 421 CAACTCAGATGCTGCACTTACAAATGTTATATCATCACT 462

Search completed: May 30, 2005, 10:27:14
Job time : 284.354 secs

| Query Match | 100.0% | Score 462 | DB 3 | Length 2627 |
|-----------------------|----------------|---------------------------------------------------------------|----------|-------------|
| Best Local Similarity | 100.0% | Pred. No. 5e-146 | | |
| Matches 462 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | GGAGGACAGCGGACGCTCCACTCAGCCAGTACCCAGATACGCTGGAGACCTTCCCAACC | 60 | |
| Db | 23 | GGAGGACAGCGGACGCTCCACTCAGCCAGTACCCAGATACGCTGGAGACCTTCCCAACC | 82 | |
| QY | 61 | ATGGCTTCCTTGGGGCAGATCTCTTCTGGAGCATTAATTAGCATCATTAATTTCGGCT | 120 | |
| Db | 83 | ATGGCTTCCTTGGGGCAGATCTCTTCTGGAGCATTAATTAGCATCATTAATTTCGGCT | 142 | |
| QY | 121 | GGAGCAATGCACTCATTCATTGGCTTTGGTATTTTCAGGAGACACTCCATCACAGTCAT | 180 | |
| Db | 143 | GGAGCAATGCACTCATTCATTGGCTTTGGTATTTTCAGGAGACACTCCATCACAGTCAT | 202 | |
| QY | 181 | ACTGTGCGCTCAGCTGGGAACATTTGGGGAGATGAAATCTTGAGCTGCACCTTTTGAACCT | 240 | |
| Db | 203 | ACTGTGCGCTCAGCTGGGAACATTTGGGGAGATGAAATCTTGAGCTGCACCTTTTGAACCT | 262 | |
| QY | 241 | GACATCAAACTTTCTGATATTCGTATACAAATGCTGAAAGAAAGTGTTTTAGCTTGCTC | 300 | |
| Db | 263 | GACATCAAACTTTCTGATATTCGTATACAAATGCTGAAAGAAAGTGTTTTAGCTTGCTC | 322 | |
| QY | 301 | CATGAGTTCAAGAAGACAAAGATGAGCTGTCCGACAGCATGAAATGTTCAAGGCGCG | 360 | |
| Db | 323 | CATGAGTTCAAGAAGACAAAGATGAGCTGTCCGACAGCATGAAATGTTCAAGGCGCG | 382 | |
| QY | 361 | ACAGCAGTGTTCGTGATCAAGTAAAGTGGCAATGCTCTTTCGGCTGAAAAACGTG | 420 | |

Db 383 ACAGCAGTGTTCGATCATGAGTATGTCGCAAGCCTCTTGGCGCTGAAAAACGCG 442
QY 421 CAACCTCAGAGTGTTCGCGACCTCAACAATGTTATATATCACT 462
Db 443 CAACCTCAGAGTGTTCGCGACCTCAACAATGTTATATATCACT 484

RESULT 2

US-09-667-857-391
Sequence 391, Application US/09667857
Patent No. 6699664
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 391
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-667-857-391

Query Match 100.0%; Score 462; DB 4; Length 2627;
Best Local Similarity 100.0%; Pred. No. Se-146;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAAGCAGCGGAGCTCCATCAGCAGATACCCAGATAGCGCTGGGAACCTTCCCGAGCC 60
Db 23 GGAAAGCAGCGGAGCTCCATCAGCAGATACCCAGATAGCGCTGGGAACCTTCCCGAGCC 82
QY 61 ATGCGTCCCTGGGCGAGATCCCTCTTGAGAGCATATTAGCATCATCTATTATTCGCT 120
Db 83 ATGCGTCCCTGGGCGAGATCCCTCTTGAGAGCATATTAGCATCATCTATTATTCGCT 142
QY 121 GAGAGCAATTCATCATCTGCTTGGATTTCAGGAGACATCTCCATCAAGTCACT 180
Db 143 GAGAGCAATTCATCATCTGCTTGGATTTCAGGAGACATCTCCATCAAGTCACT 202
QY 181 ACTGTGCGCTCAGCTGGGAAATTTGGGGAGATGGAATCCTGAGCTGGACCTTTGAACCT 240
Db 203 ACTGTGCGCTCAGCTGGGAAATTTGGGGAGATGGAATCCTGAGCTGGACCTTTGAACCT 262
QY 241 GACATCAAACTTTCGATATCGTATATCAATGCTGGAAGAAAGTGTTTAGGCTTGGTC 300
Db 263 GACATCAAACTTTCGATATCGTATATCAATGCTGGAAGAAAGTGTTTAGGCTTGGTC 322
QY 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGAGAGAGAGATGAATGTTTCAGAGCCGG 360
Db 323 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGAGAGAGAGATGAATGTTTCAGAGCCGG 382
QY 361 AAGAGAGTGTTCGATCAAGTATGATGTCGCAATGCTCTTTGGCGCTGAAAAACGCG 420
Db 383 AAGAGAGTGTTCGATCAAGTATGATGTCGCAATGCTCTTTGGCGCTGAAAAACGCG 442
QY 421 CAACCTCAGAGTGTTCGCGACCTCAACAATGTTATATCACT 462
Db 443 CAACCTCAGAGTGTTCGCGACCTCAACAATGTTATATCACT 484

RESULT 3

US-09-799-451-332
Sequence 332, Application US/09799451
Patent No. 6783969

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yuning
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No.6783969el Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_Fl_genes Version 2.0
SEQ ID NO 332
LENGTH: 1046
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (4)..(888)
US-09-799-451-332

Query Match 80.5%; Score 372; DB 4; Length 1046;
Best Local Similarity 100.0%; Pred. No. 1.1e-115;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 AGCATATTTAGCATCATATTTCTGCTGGAGCAATTGCACTCATATGGCTTGGT 150
Db 73 AGCATATTTAGCATCATATTTCTGCTGGAGCAATTGCACTCATATGGCTTGGT 132
QY 151 ATTTCAGGAGACATTCATCACTCACTACTGCTGCTCAAGCTGGGAAACATTGGGAG 210
Db 133 ATTTCAGGAGACATTCATCACTCACTACTGCTGCTCAAGCTGGGAAACATTGGGAG 192
QY 211 GATGGAATCTGAGCTGCACTTTGAACTTGACATCAAACTTCTGATATCGTATGACAA 270
Db 193 GATGGAATCTGAGCTGCACTTTGAACTTGACATCAAACTTCTGATATCGTATGACAA 252
QY 271 TGGCTGAAGAAAGTGTTCGCTTGGTTCATGATGATCAAGAAAGCAAGATGAGCTG 330
Db 253 TGGCTGAAGAAAGTGTTCGCTTGGTTCATGATGATCAAGAAAGCAAGATGAGCTG 312
QY 331 TCGAGAGAGATGAATGTTTCAGAGCCGGACAGAGTGTTCGATCAAGTATGATGTT 390
Db 313 TCGAGAGAGATGAATGTTTCAGAGCCGGACAGAGTGTTCGATCAAGTATGATGTT 372
QY 391 GGCATGCTCTTTGCGGCTGAAAAACGTGCAACTCAAGATGCTGGCACTTCAAAATGT 450
Db 373 GGCATGCTCTTTGCGGCTGAAAAACGTGCAACTCAAGATGCTGGCACTTCAAAATGT 432
QY 451 TATATCATCACT 462
Db 433 TATATCATCACT 444

RESULT 4

US-09-910-174B-27

```
; Sequence 27, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-910-174B-27

Query Match          9.4%; Score 43.6; DB 4; Length 948;
Best Local Similarity 63.2%; Pred. No. 0.00037;
Matches 67; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 357 CCGGACGACGAGTGTTCCTGATCAAGATAGTGTGGCAATGCCCTTTGGCGCTGAATAA 416
DB 273 CCGGACGACGCGCTCTCCCTGACCTGTGGTGCAGGCAATGCCCTTTGAGGCTGCAGCG 332

QY 417 CGTGCACTCAAGATGCTGCGACCTTCAAAATGTTATATCATCACT 462
DB 333 CGTCCGAGTAACGACGAGGCGACGTACCTGCTTTGTGAGCACTT 378

RESULT 5
US-09-620-461-27
; Sequence 27, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Mus
US-09-620-461-27

Query Match          9.4%; Score 43.6; DB 4; Length 948;
Best Local Similarity 63.2%; Pred. No. 0.00037;
Matches 67; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 357 CCGGACGACGAGTGTTCCTGATCAAGATAGTGTGGCAATGCCCTTTGGCGCTGAATAA 416
DB 273 CCGGACGACGCGCTCTCCCTGACCTGTGGTGCAGGCAATGCCCTTTGAGGCTGCAGCG 332

QY 417 CGTGCACTCAAGATGCTGCGACCTTCAAAATGTTATATCATCACT 462
DB 333 CGTCCGAGTAACGACGAGGCGACGTACCTGCTTTGTGAGCACTT 378

RESULT 6
US-09-949-016-876
; Sequence 876, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
```

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 876
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-876

Query Match          8.8%; Score 40.6; DB 4; Length 1964;
Best Local Similarity 47.5%; Pred. No. 0.006;
Matches 121; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 203 TTGGGGAGATGGAATCTGAGCTGCACTTTGACCTGACATCAAACTTTGATATCG 262
DB 253 TGGGGAGAGCGCGCTGTTCTCTGCTCCTCTTTCTTGAGACGACGAGGCTATGG 312

QY 263 TGATTAACAATGCGGAAGAGAGTGTGTTAGGCTGTGCTCAATGATCAAGAGGCAAG 332
DB 313 AAGTGGGGTCTTCAAGAAATCACTTCATGCTGTGTGTCACCTTCAAGAGATGGGGAAG 372

QY 323 ATGAGCTGTGCGACGAGATGAATGTTCAAGAGCGCGACGACGAGTGTTCGATCAAG 382
DB 373 ACTGGGAATCTAAGACAGATGCCACAGTATCGAGGAGAACTGAGTTGTGAAGACTCCA 432

QY 383 TGATGTTGGCAATGCTCTGTTGCGGCTGAATAAGTGAACATCAAGATGTCGACCT 442
DB 433 TTGACGGGGGCGCTGCTCTCTTAAGGCTAATAAATCAATCACTCCTCGACATCGGCTGT 492

QY 443 ACAATGTTATATCA 457
DB 493 ATGGGTGCTGTCTCA 507

RESULT 7
US-08-724-394A-12
; Sequence 12, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```



```

1  APPLICATION NUMBER:  US/08/724,394A
2  FILING DATE:  01-OCT-1996
3  CLASSIFICATION:  536
4  ATTORNEY/AGENT INFORMATION:
5  NAME:  Faltz, Renee A.
6  REGISTRATION NUMBER:  35,136
7  REFERENCE/DOCKET NUMBER:  017957-000100
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE:  415-576-0200
10 TELEFAX:  415-576-0300
11 INFORMATION FOR SEQ ID NO:  12:
12 SEQUENCE CHARACTERISTICS:
13     LENGTH:  2882 base pairs
14     TYPE:  nucleic acid
15     STRANDEDNESS:  not relevant
16     TOPOLOGY:  not relevant
17     MOLECULE TYPE:  cDNA
18     FEATURE:
19     NAME/KEY:  misc feature
20     LOCATION:  1..2882
21     OTHER INFORMATION:  /note= "cDNA 21"
22 US-08-724-394A-12

```

| | | | | |
|-----------------------|-----------------|-----------------|-----------|--------------|
| Query Match | 7.9% | Score 36.4; | DB 2; | Length 2882; |
| Best Local Similarity | 45.7%; | Pred. No. 0.2; | | |
| Matches 127; | Conservative 0; | Mismatches 151; | Indels 0; | Gaps 0 |

| QY | 179 | CTACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAAATCCTGAGCTGCACCTTTGAAAC | 238 |
|----|-----|------------------------------------------------------------------|-----|
| Db | 314 | CCACTGATGCCATCTTGCGCACGSGTTGGAGAAAAACATACGTTAGCTGCGCATCTGTACAC | 373 |
| QY | 239 | CTGACATCAAACTTTCTGATATCTGATATCAAAATGCGTGAAGGAGTGTTTAGGCTTGG | 298 |
| Db | 374 | CCGAGAAAAATGCTGAGGACATGAGAGTGTCGGTGTTCGGCTTCAGTTCTCCCCCCAG | 433 |
| QY | 299 | TTCATGATTCANAGAAAGCAAGATGAGACTGTGCGAGCAGAGATGAAATGTTTCAGAGGC | 358 |
| Db | 434 | TGTTTGTGTATTAAGGTGCGAGAGAGAAACAGAGAGCAGTTGAGAGATACGAGGAA | 493 |
| QY | 359 | GGAACAGCAGTGTTTGCTGATCAAGTATGTTGGCAATGCCCTTTTGGCGCTGAAAAACG | 418 |
| Db | 494 | GAACACACTTTTGTAGCAAAAGACATCAGCAGGGGACGGTGGCCCTGTTCATACAAACA | 553 |
| QY | 419 | TGCACCTCAACGATGCTGGGACCTTAACAAATGTTTATATC | 456 |
| Db | 554 | TCAACGCCAGGAAAAACGACCTTACCGCTGTACTTC | 591 |

```

RESULT 8
US-09-949-016-20613
; Sequence 20613, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: Cl001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20613
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-20613

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| | | | | |
|-----------------------|-----------------|------------------|-----------|-------------|
| Query Match | 7.8% | Score 36.2; | DB 4; | Length 601; |
| Best Local Similarity | 68.5%; | Pred. No. 0.091; | | |
| Matches 50; | Conservative 0; | Mismatches 23; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|-------------------------------------------------------------|-----|
| Qy | 310 | AAAGAAAGCAAGATAGCTGTGAGAGCAGATCAATATGTTCAAGGCCGAGACGCGATG | 369 |
| Db | 485 | AAAGAAAGCAAGATTTAGGGGTACGATCGGGGGCAATGCCAGAAAGGGAAACGAGAAAG | 544 |
| Qy | 370 | TTTGTGATCAAG | 382 |
| Db | 545 | TTCTGCTGGGGAAG | 557 |

RESULT 9
US-09-949-016-20614
; Sequence 20614, Application US/09949016

```

1  APPLICANT: VENTNER, J. Craig et al.
2  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
3  TITLE OF INVENTION: WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
4  FILE REFERENCE: CL001307
5  CURRENT APPLICATION NUMBER: US/09/949,016
6  CURRENT FILING DATE: 2000-04-14
7  PRIOR APPLICATION NUMBER: 60/241,755
8  PRIOR FILING DATE: 2000-10-20
9  PRIOR APPLICATION NUMBER: 60/237,768
10 PRIOR FILING DATE: 2000-10-03
11 PRIOR APPLICATION NUMBER: 60/231,498
12 PRIOR FILING DATE: 2000-09-08
13 NUMBER OF SEQ ID NOS: 207012
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO 20614
16 LENGTH: 601

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| | | | | |
|-----------------------|--------------|------------------|----------------|-------------|
| Query Match | 7.8%; | Score 36.2; | DB 4; | Length 601; |
| Best Local Similarity | 68.5%; | Pred. No. 0.091; | | |
| Matches 50; | Conservative | 0; | Mismatches 23; | Indels 0; |
| | | | Gaps | 0; |

| Qy | 310 | 370 |
|----|-----------------------------------------------------------|--------------------|
| Qy | AAAGAAAGCAAGATACGTCGCAGCAGATGAAATGTCACAGCCCGACACGACGTG | TTTGCTGCATCAAG 382 |
| Db | AAAGAAAGCAAGATTAGGGGTACGATCGGGGCAAAATGCCAAGAGGGGAACAGGAAG | TTGCTCGGGAG 560 |

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1 RESULT 10
2 US-09-949-016-69029
3 Sequence 69029, Application US/09949016
4 Patent No. 6812339
5 GENERAL INFORMATION:
6 APPLICANT: VENTER, J. Craig et al.
7 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
8 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
9 FILE REFERENCE: C1001307
10 CURRENT APPLICATION NUMBER: US/09/949,016
11 CURRENT FILING DATE: 2000-04-14
12 PRIOR APPLICATION NUMBER: 60/241,755
13 PRIOR FILING DATE: 2000-10-20
14 PRIOR APPLICATION NUMBER: 60/237,768
15 PRIOR FILING DATE: 2000-10-03
16 PRIOR APPLICATION NUMBER: 60/231,498
17 PRIOR FILING DATE: 2000-09-08
18 NUMBER OF SEQ ID NOS: 207012
19 SOFTWARE: FastSeq for Windows Version 4.0
20 SEQ ID NO 69029
21 LENGTH: 601
22 TYPE: DNA

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ORGANISM: Human
US-09-949-016-69029

Query Match
Best Local Similarity 7.8%; Score 36.2; DB 4; Length 601;
Best Local Similarity 68.5%; Pred. No. 0.091;
Matches 50; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 310 AAGAAGGCAAGATGAGCTGTGAGCAGATGAATGTTTCAGAGGCCGACAGCAGTG 369
DB 488 AAGAAGGCAAGATGAGGCTGATCGGGGCAATGCCAGAGGGGAAACAGGAAG 547

QY 370 TTTGCTGATCAAG 382
DB 548 TCTGCTGGGGAAG 560

RESULT 11
US-09-949-016-69030

Sequence 69030, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 69030

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-69030

Query Match
Best Local Similarity 7.8%; Score 36.2; DB 4; Length 601;
Best Local Similarity 68.5%; Pred. No. 0.091;
Matches 50; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 310 AAGAAGGCAAGATGAGCTGTGAGCAGATGAATGTTTCAGAGGCCGACAGCAGTG 369
DB 485 AAGAAGGCAAGATGAGGCTGATCGGGGCAATGCCAGAGGGGAAACAGGAAG 544

QY 370 TTTGCTGATCAAG 382
DB 545 TCTGCTGGGGAAG 557

RESULT 12
US-09-949-016-11887

Sequence 11887, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11887
LENGTH: 11820

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(11820)

OTHER INFORMATION: n = A,T,C or G

Query Match
Best Local Similarity 7.8%; Score 36.2; DB 4; Length 11820;
Best Local Similarity 68.5%; Pred. No. 0.56;
Matches 50; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 310 AAGAAGGCAAGATGAGCTGTGAGCAGATGAATGTTTCAGAGGCCGACAGCAGTG 369
DB 5264 AAGAAGGCAAGATGAGGCTGATCGGGGCAATGCCAGAGGGGAAACAGGAAG 5323

QY 370 TTTGCTGATCAAG 382
DB 5324 TCTGCTGGGGAAG 5336

RESULT 13
US-09-949-016-13767

Sequence 13767, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13767

LENGTH: 11826

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(11826)

OTHER INFORMATION: n = A,T,C or G

Query Match
Best Local Similarity 7.8%; Score 36.2; DB 4; Length 11826;
Best Local Similarity 68.5%; Pred. No. 0.56;
Matches 50; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 310 AAGAAGGCAAGATGAGCTGTGAGCAGATGAATGTTTCAGAGGCCGACAGCAGTG 369
DB 5264 AAGAAGGCAAGATGAGGCTGATCGGGGCAATGCCAGAGGGGAAACAGGAAG 5323

QY 370 TTTGCTGATCAAG 382
DB 5324 TCTGCTGGGGAAG 5336

RESULT 14
US-09-949-016-11547/C

Sequence 11547, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11547
LENGTH: 854
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-11547

Query Match
Best Local Similarity 55.6%; Score 36; DB 4; Length 854;
Pred. No. 0.13;
Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 54 CCAGCATGCTCCCTGGGAGATCTCTTGGAGCATATAGCATCATATAT 113
DB 628 CCTCTCCACTTTTTCCTTGAATAATCATCTTACTGACAGTTCTTCAATCTTCT 569
QY 114 TCTGCTGAGCAATGTCATCATCTTGGTATTTGAGGAGACACTGCATCAC 173
DB 568 TATGCTGATTCCTGGCAACCTTCACTTGGCTTTCCTGCGAGTCTGCTCTCAT 509
QY 174 AGTC 177
DB 508 CCTC 505

RESULT 15
US-08-724-394A-15
Sequence 15, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Teuchihaashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fille, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: misc feature
LOCATION: 1..3416
OTHER INFORMATION: /note="cDNA 44"
US-08-724-394A-15

Query Match
Best Local Similarity 46.1%; Score 34.8; DB 2; Length 3416;
Pred. No. 0.78;
Matches 117; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 203 TTGGGAGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAAACTTCTGATATCG 262
DB 490 TGGTGAAGACGCTGATCTGCCCTTGTCACTGTTCCGACCATGATGACAGACATGG 549
QY 263 TGATCAATGCTGAGAGAGATGTTTAAAGCTTGTTCATGAGTTCAAGAGGCAAG 322
DB 550 AGCTGAAGTGGGTGATGCCAGCCTAAGGCAAGTGATGAAGTATGACATGGAAGG 609
QY 323 ATGAGCTTCGAGCAGATGAATGTTCAAGGCCGAGCAGAGTGTTCATATCAG 382
DB 610 AAGTGAAGACAGGAGAGTCACTGATCGAGGAGAACTTGAATCTGCGGAGATGCA 669
QY 383 TGATAGTTGGCAATGCTCTTGGGAGCTGAAAAAGTGCACATGACAGATGCTGGACCT 442
DB 670 TCATGCGAGGAGAGCTCTCTCCGAATACAAAGTCAAGCTTGAACAGTGAAGT 729
QY 443 ACAATGTTATATC 456
DB 730 ACTTGTTATTTT 743

Search completed: May 31, 2005, 00:29:01
Job time : 86.6262 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 17:54:16 ; Search time 316.984 Seconds

(without alignments)
8948.327 Million cell updates/sec

Title: US-09-763-978B-13

Perfect score: 462
Sequence: 1 ggaaggcagcgagctcca.....acaatgtatcatcact 462

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 306979757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
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- 14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
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- 18: /cgn2_6/prodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 462 | 100.0 | 1065 | 9 | US-09-877-065-5 |
| 2 | 462 | 100.0 | 1658 | 9 | US-09-989-722-290 |
| 3 | 462 | 100.0 | 1658 | 9 | US-09-989-723-290 |
| 4 | 462 | 100.0 | 1658 | 9 | US-09-989-729-290 |
| 5 | 462 | 100.0 | 1658 | 9 | US-09-989-727-290 |
| 6 | 462 | 100.0 | 1658 | 9 | US-09-989-731-290 |
| 7 | 462 | 100.0 | 1658 | 9 | US-09-989-732-290 |
| 8 | 462 | 100.0 | 1658 | 9 | US-09-991-073-290 |
| 9 | 462 | 100.0 | 1658 | 9 | US-09-990-442-290 |
| 10 | 462 | 100.0 | 1658 | 9 | US-09-991-163-290 |
| 11 | 462 | 100.0 | 1658 | 9 | US-09-993-604-290 |

| | | | | | | |
|----|-----|-------|------|----|--------------------|-------------------|
| 12 | 462 | 100.0 | 1658 | 9 | US-09-990-456-290 | Sequence 290, App |
| 13 | 462 | 100.0 | 1658 | 9 | US-09-989-721-290 | Sequence 290, App |
| 14 | 462 | 100.0 | 1658 | 9 | US-09-992-598-290 | Sequence 290, App |
| 15 | 462 | 100.0 | 1658 | 9 | US-09-989-293A-290 | Sequence 290, App |
| 16 | 462 | 100.0 | 1658 | 9 | US-09-989-735-290 | Sequence 290, App |
| 17 | 462 | 100.0 | 1658 | 9 | US-09-990-444-290 | Sequence 290, App |
| 18 | 462 | 100.0 | 1658 | 9 | US-09-991-181-290 | Sequence 290, App |
| 19 | 462 | 100.0 | 1658 | 9 | US-09-989-730-290 | Sequence 290, App |
| 20 | 462 | 100.0 | 1658 | 9 | US-09-990-436-290 | Sequence 290, App |
| 21 | 462 | 100.0 | 1658 | 9 | US-09-993-687-290 | Sequence 290, App |
| 22 | 462 | 100.0 | 1658 | 10 | US-09-989-734-290 | Sequence 290, App |
| 23 | 462 | 100.0 | 1658 | 10 | US-09-997-653-290 | Sequence 290, App |
| 24 | 462 | 100.0 | 1658 | 10 | US-09-989-724-290 | Sequence 290, App |
| 25 | 462 | 100.0 | 1658 | 10 | US-09-990-441-290 | Sequence 290, App |
| 26 | 462 | 100.0 | 1658 | 10 | US-09-990-441-290 | Sequence 290, App |
| 27 | 462 | 100.0 | 1658 | 10 | US-09-993-667-290 | Sequence 290, App |
| 28 | 462 | 100.0 | 1658 | 10 | US-09-997-428-290 | Sequence 290, App |
| 29 | 462 | 100.0 | 1658 | 10 | US-09-997-666-290 | Sequence 290, App |
| 30 | 462 | 100.0 | 1658 | 10 | US-09-990-438-290 | Sequence 290, App |
| 31 | 462 | 100.0 | 1658 | 10 | US-09-990-562-290 | Sequence 290, App |
| 32 | 462 | 100.0 | 1658 | 10 | US-09-990-711-290 | Sequence 290, App |
| 33 | 462 | 100.0 | 1658 | 10 | US-09-989-726-290 | Sequence 290, App |
| 34 | 462 | 100.0 | 1658 | 10 | US-09-998-156-290 | Sequence 290, App |
| 35 | 462 | 100.0 | 1658 | 10 | US-09-990-437-290 | Sequence 290, App |
| 36 | 462 | 100.0 | 1658 | 10 | US-09-991-157-290 | Sequence 290, App |
| 37 | 462 | 100.0 | 1658 | 10 | US-09-997-514-290 | Sequence 290, App |
| 38 | 462 | 100.0 | 1658 | 10 | US-09-997-573-290 | Sequence 290, App |
| 39 | 462 | 100.0 | 1658 | 10 | US-09-991-172-290 | Sequence 290, App |
| 40 | 462 | 100.0 | 1658 | 10 | US-09-997-726-290 | Sequence 290, App |
| 41 | 462 | 100.0 | 1658 | 10 | US-09-997-559-290 | Sequence 290, App |
| 42 | 462 | 100.0 | 1658 | 10 | US-09-997-601-290 | Sequence 290, App |
| 43 | 462 | 100.0 | 1658 | 10 | US-09-990-443-290 | Sequence 290, App |
| 44 | 462 | 100.0 | 1658 | 10 | US-09-929-766-4 | Sequence 4, Appl1 |
| 45 | 462 | 100.0 | 1658 | 10 | US-09-991-854-290 | Sequence 290, App |

ALIGNMENTS

RESULT 1
US-09-877-065-5
; Sequence 5, Application US/09877065
; Patent No. US20020051990A1
; GENERAL INFORMATION:
; APPLICANT: OPIE, ERIC
; APPLICANT: MCILACHLAN, KAREN
; APPLICANT: HEARD, CHERYL J.
; TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR
; FILE REFERENCE: 037003-0280631
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,451
; PRIORITY FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-065-5

Query Match 100.0%; Score 462; DB 9; Length 1065;
Best Local Similarity 100.0%; Pred. No. 4.6e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 12 GGAAGGAGGCGAGGCTCCAGCAGGAGATGAGTGGAGACCTTCCGAGCC 71
QY 61 ATGGCTTCCTCGGAGGAGATCTCTTCTGAGAGCATATTAGCATCATTTATTCGGCT 120
DB 72 ATGGCTTCCTCGGAGGAGATCTCTTCTGAGAGCATATTAGCATCATTTATTCGGCT 131

;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
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;; PRIOR APPLICATION NUMBER: 60/090862
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;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
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;; PRIOR APPLICATION NUMBER: 60/091544
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGAGGCGAGGCGAGCTCCAGCTCAGCAGTACCAGATACGCTGGAACTTCCCAACC 60

Qy 61 ATGGCTTCCCTGGGGGAGATCCCTTCTGGAGCATTAATAGCATCATTAATCTGGCT 120
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Qy 121 GGAGCAATTGCACTCATCATTTGGTATTTCAGGAGCACTTCATCAGCTCACT 180
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Qy 181 ACTGTGCTCAGCTGGGAACATTTGGGGAGATGGAATCTTGAAGCTGCACTTTGAACCT 240
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Qy 241 GACATCAAACTTCTGATATCGATATCAATGCGTGAAGAAAGGTGTTTAAAGCTGGTC 300
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Qy 301 CATGAGTCAAAAGAGCAAGATGAGCTGTGAGAGCAGATGAATGTTTCAGAGCCCG 360
Db 301 CATGAGTCAAAAGAGCAAGATGAGCTGTGAGAGCAGATGAATGTTTCAGAGCCCG 360

Qy 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTGAAAAAGCG 420
Db 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTGAAAAAGCG 420

Qy 421 CAAGTCAGAGATGCTGGACCTTAACAATGTTATATCATCACT 462
Db 421 CAAGTCAGAGATGCTGGACCTTAACAATGTTATATCATCACT 462

RESULT 3
US-09-989-723-290
Sequence 290, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No.5.9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 ATGGCTTCCCTGGGCGAGATCCCTTCTTGAGACATATTGCAATCATATTTCGGCT 120
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RESULT 4
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; Sequence 290, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
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;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC56
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-989-731-290
; Sequence 290, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Grimaldi, U. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5.9e-147; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0;

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DB 1 GGAAGGACGCGAGCTCCAGCTGACGAGTACCCAGATACGCTGGGAACCTTCCCGAGCC 60
QY 61 ATGGCTTCCTGGGCGAGATCTCTTCTGGAGCATATTAGCATCATCTATTCTGGCT 120
DB 61 ATGGCTTCCTGGGCGAGATCTCTTCTGGAGCATATTAGCATCATCTATTCTGGCT 120
QY 121 GGAGCAATGCACTCATCTGCTTGGATTTCAGGAGACATCCCATGACAGTCACT 180
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QY 301 CATGAGTTCAAGAAAGAGCAAGTAGCTGTGGAGCAGAGTGAATGTTCAAGAGCCGG 360
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QY 421 CAACTTACAGATGCTGGCACTTAACAATGTATATATCACT 462
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RESULT 7
US-09-989-732-290

;; Sequence 290, Application US/09989732
;; Patent No. US20020123463A1

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desmoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Matanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2730P1C57

;; CURRENT APPLICATION NUMBER: US/09/989,732

;; PRIOR APPLICATION NUMBER: 60/049787

;; PRIOR FILING DATE: 1997-06-16

;; PRIOR APPLICATION NUMBER: 60/062250

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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred No.5.9e-147; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0;

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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
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Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 GACATCAAACTTCTGATATCGTATACATGCTGCAAGGATGTTTATAGCTTGGTC 300
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DB 361 ACAGCAGTGTTCGTATCATGATGATGATGGAATGCTCTTTGGGCTGAAAAAGCTG 420
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RESULT 9
US-09-442-290
Sequence 290, Application US/09990442
Patent No. US2002013252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730Pic8
CURRENT APPLICATION NUMBER: US/09/990,442
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25


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/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091633
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 462; DB 9; Length 1658;
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Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-991-163-290
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/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
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/ APPLICANT: Botstein, David
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/ APPLICANT: Gerber, Hanspeter
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/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
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/ APPLICANT: Napier, Mary A.
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/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
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/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C17
/ CURRENT APPLICATION NUMBER: US/09/991,163
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/049787
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5.9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 ACTGTCGCTCAGCTGGGAAACATTTGGGAGATGGAATCTTGAGCTGCACTTTGAACCT 240
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RESULT 11
US-09-993-604-290
Sequence 290, Application US/09993604
Patent No. US20020137075A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumahe, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Acids Encoding and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C25
CURRENT APPLICATION NUMBER: US/09/993,604
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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/ PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-990-456-290
Sequence 290, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
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/ APPLICANT: Paoni, Nicholas F.
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/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC22
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-06-02
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Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 ACTGTGCTCAGCTGGGAAACATTTGGGAGAGATGAAATCTGAGCTGCATTTGAACCT 240
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QY 301 CATGAGTTCAAGAGAGCAAGATGAGCTGCGAGCAGAGATGAATGTTTCAGAGCCCG 360
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RESULT 13
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Sequence 290, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auscin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC55
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CURRENT FILING DATE: 2001-11-19
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| Prior | Filing Date: | 1998-06-26 |
| Prior | Application Number: | 60/091360 |
| Prior | Filing Date: | 1998-07-01 |
| Prior | Application Number: | 60/091478 |
| Prior | Filing Date: | 1998-07-02 |
| Prior | Application Number: | 60/091544 |
| Prior | Filing Date: | 1998-07-01 |
| Prior | Application Number: | 60/091519 |
| Prior | Filing Date: | 1998-07-02 |
| Prior | Application Number: | 60/091626 |
| Prior | Filing Date: | 1998-07-02 |
| Prior | Application Number: | 60/091633 |
| Prior | Filing Date: | 1998-07-02 |
| Prior | Application Number: | 60/091978 |
| Prior | Filing Date: | 1998-07-07 |
| Prior | Application Number: | 60/091982 |
| Prior | Filing Date: | 1998-07-07 |
| Prior | Application Number: | 60/092182 |
| Prior | Filing Date: | 1998-07-09 |

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| Best Local Similarity | 100.0%; | Pred. No. 5,9e-147; | | |
| Matches 462; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

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| Db | 61 | ATGGCTTCCTCGGGGCAGATCCCTTTCTGAGCATATTAGCATCATCATATTCTGGCT | 120 |
| Qy | 121 | GGAGCAATGTGACATCATATTGGCTTTGGTAATTTCAAGSAGACATCCATCACAGTACT | 180 |
| Db | 121 | GGAGCAATGTGACATCATATTGGCTTTGGTAATTTCAAGSAGACATCCATCACAGTACT | 180 |
| Qy | 181 | ACTGTGCTTCAGCTGGGAAACATTTGGGAGAGATGAAATCTGAGCTGCATTTTGAACT | 240 |
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| Qy | 241 | GACATCAAATTTTGATATCGTATATACAATAGCTGAAAGAAGGTGTTTTAGCTTGCTC | 300 |
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| Qy | 301 | CATAGTTCAAAGAAGCAAAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGGCCGG | 360 |
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| Qy | 361 | ACAGCAGTGTGTGCTGATCAAGTAGATGTTGGCAATGCTTTTGGCGCTGAAAAACGTG | 420 |
| Db | 361 | ACAGCAGTGTGTGCTGATCAAGTAGATGTTGGCAATGCTTTTGGCGCTGAAAAACGTG | 420 |
| Qy | 421 | CAACTCAAGATGCTGGCACTTACAAATGTTATATCACTACT 462 | |
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RESULT 14

US-09-992-598-290

; Sequence 290, Application US/09992598

; Patent No. US20020160384A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAAGCAGCGGCGAGCTCCACTGAGCCAGTACCAGATACGCTGGGAACTTCCCGCAGCC 60
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Db      1 GGAAGGCAAGGCGAGCTCCACTGAGCCAGTACCAGATACGCTGGGAACTTCCCGCAGCC 60

Qy      61 ATGGCTTCCTGGGGGAGATGCTCTTCTTGAGGATTAATTGATCATGATTAATTTGGCT 120
      61 ATGGCTTCCTGGGGGAGATGCTCTTCTTGAGGATTAATTGATCATGATTAATTTGGCT 120
Db      61 ATGGCTTCCTGGGGGAGATGCTCTTCTTGAGGATTAATTGATCATGATTAATTTGGCT 120

Qy      121 GGAAGCAATTGCATCATGATTTGGCTTGTGATTTCAAGGGAGACATCCCAACAGTCACT 180
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Db      121 GGAAGCAATTGCATCATGATTTGGCTTGTGATTTCAAGGGAGACATCCCAACAGTCACT 180

Qy      181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCTTGAGCTGCACTTTTGAACCT 240
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Db      181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCTTGAGCTGCACTTTTGAACCT 240

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Db      241 GACATCAAACTTTCTGATATCGTGATTCGAATGCGCTGAGAGAGATGTTTAAAGCTTGGCT 300

Qy      301 CATGATTTCAAAAGGCAAGATGAGCTGTGAGAGAGATGAATGTTCAAGAGCCGG 360
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Db      301 CATGATTTCAAAAGGCAAGATGAGCTGTGAGAGAGATGAATGTTCAAGAGCCGG 360

Qy      361 ACAGCAGTGTTCGTATCAAGTATGATGATGGAATGCCCTTCTTGCGGCTGAATAACGTG 420
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; Sequence 290, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
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PRIOR APPLICATION NUMBER: 60/088202
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5.9e-147; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0;

Qy 1 GGAAGCAGCGGACCTCCTCAGCCAGTACCCAGATACGCTGGAGACTTCCCAACC 60
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Db 61 ATGGCTTCCCTGGGGCAGATCCTCTCTGGAGCATATTAAGCATCATCATTTATTTCTGGCT 120
QY 121 GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAAGGAGACACTCCATCAGTCACT 180
Db 121 GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAAGGAGACACTCCATCAGTCACT 180
QY 181 ACTGTGCTCAGCTGGGAACATTGGGGAGGATGGAACTCTGAGCTGCACTTTGAACT 240
Db 181 ACTGTGCTCAGCTGGGAACATTGGGGAGGATGGAACTCTGAGCTGCACTTTGAACT 240
QY 241 GACATCAAACTTTCTGATATCGTGAATCAATGGCTGAAGAGGTTGTTTAAAGCTTGGTC 300
Db 241 GACATCAAACTTTCTGATATCGTGAATCAATGGCTGAAGAGGTTGTTTAAAGCTTGGTC 300
QY 301 CATGAGTTCAAAGGCAAGAGATGAGCTGTGGAGCAGATGAATGTTCAAGGCCGG 360
Db 301 CATGAGTTCAAAGGCAAGAGATGAGCTGTGGAGCAGATGAATGTTCAAGGCCGG 360
QY 361 ACAGCAGTGTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGGGCTGAAGAAAGTG 420
Db 361 ACAGCAGTGTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGGGCTGAAGAAAGTG 420
QY 421 CAACTCAGAGATGCTGGACCTACAAATGTTATATCATCACT 462
Db 421 CAACTCAGAGATGCTGGACCTACAAATGTTATATCATCACT 462

Search completed: May 31, 2005, 10:07:40
Job time : 317.984 secs

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Db 133 GGAGCAATTGCACTCATTCATTTGGCTTTGGTATTTCAGGGAGACATTCATCAGATCACT 192

QY 181 ACTGTGGCTCAGCTGGGAACATTTGGGGAGATGAGATCCTGAGCTGCACTTTGAACCT 240

Db 193 ACTGTGGCTCAGCTGGGAACATTTGGGGAGATGAGATCCTGAGCTGCACTTTGAACCT 252

QY 241 GACATCAAACTTTCTGATATCGATATCAATGAGCTGAGAGAGTGTATTAGGCTTGTC 300

Db 253 GACATCAAACTTTCTGATATCGATATCAATGAGCTGAGAGAGTGTATTAGGCTTGTC 312

QY 301 CATGAGTTCAAAGAGCAAAAGATGAGCTGCGAGAGATGAATGTTCAAGGCCGG 360

Db 313 CATGAGTTCAAAGAGCAAAAGATGAGCTGCGAGAGATGAATGTTCAAGGCCGG 372

QY 361 ACAGCAGTGTTCGTATCAAGATGATGAGTGGCAATGCTCTTTGGCGCTGAAGAACGTG 420

Db 373 ACAGCAGTGTTCGTATCAAGATGATGAGTGGCAATGCTCTTTGGCGCTGAAGAACGTG 432

QY 421 CAATCAGAGATGCTGGCACCTTCAAAATGTTATATCACT 462

Db 433 CAATCAGAGATGCTGGCACCTTCAAAATGTTATATCACT 474

RESULT 2
BP255264 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP255264 Sugano cDNA library, kidney epithelial cell Homo sapiens
DEFINITION cDNA clone HRC08666, mRNA sequence.

ACCESSION BP255264
VERSION BP255264.1 GI:52170494
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanebaidai, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. 583
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC08664"
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ORIGIN
Query Match 100.0%; Score 462; DB 5; Length 583;
Best Local Similarity 100.0%; Pred. No. 8e-130; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGAGGAGCTCAGTCACTGAGCCAGTACCAGATGCTGGAACTTCCCGAGCC 60
Db 13 GGAAGGAGGAGGAGGAGCTCAGTCACTGAGCCAGTACCAGATGCTGGAACTTCCCGAGCC 72
QY 61 ATGGCTTCCCTGGGGAGATGCTCTTCTTGAGAGCAATTAATGATCATCATTAATTTGGCT 120
Db 73 ATGGCTTCCCTGGGGAGATGCTCTTCTTGAGAGCAATTAATGATCATCATTAATTTGGCT 132
QY 121 GGAAGCAATTCAGTCACTGATGCTGTTGGTATTTCAAGGAGACATTCATCAGATCACT 180
Db 133 GGAAGCAATTCAGTCACTGATGCTGTTGGTATTTCAAGGAGACATTCATCAGATCACT 192

QY 181 ACTGTGGCTCAGCTGGGAACATTTGGGGAGATGAGATCCTGAGCTGCACTTTGAACCT 240

Db 193 ACTGTGGCTCAGCTGGGAACATTTGGGGAGATGAGATCCTGAGCTGCACTTTGAACCT 252

QY 241 GACATCAAACTTTCTGATATCGATATCAATGAGCTGAGAGAGTGTATTAGGCTTGTC 300

Db 253 GACATCAAACTTTCTGATATCGATATCAATGAGCTGAGAGAGTGTATTAGGCTTGTC 312

QY 301 CATGAGTTCAAAGAGCAAAAGATGAGCTGCGAGAGATGAATGTTCAAGGCCGG 360

Db 313 CATGAGTTCAAAGAGCAAAAGATGAGCTGCGAGAGATGAATGTTCAAGGCCGG 372

QY 361 ACAGCAGTGTTCGTATCAAGATGATGAGTGGCAATGCTCTTTGGCGCTGAAGAACGTG 420

Db 373 ACAGCAGTGTTCGTATCAAGATGATGAGTGGCAATGCTCTTTGGCGCTGAAGAACGTG 432

QY 421 CAATCAGAGATGCTGGCACCTTCAAAATGTTATATCACT 462

Db 433 CAATCAGAGATGCTGGCACCTTCAAAATGTTATATCACT 474

RESULT 3
BX499180 604 bp mRNA linear EST 04-SEP-2003
LOCUS BX499180
DEFINITION DKFZp79B1644_r1 779 (synonym: hnccl) Homo sapiens cDNA clone
DKFZp79B1644.5, mRNA sequence.

ACCESSION BX499180
VERSION BX499180.1 GI:32017386
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 604)
AUTHORS Bloeker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Oeanger,A., Podo,G., Han,M., and Wiemann,S.

TITLE EST (Bloeker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS

FEATURES
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Location/Qualifiers
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/clone="DKFZp79B1644"
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/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN
Query Match 100.0%; Score 462; DB 5; Length 604;
Best Local Similarity 100.0%; Pred. No. 8.1e-130; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGAGGAGCTCAGTCACTGAGCCAGTACCAGATGCTGGAACTTCCCGAGCC 60
Db 12 GGAAGGAGGAGGAGGAGCTCAGTCACTGAGCCAGTACCAGATGCTGGAACTTCCCGAGCC 71
QY 61 ATGGCTTCCCTGGGGAGATGCTCTTCTTGAGAGCAATTAATGATCATCATTAATTTGGCT 120


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Db      72  ATGGCTCCCGGGGAGAGATCTCTTCGAGGAGATTAATGATCATCATTAATTCGACT 131
      121  GGAGCAATTGCACTCATCATTTGGCTTGGATTTTCAGGAGACATCTCATCACTACT 180
      Db    132  GGAGCAATTGCACTCATCATTTGGCTTGGATTTTCAGGAGACATCTCATCACTACT 191
      Qy    181  ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCGAGCTGACCTTTGAACCT 240
      Db    192  ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCGAGCTGACCTTTGAACCT 251
      Qy    241  GACATCAAACTTTCTGATATCGTATGATCAATGCTGAAAGGATGTTTAAAGCTTGGTC 300
      Db    252  GACATCAAACTTTCTGATATCGTATGATCAATGCTGAAAGGATGTTTAAAGCTTGGTC 311
      Qy    301  CATGAGTTCAAGAAGGCAAGATGAGCTGCGAGCAGATGAAATGTTCAAGGCGCG 360
      Db    312  CATGAGTTCAAGAAGGCAAGATGAGCTGCGAGCAGATGAAATGTTCAAGGCGCG 371
      Qy    361  ACAGCAGTGTTCGTATCAAGTATGATGTTGGCAATGCTCTTGGCGGCTGAAAGAGTG 420
      Db    372  ACAGCAGTGTTCGTATCAAGTATGATGTTGGCAATGCTCTTGGCGGCTGAAAGAGTG 431
      Qy    421  CAACTCAGAGTGTTCGTATCAAGTATGATGTTGGCAATGCTCTTGGCGGCTGAAAGAGTG 462
      Db    432  CAACTCAGAGTGTTCGTATCAAGTATGATGTTGGCAATGCTCTTGGCGGCTGAAAGAGTG 473

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RESULT 4
BP255229      584 bp      mRNA      linear      EST 16-SEP-2004
LOCUS         BP255229 Sugano cDNA library kidney epithelial cell Homo sapiens
DEFINITION    cDNA clone HRC08590, mRNA sequence.
ACCESSION     BP255229
VERSION       BP255229.1 GI:52170459
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

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REFERENCE
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 584)
              Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
              Mizushima-Sugano,J., Nakai,K. and Sugano,S.
              Sequence comparison in the promoter regions
              block structure in the promoter reveals a homologous
              genome Res. 14 (9), 1711-1718 (2004)
              Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
              Email: yusuzuki@ims.u-tokyo.ac.jp.

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FEATURES
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Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN

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Query Match      99.7%; Score 460.4; DB 5; Length 584;
Best Local Similarity 99.8%; Pred. No. 2.5e-129;
Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    121  GGAGCAATTGCACTCATCATTTGGCTTGGATTTTCAGGAGACATCTCATCACTACT 180
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      Qy    181  ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCGAGCTGACCTTTGAACCT 240
      Db    191  ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCGAGCTGACCTTTGAACCT 250
      Qy    241  GACATCAAACTTTCTGATATCGTATGATCAATGCTGAAAGGATGTTTAAAGCTTGGTC 300
      Db    251  GACATCAAACTTTCTGATATCGTATGATCAATGCTGAAAGGATGTTTAAAGCTTGGTC 310
      Qy    301  CATGAGTTCAAGAAGGCAAGATGAGCTGCGAGCAGATGAAATGTTCAAGGCGCG 360
      Db    311  CATGAGTTCAAGAAGGCAAGATGAGCTGCGAGCAGATGAAATGTTCAAGGCGCG 370
      Qy    361  ACAGCAGTGTTCGTATCAAGTATGATGTTGGCAATGCTCTTGGCGGCTGAAAGAGTG 420
      Db    371  ACAGCAGTGTTCGTATCAAGTATGATGTTGGCAATGCTCTTGGCGGCTGAAAGAGTG 430
      Qy    421  CAACTCAGAGTGTTCGTATCAAGTATGATGTTGGCAATGCTCTTGGCGGCTGAAAGAGTG 462
      Db    431  CAACTCAGAGTGTTCGTATCAAGTATGATGTTGGCAATGCTCTTGGCGGCTGAAAGAGTG 472

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RESULT 5
CD686218      578 bp      mRNA      linear      EST 25-JUN-2003
LOCUS         CD686218 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION    CD686218
ACCESSION     CD686218
VERSION       CD686218.1 GI:32202914
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

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REFERENCE
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 578)
              Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
              Zeng,Y.-X.
              Transcriptional Gene Expression Profile of Human Nasopharynx
              Unpublished (2003)
              Contact: Yixun Zeng
              Cancer Center
              Sun Yat-sen University
              651 Dongfeng Road East, Guangzhou 510060, China
              Tel: 86-1380-9770-743
              Fax: 86-20-8775-4506
              Email: yxzeng@zsums.edu.cn.

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FEATURES
source
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Location/Qualifiers

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/organism="Homo sapiens"
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/note="ESTs generated from a normal nasopharynx cDNA
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ORIGIN

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Best Local Similarity 99.6%; Pred. No. 7.6e-129;
Matches 460; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Db | 231 | ACTGTGCGCTCAGCTGGGAAACATTTGGGAGGATGGAAATCTGAAGCTGCATTTTGAACCT | 290 |
| Qy | 241 | GACATCAAACTTTTCTGATATCTGATATCAATAGCTGAAGGAAAGTGTTTTAGGCTTTGGTTC | 300 |
| Db | 291 | GACATCAAACTTTTCTGATATCTGATATCAATAGCTGAAGGAAAGTGTTTTAGGCTTTGGTTC | 350 |
| Qy | 301 | CATGAGTTCAAAGAAAGGCAAGATAGCTGTCGGAGCAGAGATGAATGTTTCAGAGCGCGG | 360 |
| Db | 351 | CATGAGTTCAAAGAAAGGCAAGATAGCTGTCGGAGCAGAGATGAATGTTTCAGAGCGCGG | 410 |
| Qy | 361 | ACAGCAGTGTTCGATCAAGTGTAGTTCAGTTCGCTCTTTGCGGCTGAAAAACGTG | 420 |
| Db | 411 | ACAGCAGTGTTCGATCAAGTGTAGTTCAGTTCGCTCTTTGCGGCTGAAAAACGTG | 470 |
| Qy | 421 | CAACTCACAAGATGTGGCACTTACAAATGTTATATCACTCACT | 462 |
| Db | 471 | CAACTCACAAGATGTGGCACTTACAAATGTTATATCACTCACT | 512 |

[illegible]

| Qy | 181 | ACTGTGGCTCAGTGGGGAAATTTGGGGAGATGAATCTCGAGCTGCATTTGAACCT | 240 |
|----|-----|------------------------------------------------------------|-----|
| Qy | 181 | ACTGTGGCTCAGTGGGGAAATTTGGGGAGATGAATCTCGAGCTGCATTTGAACCT | 240 |
| Db | 193 | ACTGTGGCTCAGCTGGGACATTTGGGGAGATGAATCTCGAGCTGCATTTGAACCT | 252 |
| Qy | 241 | GACATCAAACTTTCTGATATCGTGATACAAATGCTGGAAGAAAGTGTTTAGCTTGCTC | 300 |
| Db | 253 | GACATCAAACTTTCTGATATCGTGATACAAATGCTGGAAGAAAGTGTTTAGCTTGCTC | 312 |
| Qy | 301 | CATAGATTCAAGAAGGCAAGATGAGCTGTCCGAGCAGATGAATGTTTCAGAGCCGG | 360 |
| Db | 313 | CATAGATTCAAGAAGGCAAGATGAGCTGTCCGAGCAGATGAATGTTTCAGAGCCGG | 372 |
| Qy | 361 | ACAGCAGTGTTCGTGATCAAGTATGTTGGCAATGCTCTTTTCGGCTGAAAAACGTG | 420 |
| Db | 373 | ACAGCAGTGTTCGTGATCAAGTATGTTGGCAATGCTCTTTTCGGCTGAAAAACGTG | 432 |
| Qy | 421 | CAACTCACAGATGCTGGCACTTACCAAAATGTTATATCATCACT | 462 |
| Db | 433 | CACCTCACAGATGCTGGCACTTACCAAA-GTTATATCATCACT | 473 |

| | |
|---------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT 7 | |
| EXBS434 LOCUS | BX358434 767 bp mRNA linear EST 08-APR-200 |
| DEFINITION | BX358434 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI039YG21 5-PRIME, mRNA sequence. |
| ACCESSION | BX358434 |
| VERSION | BX358434.2 GI:46285747 |
| KEYWORDS | EST. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| AUTHORS | Li,W.B., Gruber,C., Jessee,J. and Polayes,D. |
| TITLE | Full-length cDNA libraries and normalization |
| JOURNAL | Unpublished (2001) |
| COMMENT | On May 5, 2003 this sequence version replaced gi:30366215. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oliigo(dt) primer. Five prim end enriched, double-strand cDNA was digested with Not I and clones into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 742.r For more information about this cluster, see http://www.genoscope.cns.fr/cdnats=CSODI039AD1IQPlc=742.r. |
| FEATURES | Location/Qualifiers |
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| | /mol_type="mRNA" |
| | /db_xref="taxon:9606" |
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| | /library="PLACENTA COT 25-NORMALIZED" |
| | /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" |
| | /note="1st strand cDNA was primed with a NotI-oliigo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." |
| ORIGIN | |
| Query Match | 90.6%; Score 418.6; DB 5; Length 767; |
| Best Local Similarity | 98.9%; Pred. No. 1.7e-116; |
| Matches 432; Conservative | 0; Mismatches 4; Indels 1; Gaps 1 |
| OY | 26 CCAAGTACCAATGCGCTGGGAACCTCCAGCAGCATGGCTTCCTGGAGCGAGATCCTCT 85 |
| DB | 1 CCGGGATCCAATGCGCTGGGA--CTTCCCAGGCATGGCTTCCCTGGGGCGAGATCCTTT 59 |
| OY | 86 TCTGGAGCATATTAGCATCATTAATTCTGGCTGGAGCAATTGCACTCATCATTTGGCT 145 |

Db 60 TCTGAGCATATTAGCATCATATTATTGGGTGGAGCAATTGCACTCATTTGGCT 119
Qy 146 TTGGTATTTCAGGAGACATCTCATCAAGTCACTACTGTGCTCAGCTGGAACTTG 205
Db 120 TTGGTATTTCAGGAGACATCTCATCAAGTCACTACTGTGCTCAGCTGGAACTTG 179
Qy 206 GGGAGATGGAATCCTGAGTGCATTTTGAACCTGACATCAATCTTCTGATATCTGGA 265
Db 180 GGGAGATGGAATCCTGAGTGCATTTTGAACCTGACATCAATCTTCTGATATCTGGA 239
Qy 266 TACATGCTGAGAGAGAGTGTGTAGGCTTGTCATGATGTTCAAGAGCAAGATG 325
Db 240 TACATGCTGAGAGAGAGTGTGTAGGCTTGTCATGATGTTCAAGAGCAAGATG 299
Qy 326 AGCTGTGAGAGAGAGTGTGTAGGCTTGTCATGATGTTCAAGAGCAAGATG 385
Db 300 AGCTGTGAGAGAGAGTGTGTAGGCTTGTCATGATGTTCAAGAGCAAGATG 359
Qy 386 TAGTTGGCAATGCTCTTGGGCTGAAAGTGCACATCAAGATGCTGGCACTTACA 445
Db 360 TAGTTGGCAATGCTCTTGGGCTGAAAGTGCACATCAAGATGCTGGCACTTACA 419
Qy 446 AATGTTATATCATCACT 462
Db 420 AATGTTATATCACT 436

RESULT 8
CN259813 714 bp mRNA linear EST 16-MAY-2004
LOCUS 1700600041697 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259813
VERSION CN259813.1 GI:47276227
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 714)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 714 Std Error: 0.00.
Location/Qualifiers

FEATURES
source 1..714
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tisue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="Oligo dT primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Query Match 89.6%; Score 414; DB 7; Length 714;
Best Local Similarity 100.0%; Pred. No. 4.2e-115;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

49 CCTTCCACAGCATGGCTTCCCTGGGACAGATCTCTTGGAGCATATATGACATATC 108
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Db 1 CCTTCCACAGCATGGCTTCCCTGGGACAGATCTCTTGGAGCATATATGACATATC 60
Qy 109 ATTATTTGCTGGAGCAATTGCACTCATATTGGCTTTGGTATTAGGAGACATCTCC 168
Db 61 ATTATTTGCTGGAGCAATTGCACTCATATTGGCTTTGGTATTAGGAGACATCTCC 120
Qy 169 ATCAGAGTCTATGTCGCTGAGTGGGAACTTGGGAGGATGGAAATCTGAGCTGC 228
Db 121 ATCAGAGTCTATGTCGCTGAGTGGGAACTTGGGAGGATGGAAATCTGAGCTGC 180
Qy 229 ACTTTGACCTGACATCAATCTTCTGATATGCTGATACATGCTGAAGAGAGTGT 288
Db 181 ACTTTGACCTGACATCAATCTTCTGATATGCTGATACATGCTGAAGAGAGTGT 240
Qy 289 TTAGGCTTGGTCCATGAGTTCAAGAGCAAGATGAGTGTGAGCAGAGATGAATG 348
Db 241 TTAGGCTTGGTCCATGAGTTCAAGAGCAAGATGAGTGTGAGCAGAGATGAATG 300
Qy 349 TTGAGAGCCGAGCAGAGTGTGCTGATCAAGTATAGTTGGCAATGCTCTTGGCG 408
Db 301 TTGAGAGCCGAGCAGAGTGTGCTGATCAAGTATAGTTGGCAATGCTCTTGGCG 360
Qy 409 CTGAAAAAGCTGCACTCAGATGCTGGCACTTCAATGTTATATCATCACT 462
Db 361 CTGAAAAAGCTGCACTCAGATGCTGGCACTTCAATGTTATATCATCACT 414

RESULT 9
BF680206 845 bp mRNA linear EST 21-DEC-2000
LOCUS 602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5',
DEFINITION mRNA sequence.
ACCESSION BF680206
VERSION BF680206.1 GI:11954101
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 845)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: c9abds-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM147 row: d column: 16
High quality sequence stop: 657.
Location/Qualifiers

FEATURES
source 1..845
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4295775"
/lab_host="DH10B (tr phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgccg); Site 2: SfiI
(ggccatctggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGAGCC-3'
and 3' adaptor sequence:
5'-ATCTGAGGCGCAGGCGCCGACATG-dt(30)-BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 clones contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

Query Match 89.6%; Score 414; DB 7; Length 714;
Best Local Similarity 100.0%; Pred. No. 4.2e-115;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Query Match 77.6%; Score 358.6; DB 2; Length 845;

Best Local Similarity 83.4%; Pred. No. 3.9e-98; Mismatches 4; Indels 87; Gaps 1;

Matches 458; Conservative 0; Mismatches 4; Indels 87; Gaps 1;

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QY 1 GGAAGCAGCGAGCGAGCTCCACTGAGCAGTACCAGATACGCTGGAACTTCCCGAGCC 60
DB 14 GGAAGCAGCGAGCGAGCTCCACTGAGCAGTACCAGATACGCTGGAACTTCCCGAGCC 73
QY 61 ATGGCTTCCCTGGGCGAGATCTCTTCTGGAGCATTAATGACATCATTAATTTCTGGCT 120
DB 74 ATGGCTTCCCTGGGCGAGATCTCTTCTGGAGCATTAATGACATCATTAATTTCTGGCT 133
QY 121 GGAGCAATTGCACTCATCATTTGGCTTTG----- 148
DB 134 GGAGCAATTGCACTCATCATTTGGCTTTGTAATTTCAGAACTCTCTGCTGGCTTCAGCAA 193
QY 149 -----GTAAT 153
DB 194 TGAAGGTTGGTGTAGAAAGTTCCAAAGGCTTCCCTTAGCATTAATCTTGGCTTCGTAAC 253
QY 154 TCAGGAGACATCTCATCATCATCTACTGTGCTGCTGAGGAACTTGGGAGAT 213
DB 254 GCAAGGAGACATCTCATCATCTACTGTGCTGCTGAGGAACTTGGGAGAT 313
QY 214 GGAATCCTGAGCTGCACTTTTGAACCTGATCAAACTTTCTGATATCGTATACATGG 273
DB 314 GGAATCCTGAGCTGCACTTTTGAACCTGATCAAACTTTCTGATATCGTATACATGG 373
QY 274 CTGAAGAGAGGTGTTTGAAGCTTGTGCTGATGATTCAGAAAGCAAAAGATGAGCTGCG 333
DB 374 CTGAAGAGAGGTGTTTGAAGCTTGTGCTGATGATTCAGAAAGCAAAAGATGAGCTGCG 433
QY 334 GAGCAGGATTAATGTTTCAAGGCGGAGCAGCTGTTTCTGATCAAGTATGTTGGC 393
DB 434 GAGCAGGATTAATGTTTCAAGGCGGAGCAGCTGTTTCTGATCAAGTATGTTGGC 493
QY 394 AATGCCCTTTGGGCGCTGAAAAAGTCACTCAAGATGCTGGCACTTCAATATGTTAT 453
DB 494 AATGCCCTTTGGGCGCTGAAAAAGTCACTCAAGATGCTGGCACTTCAATATGTTAT 553
QY 454 ATCATCACT 462
DB 554 ATCATCACT 562
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RESULT 10
CR603772 2431 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSOD1039YG21 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR603772
VERSION CR603772.1 GI:50484579
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 2431)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue (bases 1 to 2431)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

FEATURES

source

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1..2431

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOD1039YG21"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 68.3%; Score 315.4; DB 3; Length 2431;

Best Local Similarity 96.7%; Pred. No. 9.3e-85; Mismatches 11; Indels 0; Gaps 0;

Matches 322; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 130 GCATCATCATTTGGCTTGGTATTTGAGGAGACACTCCATCAGTACTGTCCGC 189
DB 1 GCATCATCATTTGGCTTGGTATTTGAGGAGACACTCCATCAGTACTGTCCGC 60
QY 190 TCAGCTGGGAAATTTGGGAGAGATGGAATCCGAGCTGCACTTTGAACCTGACATCAA 249
DB 61 TCAGCTGGGAAATTTGGGAGAGATGGAATCCGAGCTGCACTTTGAACCTGACATCAA 120
QY 250 CTTTCTGATATGCTGATACATGCTGGAAGAGTGTGTTAGGCTTGGTCCATGATTC 309
DB 121 CTTTCTGATATGCTGATACATGCTGGAAGAGTGTGTTAGGCTTGGTCCATGATTC 180
QY 310 AAAGAGGCAAAAGATGAGCTGTGCGAGCAGATGAATGTTTGAAGGCCGAGCAGAGTG 369
DB 181 AAAGAGGCAAAAGATGAGCTGTGCGAGCAGATGAATGTTTGAAGGCCGAGCAGAGTG 240
QY 370 TTTTCTGATCACTGATTAATTTGCAATGCTTTTGGCGCTGAAAAAGTGAATCACA 429
DB 241 TTTTCTGATCACTGATTAATTTGCAATGCTTTTGGCGCTGAAAAAGTGAATCACA 300
QY 430 GATGCTGGACCTACCAATGTTATATCATCACT 462
DB 301 GATGCTGGACCTACCAATGTTATATCATCACT 333
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RESULT 11

BB666051

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BB666051 670 bp mRNA linear EST 26-OCT-2001
BB666051 RIKEN full-length enriched, 2 days pregnant adult female
covidict Mus musculus cDNA clone B230029B13 5', mRNA sequence.
BB666051 GI:16499684
EST.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 670)
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

Wagii, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Onara, E., Wachihi, M., Yoneda, S., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN Integrated sequence analysis (RISA) system--334-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamakata, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

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Location/Qualifiers
1. 670
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="E230029B13"
/sex="female"
/tissue_type="oviduct"
/dev_stage="2 days pregnant adult"
/lab_host="RD10B"
/clone_lib="RIKEN full-length enriched, 2 days pregnant
adult female oviduct"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGGAGAGGAGCGCCGCGACCTGAGTTTTTTTTTTTTNN 3', cDNA was
prepared by using triosephosphate dehydrogenase-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence 15'
GAGGAGAGGATTCGACGATTAAATTAATTAATTCGCCCCCCCC 3'. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
Bluescript KS(+) after bulk excision from Lambda FLC I."

```

ORIGIN

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|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 65.5% | Score 302.8; | DB 2; | Length 670; |
| Best Local Similarity | 83.7% | Pred. No. 4.3e-81; | | |
| Matches 343; Conservative | 0; | Mismatches 67; | Indels 0; | Gaps 0 |

| | | | |
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| Qy | 52 | TCGCCAGGCATGCGTTCCCTGGGGGAGATCCCTCTGGAGCATATTGACATCATC | 111 |
| Db | 93 | TCCCTCTGCATGGCTTCCTTGGGGGAGATCATCTTTTGGAGTATTATTAACTCATC | 152 |
| Qy | 112 | ATTCTGGCTGAGCAATTGCACTCATCATTTGGCTTTGGTATTTCAGGAGACATCCATC | 171 |
| Db | 153 | ATCTGGGCTGGGGCATCGCACTCATCATTTGGCTTTTGGCATTTTCAGGCAAGCATTCATC | 212 |
| Qy | 172 | ACAGTCACTACTGTGCGCTCAGCTGGGAACATTGGGAGATGGAATCCTGAGCTGACT | 231 |
| Db | 213 | ACGGTCAAGACCTTCACTCAGCTGGAAACATTGGAGAGGAGCGGACCTTGAGCTGCACT | 272 |
| Qy | 232 | TTTGAACCTGCATCAAACTTTCTGTATCGGATGACAATGGCTGAAGGAAGGTGTTTA | 291 |
| Db | 273 | TTTGAACCTGCATCAAACTCAACGGCATCGTCATCATGAGTCTTAAGAAAGGCATCAAA | 332 |

| | | | |
|----|-----|------------------------------------------------------------|-----|
| QY | 292 | GGCTTGGTCATGAGTTCAAAAGGACAAATATAGCTGTGAGGACAGATGAAATGTC | 351 |
| Db | 333 | GGTTTGTGTCAAGAGTTAAAGAAAGCAAAACGACTTCCACGACAGATGAGATGTTTC | 392 |
| QY | 352 | AGAGGCGCGACAGCAGTGTTCGTGATCAATGATGATGTGGCAATGCTCTTTGGCGCTG | 411 |
| Db | 393 | AGAGGCGCGACAGCAGTGTTCGTGATGAGGTGATGTGGCAATGCTTCTTGAGACTG | 452 |
| QY | 412 | AAAAAGTGCACACTCAGAGATGCTGGACCTACCAATGTTATATCATCAC | 461 |
| Db | 453 | AAAAAGTGCACACTCAGAGATGCTGGACCTACCAATGTTATATCATCCGAC | 502 |

D'o

| RESULT 12 | LOCUS | DEFINITION |
|-----------|----------------------------------------------------------------------------------------------|-----------------|
| BY736335 | 702 bp mRNA linear | EST 17-DEC-2002 |
| BY736335 | Riken full-length enriched, blastocyst Mus musculus cDNA clone 11C0027J19 5', mRNA sequence. | |

| | |
|-----------|-------------------------------------------------------------------|
| SOURCE | Mus musculus (house mouse) |
| ORGANISM | Mus musculus |
| | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; |
| | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus |
| REFERENCE | 1 (bases 1 to 702) |
| AUTHORS | Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., |

TITLE

| | |
|---------|--------------------------------|
| JOURNAL | Nature 420, 563-573 (2002) |
| MEDLINE | 22354683 |
| PUBMED | 12466851 |
| COMMENT | Contact: Yoshihide Hayashizaki |

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome@gsc.riken.jp; <http://genome.gsc.riken.jp/>
Adachi, Y., Aizawa, K., Akiura, T., Arikawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Kumotani, K., Ishii, Y., Itoh, M., Kageura, I., Kawai, J., Kojima, Y.,
Kondo, S., Komori, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohashi, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,

Takeda, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct SubMISSION
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source

Location/Qualifiers
1..702
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I1C0027J19"
/dev_stage="blastocyst"
/clone_lib="RIKEN full-length enriched, blastocyst"

ORIGIN

Query Match 65.5%; Score 302.8; DB 6; Length 702;
Best Local Similarity 83.7%; Pred. No. 4.4e-81;
Matches 343; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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OY 52 TCCCGAGCAGTGGCTTCCCTGGGAGATCCTCTTCTGGAGCATTAATGATCATCTT 111
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Db 92 TCCCTCTCAGTGGCTTCCCTGGGAGATCATCTTTTGAAGTATTAATGATCATCTC 151
OY 112 ATTCGAGTGGAGCAATTCAGTCAATGAGCTTTGGTATTTTCAGGAGACACTCCATC 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 152 ATCTGGGCTGGGCGCATGCACTCATTCATTTGGCTTTGCAATTTCAAGGACATCTTC 211
OY 172 ACAGTCACTACTGTGCTGCTGAGTGAACATTTGGAGAGATGAATCTGAGCTGACT 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 ACGGTCAGACCTTCACTCAGCTGGAACATTTGAGAGACGAGACCTGAGCTGCACT 271
OY 232 TTGAACCTGACATTAACCTTTTGTATATCGTGAATACATGGCTGAAGAGGTGTTTA 291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 TTTGAACCTGACATTAACCTCAACGCGCATCGTCACTGCGTGAAGAGGCGATCAAA 331
OY 292 GCGTTGTCATGATTAAGAAAGAAAGATGAGTGTGCGAGCAGATGAATGTTTC 351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 GGTTCGTCACGATTCAGAAAGAGCAAGACGACCTCTACAGCAGACATGAGATGTC 391
OY 352 AGAGCCCGAGACGAGTGTTCATGATCAAGTATGATGGCAATGCTCTTTGGGCTG 411
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Db 392 AGAGCCCGACAGAGTGTTCATGATCAAGTATGATGGCAATGCTCTCTGAGACTG 451
OY 412 AAAAAGTGAACACTACAGATGCTGGACCTTACCAATGTTATATATATC 461
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 452 AAAAAGTGAACACTACAGATGCTGGACCTTACCAATGTTATATATC 501
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RESULT 13
BI454643
LOCUS 757 bp mRNA linear EST 21-AUG-2001
DEFINITION 603170538P1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5250177 5',
mRNA sequence.
ACCESSION BI454643
VERSION BI454643.1 GI:15245299
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
plate: L1AM1631 row: k column: 10
High quality sequence stop: 742.

FEATURES
source

Location/Qualifiers
1..757
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5250177"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN

Query Match 65.5%; Score 302.8; DB 4; Length 757;
Best Local Similarity 83.7%; Pred. No. 4.5e-81;
Matches 343; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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OY 52 TCCCGAGCAGTGGCTTCCCTGGGAGATCCTCTTCTGGAGCATTAATGATCATCTT 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 TCCCTCTCAGTGGCTTCCCTGGGAGATCATCTTTTGAAGTATTAATGATCATCTC 122
OY 112 ATTCGAGTGGAGCAATTCAGTCAATGAGCTTTGGTATTTTCAGGAGACACTCCATC 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 ATCTGGGCTGGGCGCATGCACTCATTCATTTGGCAATTTCAAGGACATCTTCATC 182
OY 172 ACAGTCACTACTGTGCTGCTGAGTGAACATTTGGAGAGATGAATCTGAGCTGACT 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 ACGGTCAGACCTTCACTCAGCTGGAACATTTGAGAGACGAGACCTGAGCTGCACT 242
OY 232 TTGAACCTGACATTAACCTTTTGTATATCGTGAATACATGGCTGAAGAGGTGTTTA 291
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Db 243 TTTGAACCTGACATTAACCTCAACGCGATGCTCATCGATGCTGAAGAGAGATCAAA 302
OY 292 GCGTTGTCATGATTAAGAAAGAAAGATGAGTGTGCGAGCAGATGAATGTTTC 351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 303 GGTTCGTCACGATTCAGAAAGAGCAAGACGACCTCTACAGCAGACATGAGATGTC 362
OY 352 AGAGCCCGAGACGAGTGTTCATGATCAAGTATGATGGCAATGCTCTTTGGGCTG 411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 363 AGAGCCCGACAGAGTGTTCATGATCAAGTATGATGGCAATGCTCTCTGAGACTG 422
OY 412 AAAAAGTGAACACTACAGATGCTGGAGCTTACCAATGTTATATATCATC 461
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Db 423 AAAAAGTGAACACTACAGATGCTGGAGCTTACCAATGTTATATCATC 472
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RESULT 14
CV079354
LOCUS 827 bp mRNA linear EST 25-AUG-2004
DEFINITION AGENCOURT_31473506 NIH_MGC_251 Rattus norvegicus cDNA clone

IMAGE:7389454 5', mRNA sequence.
ACCESSION CV079354
VERSION CV079354.1 GI:51546385
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 827)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: csgrabs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: LLM15562 row: g column: 20
High quality sequence stop: 719.
Location/Qualifiers
1..827
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7389454"
/lab_host="DH10B TONa"
/clone_1ib="NIH_MGC_251"
/note="Organ: thymus; Vector: pXpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTGATCGACGCGCCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pXpress-1. Size-selection >1.25kb resulted in an average insert size of 1.6 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_250) and was constructed by Open Biosystems. Note: this is a NIH_MGC library"

ORIGIN
Query Match 64.2%; Score 296.4; DB 7; Length 827;
Best Local Similarity 82.7%; Pred. No. 4.ee-79;
Matches 339; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

52 TCCCGACCATGAGCTTCCCTGGGGCAGATCTCTTGAGAGATAATTAGCATCATCT 111
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85 TCCCTGACATGAGCTTCTGGGGCAGATCATCTTTGGAGTATTTAATCGTCAATC 144
|||||
112 ATTCTGGCTGAGCAATTGCACTCATCTATTGCTTTGGTATTTTCAAGGAGACATCC 171
|||||
145 ATCTGGCTGAGCAATCGTACTCATCTATTGGCTTTGGTATTTCAAGCAAGCACTTC 204
|||||
172 AAGTCACTACTGTCCTCCCTCAGCTGGAGACATTGGGAGAGATGGAATCCGACCTC 231
|||||
205 ACGGTACAACCTTCACTCAGCTGGAATAATTGGAGAGACGCGACCTTGAGCTGCAC 264
|||||
232 TTGAACCTGACATCAAACTTTCTGATATCGTATCAATAGCTGAAGAAAGGTGTTT 291
|||||
265 TTGAACCTGACATCAAACTCAACGAGATGCTATCAGTGCCTGAAGAAAGCATCA 324
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292 GGTTCGTCATGATTTCAAGAAAGCAAGATGAGCTGTGAGAGAGATGAATGTT 351
|||||
325 GGTTCGTCATGATTTCAAGAAAGCAAGATGAGCTGTGAGAGAGATGAATGTT 384
|||||

352 AGAGCCCGACAGACAGTGTGCTGATCAAGTATAGTGGCAATGCTCTTTGCGAGCT 411
|||||
385 CGAGCCCGACAGACATGTTTGCAGATCAAGTGTGTTGGCAATGCTCTTCCGAGACT 444
|||||
412 AAAACGTGCACTCAAGATGCTGCACCTTCAAAATGTTATTCATCAC 461
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445 AAAAATGTCAGCTCACTGATGCTGCACCTTCAACATGTTATTCACAC 494
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RESULT 15
CN259818 487 bp mRNA linear EST 16-MAY-2004
LOCUS 1700600021115 GRN_PREHP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN259818
ACCESSION CN259818
VERSION CN259818.1 GI:47276232
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Fisk, G. J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J. and Stanton, L. W.
TITLE Transcription characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 487 Std Error: 0.00.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_1ib="GRN_PREHP"
/note="oligo dT primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN
Query Match 64.1%; Score 296; DB 7; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.6e-79;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

167 CCATCACTGCTACTGTCGCTCAGCTGGAAACATTGGGAGATGGAATCTGAGCT 226
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1 CCATCACTGCTACTGTCGCTCAGCTGGAAACATTGGGAGATGGAATCTGAGCT 60
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227 GCACCTTTGAACCTGACATCAAACTTTCTGATATCGTATTAATAGCTGAAGAAAG 286
|||||
61 GCACCTTTGAACCTGACATCAAACTTTCTGATATCGTATTAATAGCTGAAGAAAG 120
|||||
287 TTTTAGCTGTGCTCACTGATTCAAAGAAAGGCAAGATGAGCTGTGAGAGAGATG 346
|||||
121 TTTTAGCTGTGCTCACTGATTCAAAGAAAGGCAAGATGAGCTGTGAGAGAGATG 180
|||||
347 TGTTCAGAGCCGAGCAGAGTGTGCTGATCAAGTGAATGCTGCTTTTC 406
|||||
181 TGTTCAGAGCCGAGCAGAGTGTGCTGATCAAGTGAATGCTGCTTTTC 240
|||||
407 GGTGAAAAAGCTGCACTCAAGATGCTGCGACCTTCAAAATGTTATATCATCACT 462
|||||
241 GGTGAAAAAGCTGCACTCAAGATGCTGCGACCTTCAAAATGTTATATCATCACT 296
|||||

Search completed: May 31, 2005, 00:10:57
Job time : 1798.88 secs

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source
    location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
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|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|-----------------|
| Qy | 841 | TGATTTTGAAGTTCTGCATCGTTCAAGAGAAATGATTAATATACATTTCT | 890 |
| Db | 2560 | TGATTTTGAAGTTCTGCATCGTTCAAGAGAAATGATTAATATACATTTCT | 2609 |
| RESULT 3 | | | |
| LOCUS | AR478744 | 2627 bp | DNA |
| DEFINITION | Sequence 391 from Patent US 6699664. | linear | PAT 14-MAY-2004 |
| ACCESSION | AR478744 | | |
| VERSION | AR478744.1 | GI:47237396 | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | Unclassified. | | |
| AUTHORS | 1 (bases 1 to 2627) | | |
| TITLE | MITCHEM, J. L., KING, G. E., ALGATE, P. A., FLING, S. P., RETTER, M. W., FANGER, G. R., REED, S. G., VEDVICK, T. S. and CARTER, D. Compositions and methods for the therapy and diagnosis of ovarian cancer | | |
| JOURNAL | Patent: US 6699664-A 391 02-MAR-2004; | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..2627 | | |
| ORIGIN | /organism="unknown" | | |
| | /mol_type="genomic DNA" | | |
| Query Match | 90.6%; Score 806.4; DB 6; Length 2627; | | |
| Best Local Similarity | 91.9%; Pred. No. 8.8e-239; | | |
| Matches | 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1; | | |
| Qy | 1 | CAAGCTCGAGGCTTCTCTTCCATCTCTGCGTGACAGCTTAAGACTCTCAATTA | 60 |
| Db | 1721 | CAAGCTCGAGGCTTCTCTTCCATCTCTGCGTGACAGCTTAAGACTCTCAATTA | 1780 |
| Qy | 61 | GCATCTGAGAGAGTGGGACTCAGCTGGGGGTGATTTGCGCCCAATCTCCGGGGAAATGC | 120 |
| Db | 1781 | GCATCTGAGAGAGTGGGACTCAGCTGGGGGTGATTTGCGCCCAATCTCCGGGGAAATGC | 1840 |
| Qy | 121 | TGAAGACAATTTGGTTACTCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNNNN | 180 |
| Db | 1841 | TGAAGACAATTTGGTTACTCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNNNN | 1900 |
| Qy | 181 | NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN | 240 |
| Db | 1901 | TAGTGGATTAAGAGGCCAGGATGCTGCTCAACCTCTTACATGTACAGAGCGTCCCAT | 1960 |
| Qy | 241 | TACAACCTACCAATCCGAAGTGTCAATCTGTGTGAGGACTAGAAACCCTGGTTTGA | 300 |
| Db | 1961 | TACAACCTACCAATCCGAAGTGTCAATCTGTGTGAGGACTAGAAACCCTGGTTTGA | 2020 |
| Qy | 301 | GAAAAGGCGCTGGGAAAGAGGGGAGCCAAATCTGTCTGCTCTCTCAATTAATC | 360 |
| Db | 2021 | GAAAAGGCGCTGGGAAAGAGGGGAGCCAAATCTGTCTGCTCTCTCAATTAATC | 2079 |
| Qy | 361 | GGCAATTAAGACTTCTGTCTTTTGGGCTGTGCTCTCAGACAGAGAGCCAGAACTATC | 420 |
| Db | 2080 | GGCAATTAAGACTTCTGTCTTTTGGGCTGTGCTCTCAGACAGAGAGCCAGAACTATC | 2139 |
| Qy | 421 | GGGACACAGATTAACATCTCAGTGAAACAGAGTTGACAAAGGCGCTATGGGAAAGCGCTGA | 480 |
| Db | 2140 | GGGACACAGATTAACATCTCAGTGAAACAGAGTTGACAAAGGCGCTATGGGAAAGCGCTGA | 2199 |
| Qy | 481 | TGGGATTAATCTTCAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCATTTACCTGCAAG | 540 |
| Db | 2200 | TGGGATTAATCTTCAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCATTTACCTGCAAG | 2259 |
| Qy | 541 | CCAAAGTCTGTAAGAGAAATCCGAGTTTCTAGCTCAGCTTTTCTTACTGGAATTTAGA | 600 |
| Db | 2260 | CCAAAGTCTGTAAGAGAAATCCGAGTTTCTAGCTCAGCTTTTCTTACTGGAATTTAGA | 2319 |

| | | | |
|-----------------------|-----------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|-----------------|
| Qy | 601 | TTCTCAGACCCCTGCCTCCGCCACATTTGAATTAAGCAACAAACATATPACCTTCACATGA | 660 |
| Db | 2320 | TTCTCAGACCCCTTCCTG3CCACAAATTAAATTAAG3CAACAAACATATPACCTTCACATGA | 23797 |
| Qy | 661 | GCACACACAGACTTTTGAAGCAAGACAATATGACTGCTTGAATTGAGGCTTGAAGATG | 720 |
| Db | 2380 | GCACACACAGACTTTTGAAGCAAGACANTGACTGCTTGAATTGAGGCTTGAAGATG | 24399 |
| Qy | 721 | AAGCTTGAAGAAAAGAAATPCTTTGTTTCCAGCCCTTCCACACTCTTCATGTGTTA | 780 |
| Db | 2440 | AAGCTTGAAGAAAAGAAATPCTTTGTTTCCAGCCCTTCCACACTCTTCATGTGTTA | 24999 |
| Qy | 781 | ACCACTGCTTCCGAGACTTGGAGCGACGGGTGACGTATATACATGTTGTTATGAAGAAC | 840 |
| Db | 2500 | ACCACTGCTTCCGAGACTTGGAGCGACGGGTGCTGTATACATGTTGTTATGAAGAAC | 25585 |
| Qy | 841 | TGATTTTGAAGTTCTGATCGTTCAAGAGAAATGATTAATATACATTTCT | 890 |
| Db | 2560 | TGATTTTGAAGTTCTGATCGTTCAAGAGAAATGATTAATATACATTTCT | 2609 |
| RESULT 4 | | | |
| AX156350 | | 2627 bp | DNA |
| LOCUS | | | linear |
| DEFINITION | Sequence 207 from Patent WO0140269. | | PAT 22-JUN-2001 |
| ACCESSION | AX156350 | | |
| VERSION | AX156350.1 | | GI:14537350 |
| KEYWORDS | | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| AUTHORS | Dillon, D.C., Day, C.H., Jiang, Y., Houghton, R.L., Mitcham, J.L. and Wang, A. | | |
| TITLE | Compositions and methods for therapy and diagnosis of breast cancer | | |
| JOURNAL | Patent: WO 0140269-A 207 07-JUN-2001; CORIXA CORPORATION (US) | | |
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| source | Location/Qualifiers | | |
| | 1..2627 | | |
| | /organism="Homo sapiens" | | |
| | /mol_type="unassigned DNA" | | |
| | /db_xref="taxon:9606" | | |
| ORIGIN | | | |
| Query Match | 90.6%; | Score 806.4; | DB 6; |
| Best Local Similarity | 91.9%; | Pred. No. 8.8e-239; | Length 2627; |
| Matches 818; | Conservative 0; | Mismatches 71; | Indels 1; |
| Gaps 1; | | | |
| Qy | 1 | CAAGCTCTGAGGCTTCCTTCCTCCATCTCTGCGTGAAGACTGAAGCTCAAGTTTCAATA | 60 |
| Db | 1721 | CAAGCTCTGAGGCTTCCTTCCTTCATCTCTCGTGAAGACTGAAGCTCAAGTTTCAATA | 1780 |
| Qy | 61 | GCACTCTGAGCAGTGGGACTCAGCTGGGATGATTTGCGCCCCCATCTCCGGGGAAATGTC | 120 |
| Db | 1781 | GCACTCTGAGCAGTGGGACTCAGCTGGGATGATTTGCGCCCCCATCTCCGGGGAAATGTC | 1840 |
| Qy | 121 | TGAAGACAATTTTGTTGTTTACTCTCAATGAGGAGTGGAGAGAGATPACAGNNNNNNNNNN | 180 |
| Db | 1841 | TGAAGACAATTTTGTTGTTTACTCTCAATGAGGAGTGGAGAGAGATPACAGTCTACTACCAAC | 1900 |
| Qy | 181 | NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN | 240 |
| Db | 1901 | TAGTGGATTAAGGCGAGGAGTCTGCTCAACCTTCACATGTACAGAGAGTCTCCCCAT | 1960 |
| Qy | 241 | TACAACCTACCCAAATCCGAAGTGTCAACTGTGTGACAGACTAAGAAACCTGTGTTTGAAGTA | 300 |
| Db | 1961 | TACAACCTACCCAAATCCGAAGTGTCAACTGTGTGACAGACTAAGAAACCTGTGTTTGAAGTA | 2020 |
| Qy | 301 | GAAGAGGCGCTGGGAAAGAGGGAGCCAAATATGTCTGTGCTTCTTCCACATTAATGATAT | 360 |
| Db | 2021 | GAAGAGGCGCT- GGAAGAGAGGGAGCCAAATATGTCTGTGCTTCTTCCACATTAATGATAT | 2079 |

| RESULT 5 | | | | |
|------------|----------------------------------------------------------------------------|-------------|-----|--------|
| AX366624 | | | | |
| LOCUS | AX366624 | 2627 bp | DNA | linear |
| DEFINITION | Sequence 391 from Patent WO0206317. | | | |
| ACCESSION | AX366624 | | | |
| VERSION | AX366624.1 | GI:18698046 | | |
| KEYWORDS | . | | | |
| SOURCE | Homo sapiens (human) | | | |
| ORGANISM | Homo sapiens | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| REFERENCE | 1 Mitcham, J. L., King, G. B., Algate, P. A., Flinn, S. P., Retter, M. W., | | | |
| AUTHORS | Fanger, G. R., Reed, S. G., Vedvick, T. S., Carter, D., Hill, P. and | | | |
| | Albone, E. | | | |
| TITLE | Compositions and methods for the therapy and diagnosis of ovarian | | | |

[illegible]

| | | | | | |
|------------|-------------------------------------------------------------------------------------------------------------------------------|-------------|-----|--------|-----------------|
| RESULT 6 | AL391476/c | 171595 bp | DNA | linear | PRI 03-AUG-2001 |
| LOCUS | AL391476/c | | | | |
| DEFINITION | Human DNA sequence from clone RP11-229A19 on chromosome 1, complete sequence. | | | | |
| ACCESSION | AL391476 | | | | |
| VERSION | AL391476.20 | GI:15131484 | | | |
| KEYWORDS | HTG. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | | | |
| REFERENCE | 1 (bases 1 to 171595) | | | | |
| AUTHORS | Wallis, V. | | | | |
| TITLE | Direct Submision | | | | |
| JOURNAL | Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk | | | | |
| | requesta: clonerequest@sanger.ac.uk | | | | |

COMMENT

On Aug 9, 2001 this sequence version replaced gi:14970375. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> RP11-229A19 is from the library RP11-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBAC3.6 This sequence is the entire insert of clone RP11-229A19 The true left end of clone RP11-287H7 is at 67254 in this sequence. The true right end of clone RP11-570D9 is at 57439 in this sequence.

FEATURES

source

1..171595
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/db_xref="taxon:9606"
/chromosome="1"
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/clone_1kb="RP11-11.1"
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745..1182
/note="LIMD2 repeat: matches 5890..6341 of consensus"
1261..1466
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1471..1567
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1568..1880
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1881..2391
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2392..2668
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2669..2813
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3066..3198
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3264..3367
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3758..4064
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4312..4610
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5330..5607
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6639..6803
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7176..7218
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7287..7593
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9335..9484

/note="LIMC5 repeat: matches 7699..7849 of consensus"
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9812..9975
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9976..10469
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11613..11858
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16726..16892
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31909..32321
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35687..35843
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36338..36699
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36702..36938
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37430..37621
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37655..38005
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38922..39220
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39802..39885
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39931..40073
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40191..40247
/note="Charlie4 repeat: matches 1906..1961 of consensus"
40286..40363
/note="MIR11 repeat: matches 288..372 of consensus"
40657..40734
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repeat_region 41248..41351
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repeat_region 42498..42761
/note="AluSg repeat: matches 1..265 of consensus"
repeat_region 43527..43770
/note="L2 repeat: matches 2465..2742 of consensus"
repeat_region 44795..44944
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repeat_region 44945..45231
/note="AluSg repeat: matches 21..307 of consensus"
repeat_region 45232..45629
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repeat_region 45628..45864
/note="L2 repeat: matches 1162..1409 of consensus"
repeat_region 45880..46206
/note="MLT1B repeat: matches 43..390 of consensus"
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1 CAAGCTCGAGGCTTCTCTTCCTTCATCTCGCTGAGCAAGTAAAGCTTCAATTA 60
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81483 GCATCTAGAGCAGTGGGACTCAGCTGGGCTGATTTCCGCCCATCTCCGGGGAATGTC 81424
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81423 TGAAGACAATTTGGTTACCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNN 81364
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LOCUS
DEFINITION Sequence 1 from Patent WO0202624.
ACCESSION AX403048
VERSION AX403048.1 GI:21388028
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Fox,G., Sullivan,J.K. and Fang,M.
B7-like molecules and uses thereof
Patent: WO 0202624-A 1 10-JAN-2002;
Amgen, Inc. (US)

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Query Match 90.6%; Score 806; DB 6; Length 2603;
Best Local Similarity 91.8%; Pred. No. 1.2e-238;
Matches 817; Conservative 1; Mismatches 71; Indels 1; Gaps 1;

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Db 1931 TACAATCAATCCCAATCCGAAGTGTCACTGTCTCAGAGCTAAGAACTGTGTTGAGA 1990
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LOCUS AX375860
DEFINITION Sequence 7 from Patent WO0194641.
ACCESSION AX375860
VERSION AX375860.1 GI:19170332
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Ople, E., McLachlan, K. and Heard, C.
AUTHORS Gene targets and ligands that bind thereto for treatment and
TITLE diagnosis of ovarian carcinomas
JOURNAL Patent: WO 0194641-A 7 13-DEC-2001.

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Best Local Similarity 91.8%; Pred. No. 2.8e-238;
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RESULT 9
LOCUS   HSM808167
DEFINITION Homo sapiens mRNA, cDNA DKFZp779B1717 (from clone DKFZp779B1717).
ACCESSION BX648021
VERSION  BX648021.1 GI:34367180
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ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
  1 (bases 1 to 2671)
    Poustek,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
    Mewes,H.W., Weil,B., Amid,C., Oesanger,A., Fobo,G., Han,M. and
    Wiemann,S.
CONSTRM The German Human cDNA Consortium
TITLE    Direct Submission
JOURNAL  Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
          Neuherberg, GERMANY
COMMENT  Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
          Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
          sequenced by DKFZ (German Cancer Research Center,
          Heidelberg/Germany) within the cDNA sequencing consortium of the
          German Genome Project.
          This clone (DKFZp779B1717) is available at the RZPD in Berlin.
          Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
          Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
          information about the clone and the sequencing project is available
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LOCUS   BD235840
DEFINITION A novel method of diagnosing, monitoring, staging, imaging and
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ACCESSION BD235840
VERSION   BD235840.1 GI:33045610
KEYWORDS  JP 2002523760-A/11.
          Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
  1 (bases 1 to 890)
    Salceda,S., Sun,Y., Recipon,H. and Cafferkey,R.
    A novel method of diagnosing, monitoring, staging, imaging and
    treating various cancers
    Patent: JP 2002523760-A 11 30-JUL-2002;
    DIADEXUS INC
COMMENT   OS Homo sapiens (human)
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          PD 30-JUL-2002
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          PF 02-SEP-1998 US 60/098880
          PI SUSANA SALCEDA, YONGMING SUN, HERVE RECIPON, ROBERT CAFFERKEY PC
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          , A61K49/00, A61K49/00,
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LOCUS AR283679
DEFINITION Sequence 74 from patent US 6528253.
ACCESSION AR283679
VERSION AR283679.1 GI:29720576
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLES Compositions and methods for diagnosis of ovarian cancer
JOURNAL Patent: US 6528253-A 74 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..1567

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Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;
QY 1 CAAGCTTGAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
| | | | |
Db 679 CAAGCTTGAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 738
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGATTTGCCCCCCTCTCCGGGAAATGTC 120
| | | | |
Db 739 GCATCTAGAGCAGTGGGACTCAGCTGGGATTTGCCCCCCTCTCCGGGAAATGTC 798
QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNN 180
| | | | |
Db 799 TGAAGCAATTTT-GTTACTCTCAATGAGGAGTGAAGAGATACAGTGTCTACTACCAAC 857
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
| | | | |
Db 858 TAGTGATTAAGGCGCAGGAGTGTCTCTCAACCTCTCACTAGACAGAGCTCTCCCAT 917
QY 241 TACAATCAATCCCAATCCGAAGTGTCAACTGTCTCAGAGCTTAAGAAACCTGTGTTAGTA 300
| | | | |
Db 918 TACAATCAATCCCAATCCGAAGTGTCAACTGTCTCAGAGCTTAAGAAACCTGTGTTAGTA 977
QY 301 GAAAAGGCGCTGGGAAAAGAGGAGCCAACTGTCTCTCTCTCTCACTTATGTCATT 360
| | | | |
Db 978 GAAAAGGCGCT-GGAAAAGAGGAGCCAACTGTCTCTCTCTCTCACTTATGTCATT 1036
QY 361 GCGAATTAAGCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
| | | | |
Db 1037 GCGAATTAAGCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1096
QY 421 GGGACACAGATTAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
| | | | |
Db 1097 GGGACACAGATTAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1156
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCTCTCTCTCTCTCTCA 540
| | | | |
Db 1157 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCTCTCTCTCTCTCTCA 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTTCTACTCAGGTTTCTTACTCTGAATTTAGA 600
| | | | |
Db 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTTCTACTCAGGTTTCTTACTCTGAATTTAGA 1276
QY 601 TCTCCAGACCCCTGCTGGCCACAATTCAATTAAAGCAACAATATACCTTCATGAA 660
| | | | |
Db 1277 TCTCCAGACCCCTGCTGGCCACAATTCAATTAAAGCAACAATATACCTTCATGAA 1336
QY 661 GCACACACAGATTTTGAAGCAAGACATGACTCTTGAATGAGGCTTGAAGAAATG 720
| | | | |
Db 1337 GCACACACAGATTTTGAAGCAAGACATGACTCTTGAATGAGGCTTGAAGAAATG 1396
QY 721 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTTCAATGTTA 780
| | | | |
Db 1397 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTTCAATGTTA 1456
QY 781 ACCACTGCTCTCTGAGACCTTGAAGCAGGAGTGTATTAATGTTGTTAAGAAAAC 840
| | | | |
Db 1457 ACCACTGCTCTCTGAGACCTTGAAGCAGGAGTGTATTAATGTTGTTAAGAAAAC 1516
QY 841 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTCT 890
| | | | |
Db 1517 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTCT 1566
RESULT 15
AR443353 1567 bp DNA linear PAT 20-FEB-2004
LOCUS AR443353
DEFINITION Sequence 74 from patent US 6670463.

| | | | |
|----|---------------------------------------------------------------------------|---------------------------------------|-------------------------------------------|
| | (COLP//) | COLPIITS T L. | |
| PA | (FRIE//) | FRIEDMAN P N. | |
| PA | (GORD//) | GORDON J. | |
| PA | (GRAN//) | GRAMADOS E N. | |
| PA | (HODG//) | HODGES S C. | |
| PA | (KLAS//) | KLASS M R. | |
| PA | (KRAT//) | KRATOCHVIL J D. | |
| PA | (ROBE//) | ROBERTS-RAPP L A. | |
| PA | (RUSS//) | RUSSELL J C. | |
| PA | (STRO//) | STROUPPE S D. | |
| PB | Billingel PA, | Cohen M | Colpites TL, Friedman PN, Gordon J; |
| PI | Grenados EN, | Hodges SC, | Klass MR, Kratochvil JD, Roberts-Rapp LA; |
| PT | Russell JC, | Stroupe SD; | |
| XX | | | |
| DR | WPI; 2002-403712/43. | | |
| XX | | | |
| PR | New BS265 proteins and nucleic acids, | | useful for detecting, diagnosing, |
| PT | staging, monitoring, prognosticating, | | in vivo imaging, preventing, |
| PT | treating, or determining the predisposition | | of an individual to breast cancer: |
| PS | | | |
| XX | Claim 1; Page 37; 52pp; English. | | |
| CC | The present sequence is of BS265 gene expressed sequence tag (EST) full- | | |
| CC | length sequence clone 3090742H1 (ATCC 98683). ESTs were derived from cDNA | | |
| CC | libraries made from breast tumour tissues, breast non-tumour tissues and | | |
| CC | numerous other tissues, and entered into a database as gene transcript | | |
| CC | images. They were then evaluated to identify EST sequences that were | | |
| CC | representative primarily of the breast tissue libraries, and were ranked | | |
| CC | according to their abundance in target libraries and absence from | | |
| CC | background libraries. Partial clones 3090742H1, g991752, g2058967 and | | |
| CC | g1615448 (see ABLS7345-48) represent the minimum number of clones that, | | |
| CC | together with the present full-length sequence of clone 3090752H1, were | | |
| CC | needed to form a config and from which a consensus sequence (see | | |
| CC | ABLS7350) was derived. ESTs corresponding to the consenus sequence of | | |
| CC | BS265 were found in 33.3% (9/27) of breast tissue libraries, and in 0.6% | | |
| CC | (3/476) of non-breast libraries. This set of contiguous and partially | | |
| CC | overlapping cDNA sequences, designated as BS265 and transcribed from | | |
| CC | breast tissue, and the polypeptides encoded by them, are useful for | | |
| CC | detecting, diagnosing, staging, monitoring, prognosticating, in vivo | | |
| CC | imaging, preventing, treating, or determining the predisposition of an | | |
| CC | individual to diseases and conditions of the breast, such as breast | | |
| CC | cancer. Also provided are antibodies which specifically bind to BS265 | | |
| CC | proteins, and agonists or inhibitors which prevent action of the | | |
| CC | proteins, and which are useful for treatment of breast disease, | | |
| CC | especially tumours and metastases | | |
| SQ | | | |
| XX | Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other; | | |
| Dn | Query Match | 90.6%; Score 806.4; DB 6; Length 893; | |
| Dn | Best Local Similarity | 91.9%; Pred. No. 9.9e-263; | |
| Dn | Matches 818; Conservative | 0; Mismatches 71; Indels 1; Gaps 1; | |
| Oy | 1 CAAGCTTGAGGGTTCCTTTCCATTCTCGGTGAACAGCTAAGACTCAGTTTTGCATA | 60 | |
| Dd | 1 CAAGCTTGAGGGTTCCTTTCCATTCTCGGTGAACAGCTAAGACTCAGTTTTGCATA | 60 | |
| Oy | 61 GCATCTNAGCAAGTGGAGCTCACGTGGGGTGAATTTGCCCCCCCATCTCGGGGGAAATGTC | 120 | |
| Dd | 61 GCATCTNAGCAAGTGGAGCTCACGTGGGGTGAATTTGCCCCCCCATCTCGGGGGAAATGTC | 120 | |
| Oy | 121 TGAGAACAATTTTGTTGTAAGTCAAATAGAAGGAGTAGAGAGAGATACAGNNNNNNNNNNNN | 180 | |
| Dd | 121 TGAGAACAATTTTGTTGTAAGTCAAATAGAAGGAGTAGAGAGAGATACAGNNNNNNNNNNNN | 180 | |
| Oy | 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN | 240 | |
| Dd | 181 TAGTGNATTAAGGCCAGGAGATGCTGCTCAACCTCTTAACATGTACAGAACGTCTCCCACAT | 240 | |
| Oy | 241 TACAATACCACCAATCCGAAGTGTCAACTGTGTGACAGCTTAAGAAACCTGTGTTTGAGTA | 300 | |
| Dd | 241 TACAATACCACCAATCCGAAGTGTCAACTGTGTGACAGCTTAAGAAACCTGTGTTTGAGTA | 300 | |


```

QY 301 GAAAGGGCTGGGAAAGAGGAGCCAAATCTGTCTGCTTCTCAATTAGTCATT 360
DB 301 GAAAAGGGGCT-GGAAAAGGGGAGGCAAAATCTGTCTGCTTCTCAATTAGTCATT 359
QY 361 GCGAATTAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 360 GCGAATTAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 419
QY 421 GGGGACCAAGATTAATCTCTAGTGAACAGAGTTGACAAAGGCTATGGGAAATGCTGA 480
DB 420 GGGGACCAAGATTAATCTCTAGTGAACAGAGTTGACAAAGGCTATGGGAAATGCTGA 479
QY 481 TGGGATTAATCTCTAGCTTGTGAGCTTCAAGTTTCTTCCCTTCATTTCACTCAAG 540
DB 480 TGGGATTAATCTCTAGCTTGTGAGCTTCAAGTTTCTTCCCTTCATTTCACTCAAG 539
QY 541 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTGA 600
DB 540 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTGA 599
QY 601 TCTCAGACCTTGCCTGGCCACAAATTAAGGCAACAAATATATCTTCATGA 660
DB 600 TCTCAGACCTTGCCTGGCCACAAATTAAGGCAACAAATATATCTTCATGA 659
QY 661 GCACACACAGCTTTGAAAGCAGAGCAATGACTGCTGAATTTGAGGCTTGAAGAAATG 720
DB 660 GCACACACAGCTTTGAAAGCAGAGCAATGACTGCTGAATTTGAGGCTTGAAGAAATG 719
QY 721 AAGCTTTGAAGAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTTATGTTA 780
DB 720 AAGCTTTGAAGAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTTATGTTA 779
QY 781 ACCACTGCTTCTGAGACCTTGAAGCAGGAGTGAAGTATTAATTAAGAAAC 840
DB 780 ACCACTGCTTCTGAGACCTTGAAGCAGGAGTGAAGTATTAATTAAGAAAC 839
QY 841 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATTAATTAATTTCT 890
DB 840 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATTAATTAATTTCT 889

RESULT 4
ABL57350
ID ABL57350 standard; cDNA; 893 BP.
AC ABL57350;
XX 12-AUG-2002 (first entry)
DT 12-AUG-2002 (first entry)
XX
DE Breast BS265 gene consensus sequence.
XX
KM BS265; human; breast; cancer; tumour; metastasis; diagnosis;
KW gene therapy; expressed sequence tag; EST; gene; ss.
XX
OS Homo sapiens.
XX
FH Key 1, 123 Location/Qualifiers
FT CDS /tag= a
FT /product= "BS265"
FT /partial
FT /note= "the CDS does not include a start codon"
XX
XX US2002034749-A1.
XX 21-MAR-2002.
XX
XX 07-MAY-2001; 2001US-00850178.
XX
XX 18-NOV-1997; 97US-00972376.
XX
XX 18-NOV-1998; 98US-00193944.
XX

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PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L A.
PA (RUS/) RUSSELL J C.
PA (STRO/) STROUBE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI Granados EN, Hodges SC, Kلاس MR, Kratochvil JD, Roberts-Rapp LA;
PI Russell JC, Stroupe SD;
XX
DR WPI, 2002-403712/43.
XX
XX P-PSDB; ABB76272.
XX
PT New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
PT staging, monitoring, prognosticating, in vivo imaging, preventing,
PT treating, or determining the predisposition of an individual to breast
PT cancer.
XX
XX Claim 1; Page 38; 52p; English.
XX
PS The present sequence is a consensus sequence of the human breast BS265
XX gene. Expressed sequence tags (ESTs) were derived from cDNA libraries
XX made from breast tumour tissues, breast non-tumour tissues and numerous
XX other tissues, and entered into a database as gene transcript images.
XX CC They were then evaluated to identify EST sequences that were
XX CC representative primarily of the breast tissue libraries, and were ranked
XX CC according to their abundance in target libraries and absence from
XX CC background libraries. 4 Overlapping EST clones, together with a full-
XX CC length sequence (see ABL57345-49), were used to form a contig from which
XX CC the present consensus sequence was derived. ESTs corresponding to the
XX CC consensus sequence were found in 33.3% (9/27) of breast tissue libraries,
XX CC and in 0.6% (3/476) of non-breast libraries. The set of contiguous and
XX CC partially overlapping cDNA sequences, designated as BS265 and transcribed
XX CC from breast tissue, and the polypeptides encoded by them, are useful for
XX CC detecting, diagnosing, staging, monitoring, prognosticating, in vivo
XX CC imaging, preventing, treating, or determining the predisposition of an
XX CC individual to diseases and conditions of the breast, such as breast
XX CC cancer. Also provided are antibodies which specifically bind to BS265
XX CC proteins, and agonists or inhibitors which prevent action of the
XX CC proteins, and which are useful for treatment of breast disease,
XX CC especially tumours and metastases
XX
SQ Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other;
XX
Query Match 90.6%; Score 806.4; DB 6; Length 893;
Best Local Similarity 91.9%; Pred. No. 9.9e-263;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1,
QY 1 CAAGCTTGAGGCTTCTCTTCATCTGCTGAGACAGTAAAGACTCACTTTCAATA 60
DB 1 CAAGCTTGAGGCTTCTCTTCATCTGCTGAGACAGTAAAGACTCACTTTCAATA 60
QY 61 GCATCTAAGAGAGGAGCTAGCTGGGAGTATTTGCCCCCATTCGCGGAGAAATGTC 120
DB 61 GCATCTAAGAGAGGAGCTAGCTGGGAGTATTTGCCCCCATTCGCGGAGAAATGTC 120
QY 121 TGAAGACAATTTGGTTACTCAATGAGAGGAGTGAAGAGATACAGNNNNNNNNNN 180
DB 121 TGAAGACAATTTGGTTACTCAATGAGAGGAGTGAAGAGATACAGNNNNNNNNNN 180
QY 181 TGAAGACAATTTGGTTACTCAATGAGAGGAGTGAAGAGATACAGNNNNNNNNNN 180
DB 181 TGAAGACAATTTGGTTACTCAATGAGAGGAGTGAAGAGATACAGNNNNNNNNNN 180
QY 241 TCAACTACCAATCCGAAGGTGCACTGTCTCAGAGCTAAGAAACCTGTTTGAGTA 300
DB 241 TCAACTACCAATCCGAAGGTGCACTGTCTCAGAGCTAAGAAACCTGTTTGAGTA 300

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| Query Match | Best Local Similarity | Matches | Score | DB | Length |
|--------------|-----------------------|------------|-------|--------|---------|
| 90.6% | 91.9% | 0 | 806.4 | 12 | 1004 |
| Conservative | 0 | Mismatches | 71 | Indels | Gaps |
| Sequence | 1004 BP | 276 A | 234 C | 214 G | 280 T |
| | | 0 U | | | 0 Other |

The present sequence is that of a cancer-specific gene, linked especially to breast cancer and endometrium cancer. It represents one of four different transcripts ADH50890-ADH50893 identified from the Genbank expressed sequence tag (EST) database which exhibit cancer-specific expression. An elevated expression of the gene relative to a known non-cancerous cell, especially due to an increased copy number, indicates a cancerous state or potentially cancerous state. Cancer-linked gene sequences, polypeptides encoded by such sequences, and antibodies reactive with such polypeptides, can be used in methods of treating and diagnosing cancer, preferably breast or endometrium cancer, and in carrying out screening assays for agents effective in reducing the activity of cancer-linked genes and hence for the treatment of cancer. Immunocjugates comprising an antibody of the invention and a cytotoxic agent are useful for cancer therapy.

Claim 1; SEQ ID NO 2; 52pp; English.

Db 765 GCACACAGACGCTTTTGAAGCAAGACATGCTGTAATTGAGGCTTGAGGAATG 824
Qy 721 AAGCTTTGAGGAAAGATACTTGTTCAGCCCTTCCACACTTTCATGTGTTA 780
Db 825 AAGCTTTGAGGAAAGATACTTGTTCAGCCCTTCCACACTTTCATGTGTTA 884
Qy 781 ACCACTGCTTCTGAGACCTTGAGCCAGCGTGAATTAATGATGTTGTAAGAAAAC 840
Db 885 ACCACTGCTTCTGAGACCTTGAGCCAGCGTGAATTAATGATGTTGTAAGAAAAC 944
Qy 841 TGATTTAGAGTTCTGATCGTTCAGAGAAATTAATTAATCAATTTCT 890
Db 945 TGATTTAGAGTTCTGATCGTTCAGAGAAATTAATTAATCAATTTCT 994

RESULT 6

AAA70077 standard; cDNA; 2627 BP.

AAA70077;

07-NOV-2000 (first entry)

Human ovarian carcinoma antigen polynucleotide SEQ ID NO:391.

Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis; tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.

Homo sapiens.

WO20036107-A2.

22-JUN-2000.

17-DEC-1999; 99WO-US030270.

17-DEC-1998; 98US-00215681.

17-DEC-1998; 98US-00216003.

23-JUN-1999; 99US-0038933.

24-SEP-1999; 99US-00404879.

(CORI-) CORIXA CORP.

MITCHELL JL, KING GE, ALGATE PA, FRUDAKIS TN;

WPI; 2000-431589/37.

Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of cancer, preferably ovarian cancer.

Claim 1; Page 204-205; 299pp; English.

The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants).

Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human exemplification of the present invention

CC The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants).

CC Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human exemplification of the present invention

CC CC

Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 90.6%; Score 806.4; DB 3; Length 2627;

Best Local Similarity 91.9%; Pred. No. 1.9e-262;

Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

1 CAAGCTGAGGCTTCTCTCCATCCGCGTGAAGCTTAAGCTTCAGTTTCATA 60
1721 CAAGCTGAGGCTTCTCTCCATCCGCGTGAAGCTTAAGCTTCAGTTTCATA 1780

Qy 61 GCATCTAGAGAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGAATGTC 120
Db 1781 GCATCTAGAGAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGAATGTC 1840
Qy 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 1841 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGGCTACTACCAAC 1900
Qy 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
Db 1901 TAGTGATAAAGGCGAGGAGATGCTGCTCAACCTCCTACATGTAAGAGAGTCTCCCAT 1960
Qy 241 TACAATACCAATCCGAATCGAATGTCATGTCGAGACTAAGAAACCTGTTTGAATA 300
Db 1961 TACAATACCAATCCGAATGTCATGTCGAGACTAAGAAACCTGTTTGAATA 2020
Qy 301 GAAAAAGGCTGGGAAAGGAGGAGCCAAATCTGCTGCTCCCTACATTAATGTCAT 360
Db 2021 GAAAAAGGCTGGGAAAGGAGGAGCCAAATCTGCTGCTCCCTACATTAATGTCAT 2079
Qy 361 GGCATAATGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 2080 GGCATAATGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2139
Qy 421 GGGCAACAGATTAATCTCTGAGTGAACAGAGTTGACAGGCTTATGGAAATGCTGCA 480
Db 2140 GGGCAACAGATTAATCTCTGAGTGAACAGAGTTGACAGGCTTATGGAAATGCTGCA 2199
Qy 481 TGGGATTAATCTCTGAGTGAACAGAGTTGACAGGCTTATGGAAATGCTGCA 540
Db 2200 TGGGATTAATCTCTGAGTGAACAGAGTTGACAGGCTTATGGAAATGCTGCA 2259
Qy 541 CCAAGTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGAAATTTAGA 600
Db 2260 CCAAGTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGAAATTTAGA 2319
Qy 601 TCTCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 2320 TCTCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2379
Qy 661 GCACACAGACTTTTGAAGCAAGGCAATGACGCTGTAATGAGGCTTGAAGAAATG 720
Db 2380 GCACACAGACTTTTGAAGCAAGGCAATGACGCTGTAATGAGGCTTGAAGAAATG 2439
Qy 721 AAGCTTTGAGGAAAGAAATATCTTTGTTCCAGCCCTTCCACACTTTCATGTGTTA 780
Db 2440 AAGCTTTGAGGAAAGAAATATCTTTGTTCCAGCCCTTCCACACTTTCATGTGTTA 2499
Qy 781 ACCACTGCTTCTGAGACCTTGAGCCAGCGTGAATTAATGATGTTGTAAGAAAAC 840
Db 2500 ACCACTGCTTCTGAGACCTTGAGCCAGCGTGAATTAATGATGTTGTAAGAAAAC 2559
Qy 841 TGATTTAGAGTTCTGATCGTTCAGAGAAATTAATTAATCAATTTCT 890
Db 2560 TGATTTAGAGTTCTGATCGTTCAGAGAAATTAATTAATCAATTTCT 2609

RESULT 7

AAH55681 standard; DNA; 2627 BP.

AAH55681;

04-SEP-2001 (first entry)

Human ovarian tumour-derived antigen O88 DNA sequence.

Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour; antigen; O88; ds.

Homo sapiens.

WO200140269-A2.

XX 07-JUN-2001.
 PD
 XX
 PF 29-NOV-2000; 2000MO-US032520.
 XX
 XX 30-NOV-1999; 990US-00451651.
 PR 22-FEB-2000; 2000US-00510662.
 PR 10-MAR-2000; 2000US-0052386.
 PR 07-APR-2000; 2000US-00545068.
 PR 15-MAY-2000; 2000US-00571025.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
 XX
 DR WPI; 2001-356154/37.
 XX
 DR N-PSDB; AAB99204, AAB99205.
 XX
 PT Breast tumor polypeptides and the nucleic acids that encode them, useful
 PT for the prevention, diagnosis and treatment of breast cancer.
 XX
 PS Claim 24; Page 189; 221pp; English.
 XX
 CC The present invention relates to human breast tumour protein coding
 CC sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-
 CC AAH55762). The breast tumour protein DNA sequences may be used in the
 CC prevention, diagnosis and treatment of diseases associated with the
 CC inappropriate expression of the breast tumour protein e.g. breast cancer.
 CC The present sequence is a human ovarian tumour-derived antigen coding
 CC sequence, which was used in an example from the present invention
 XX
 SO Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
 Query Match 90.6%; Score 806.4; DB 4; Length 2627;
 Best Local Similarity 91.9%; Pred. No. 1.9e-262;
 Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
 QY 1 CAAGCTCTGAGGCTTCCTTCATCCCTGCGAGCAAGCTAAGACTGTTTCAATA 60
 DB 1721 CAAGCTCTGAGGCTTCCTTCATCCCTGCGAGCAAGCTAAGACTGTTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGATTTGCGCCCATCTCCGGGGAATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGATTTGCGCCCATCTCCGGGGAATGTC 1840
 QY 121 TGAAGCAATTTGTTTACTCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNN 180
 DB 1841 TGAAGCAATTTGTTTACTCTCAATGAGGAGTGGAGAGATACAGTCTACTACCAAC 1900
 QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
 DB 1901 TAGTGATTAAGGCCAGGAGTGTCTCAACTCTCACTAGTACAGAGCTCTCCCAT 1960
 QY 241 TACAATACCCATCCGAAAGTGTCAACTGTGTGAGGACTAAGAAACCTGTGTTAGTA 300
 DB 1961 TACAATACCCATCCGAAAGTGTCAACTGTGTGAGGACTAAGAAACCTGTGTTAGTA 2020
 QY 301 GAAAAGGCGCTGGGAAAAGGGGAGCCAACTGTGTCTGTTCTCTCAATTAGTCATT 360
 DB 2021 GAAAAGGCGCT-GGAAAAGGGGAGCCAACTGTGTCTGTTCTCTCAATTAGTCATT 2079
 QY 361 GGCAATTAAGCATTGTCTGTTGCTGTGCTGCTGAGCAGAGAGCCAGAACTATAC 420
 DB 2080 GGCAATTAAGCATTGTCTGTTGCTGTGCTGCTGAGCAGAGAGCCAGAACTATAC 2139
 QY 421 GGGCACCAGATTAACATCTCTCAGTGAAGAGAGTGAAGAGCCCTATGGAAATGCTGA 480
 DB 2140 GGGCACCAGATTAACATCTCTCAGTGAAGAGAGTGAAGAGCCCTATGGAAATGCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATCTCAGAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATCTCAGAG 2259

QY 541 CCAGTCTGTGAAGAAATGCTGAGTCTAGCTCAGGTTTTTCTTACTCTGAATTTAGA 600
 DB 2260 CCAGTCTGTGAAGAAATGCTGAGTCTAGCTCAGGTTTTTCTTACTCTGAATTTAGA 2319
 QY 601 TCTCAGAGCCCTGCTGCGCAACATTTCAATTAAAGGCAACAAACATATACCTTCCATGAA 660
 DB 2320 TCTCAGAGCCCTGCTGCGCAACATTTCAATTAAAGGCAACAAACATATACCTTCCATGAA 2379
 QY 661 GCACACACAGACTTTTGAAGAGAGACATAGCTCTGAATTGAGGCTTGAAGAAATG 720
 DB 2380 GCACACACAGACTTTTGAAGAGAGACATAGCTCTGAATTGAGGCTTGAAGAAATG 2439
 QY 721 AAGCTTTGAAGAAAGAAATATCTTGTTCAGCCCTTCCACACTCTTCAATGTGTTA 780
 DB 2440 AAGCTTTGAAGAAAGAAATATCTTGTTCAGCCCTTCCACACTCTTCAATGTGTTA 2499
 QY 781 ACCACTGCTTCTGAGACCTTGGAGCCAGGAGTACTGTATTAATAGTTGTTATAGAAAC 840
 DB 2500 ACCACTGCTTCTGAGACCTTGGAGCCAGGAGTACTGTATTAATAGTTGTTATAGAAAC 2559
 QY 841 TGATTTTGAAGTTTCAATGCTTCAAGAGAAATGATTAAATATACATTTCT 890
 DB 2560 TGATTTTGAAGTTTCAATGCTTCAAGAGAAATGATTAAATATACATTTCT 2609
 RESULT 8
 ID ABN72971 standard; DNA; 2627 BP.
 XX
 XX ABN72971;
 AC
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Ovarian carcinoma polynucleotide OBE.
 XX
 DE Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
 KW
 XX Homo sapiens.
 OS
 PN WO200206317-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-US022635.
 XX
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-0067857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00884441.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
 PI Reed SG, Vedrick TS, Carter D, Hill P, Albone E;
 XX
 XX WPI; 2002-164781/21.
 DR P-PSDB; ABB30900, ABB30901.
 XX
 PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
 PT protein or its variants, useful for stimulating an immune response in a
 PT patient and treating ovarian cancer.
 PS
 PS Example 2; Page 319-320; 408pp; English.
 XX
 CC This invention relates to polypeptides comprising an immunogenic portion
 CC of an ovarian carcinoma protein which acts as an immunostimulant and is
 CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations and antigen presenting cells that express
 CC the polypeptides are useful for stimulating an immune response in a
 CC patient and treating ovarian cancer. This sequence represents DNA related
 CC to the invention
 XX

Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 90.6%; Score 806.4; DB 6; Length 2627;
Best Local Similarity 91.9%; Pred. No. 1.9e-262;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGCTTAAGACCTTCAATTTCAATA 60
DB 1721 CAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGCTTAAGACCTTCAATTTCAATA 1780
QY 61 GCATCTAAGACAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 120
DB 1781 GCATCTAAGACAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 1840
QY 121 TGAAGCAATTTTGGTTACTCCTCAATGAGGAGTGAGAGAGATACAGNNNNNNNNNNNN 180
DB 1841 TGAAGCAATTTTGGTTACTCCTCAATGAGGAGTGAGAGAGATACAGNNNNNNNNNNNN 1900
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
DB 1901 TAGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTACCATGTACAGAGCTCTCCCAT 1960
QY 241 TACAACTACCCAAATCCGAAGTGTCACTGTCTCAGAGACTTAAGAAACCTGGTTTGAATA 300
DB 1961 TACAACTACCCAAATCCGAAGTGTCACTGTCTCAGAGACTTAAGAAACCTGGTTTGAATA 2020
QY 301 GAAAAGGCGCTGGGAAAGAGGAGGAGCAACAATCTGTCTGCTTCTCAATTAAGTCAAT 360
DB 2021 GAAAAGGCGCT- GGAAGAGGAGGAGGAGGAGCAACAATCTGTCTGCTTCTCAATTAAGTCAAT 2079
QY 361 GGCATAATAGCAATCTGTCTCTTTGGCTGCTGCTCTCAGACAGAGAGCCAGAACTCTATC 420
DB 2080 GGCATAATAGCAATCTGTCTCTTTGGCTGCTGCTCTCAGACAGAGAGCCAGAACTCTATC 2139
QY 421 GGGACACAGAGTAATCTCTCAAGTAAGAGAGTTGACAAAGGCTTAAGGAAATCCCTGA 480
DB 2140 GGGACACAGAGTAATCTCTCAAGTAAGAGAGTTGACAAAGGCTTAAGGAAATCCCTGA 2199
QY 481 TGGGATTAATCTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTCAATTTACCTGCAAG 540
DB 2200 TGGGATTAATCTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTCAATTTACCTGCAAG 2259
QY 541 CCAAGTCTGTAAAGAAATGCTGAGTCTAAGCTCAAGTTTCTTACTCTGAATTTAGA 600
DB 2260 CCAAGTCTGTAAAGAAATGCTGAGTCTAAGCTCAAGTTTCTTACTCTGAATTTAGA 2319
QY 601 TCTCCAGACCTGCTGCGCCACAATTTAAGCAACAAACATATACCTTCATGAA 660
DB 2320 TCTCCAGACCTGCTGCGCCACAATTTAAGCAACAAACATATACCTTCATGAA 2379
QY 661 GCACACAGACCTTTGAAAGCAAGGACATGACTGCTGAATTTGAGGCTTGAAGAAATG 720
DB 2380 GCACACAGACCTTTGAAAGCAAGGACATGACTGCTGAATTTGAGGCTTGAAGAAATG 2439
QY 721 AAGCTTTGAAGAAAAGAAATACTTTGTTTCAAGCCCCCTTCCACACTCTTCAATGTGTA 780
DB 2440 AAGCTTTGAAGAAAAGAAATACTTTGTTTCAAGCCCCCTTCCACACTCTTCAATGTGTA 2499
QY 781 ACCACCTGCTTCTCTGAGACCTTGAAGCAAGGTGACGTATTTACAGTTTGTATTAAGAAAC 840
DB 2500 ACCACCTGCTTCTCTGAGACCTTGAAGCAAGGTGACGTATTTACAGTTTGTATTAAGAAAC 2559
QY 841 TGATTTTGAAGTTTGAATCGTTCAGAGAAATGATTTAAATATACATTTCT 890
DB 2560 TGATTTTGAAGTTTGAATCGTTCAGAGAAATGATTTAAATATACATTTCT 2609

RESULT 9

ADA08544

ID ADA08544 strand: cDNA; 2627 BP.

AC ADA08544;

XX

DT 06-NOV-2003 (first entry)
XX Human ovarian carcinoma polynucleotide O8E.
DE ss; human; gene therapy; ovarian cancer; cancer.
XX

OS Homo sapiens.

PN US2003091580-A1.

PD 15-MAY-2003.

PF 17-JUN-2001; 2001US-00907969.

PR 18-JUN-2001; 2001US-00884441.

PA (MITC/) MITCHAM J L.

PA (KING/) KING G E.

PA (ALGA/) ALGATE P A.

PA (FLIN/) FLING S P.

PA (RETT/) RETTER M W.

PA (FANG/) FANGER G R.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (HILL/) HILL P.

PA (ALBO/) ALBONE E.

PI Mitcham JI, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;

PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;

DR WPI; 2003-532352/50.

PT New isolated O772P polypeptides and polynucleotides, useful in gene

PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian

PT cancer.

PS Example 2; SEQ ID NO 391; 371pp; English.

XX The invention relates to an isolated O772P polypeptide, which has the

XX structure fully defined in the specification. The composition containing

XX the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells

XX or antigen presenting cells are useful for stimulating an immune response

XX CC and treating ovarian cancer. Detecting the presence of the

XX CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian

XX CC carcinoma cDNAs and protein cDNAs were identified using microarray

XX CC technology. The present sequence represents a human ovarian carcinoma

XX antigen polynucleotide.

QY Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

QY Query Match 90.6%; Score 806.4; DB 9; Length 2627;

QY Best Local Similarity 91.9%; Pred. No. 1.9e-262;

QY Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGCTTAAGACCTTCAATTTCAATA 60

QY DB 1721 CAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGCTTAAGACCTTCAATTTCAATA 1780

QY 61 GCATCTAAGACAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 120

QY DB 1781 GCATCTAAGACAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 1840

QY 121 TGAAGCAATTTTGGTTACTCCTCAATGAGGAGTGAGAGAGATACAGNNNNNNNNNNNN 180

QY DB 1841 TGAAGCAATTTTGGTTACTCCTCAATGAGGAGTGAGAGAGATACAGNNNNNNNNNNNN 1900

QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240

QY DB 1901 TAGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTACCATGTACAGAGCTCTCCCAT 1960

QY 241 TACAACTACCCAAATCCGAAGTGTCACTGTCTCAGAGACTTAAGAAACCTGGTTTGAATA 300

Db 1961 TACAACTACCCAAATCCGAGTGTCACTGTGTGACAGTAAGAAACCTGGTTTGAGTA 2020
Qy 301 GAAAGGGGCTGGGAAAGAGGGAGCCAAATAATCTGTCTGCTTCCACATAGTAT 360
Db 2021 GAAAGGGGCTT-GGAAAGAGGGAGCCAAATAATCTGTCTGCTTCCACATAGTAT 2079
Qy 361 GGCAAATAGCATTTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 420
Db 2080 GGCAAATAGCATTTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 2139
Qy 421 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGA 480
Db 2140 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGA 2199
Qy 481 TGGATTTATCTTACGCTTGTGAGCTTCAAGTTTCTTCCCTTCAATTCACCTGAG 540
Db 2200 TGGATTTATCTTACGCTTGTGAGCTTCAAGTTTCTTCCCTTCAATTCACCTGAG 2259
Qy 541 CCAAGTTCTGTAAAGAGAAATGCTGAGTTCTAGCTCAGTTTCTTACTGGAATTAGA 600
Db 2260 CCAAGTTCTGTAAAGAGAAATGCTGAGTTCTAGCTCAGTTTCTTACTGGAATTAGA 2319
Qy 601 TCTCCAGACCTCTGCTGGCCAAATTCAAATTAAGGCAACAAATATACCTTCATGAA 660
Db 2320 TCTCCAGACCTCTGCTGGCCAAATTCAAATTAAGGCAACAAATATACCTTCATGAA 2379
Qy 661 GCACACACAGATTTTGAAGGCAAGCAATGACTGTGTAATTGAGGCTTGAAGCAATG 720
Db 2380 GCACACACAGATTTTGAAGGCAAGCAATGACTGTGTAATTGAGGCTTGAAGCAATG 2439
Qy 721 AAGCTTGAAGAAAGAAATACTTGTGTTCCAGCCCTTCCCACTCTTCATGTGTA 780
Db 2440 AAGCTTGAAGAAAGAAATACTTGTGTTCCAGCCCTTCCCACTCTTCATGTGTA 2499
Qy 781 ACCACTGCTTCTCTGACCTTGAAGCCAGGTGATGATTAATGATTTGTTATAGAAAC 840
Db 2500 ACCACTGCTTCTCTGACCTTGAAGCCAGGTGATGATTAATGATTTGTTATAGAAAC 2559
Qy 841 TGAATTTAGATTCGATTCGTTCAAGAGATGATTAATTAATTAATTTCCCT 890
Db 2560 TGAATTTAGATTCGATTCGTTCAAGAGATGATTAATTAATTAATTTCCCT 2609

RESULT 10
ADP08887
ID ADP08887 standard; cDNA; 2627 BP.
XX
AC ADP08887;
XX
DT 12-FEB-2004 (first entry)
XX
DE cDNA encoding secreted ovarian carcinoma antigen segid 391.
XX
KM Gene therapy; protein therapy; vaccine; antibody inhibition;
KM breast cancer; restorative therapy; diagnostic agent; immunoassay;
KM secreted ovarian carcinoma antigen; gene; ss.
XX
OS Homo sapiens.
OS
PN US2003124140-A1.
XX
PD 03-JUL-2003.
PF 17-JUL-2002; 2002US-00198053.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00215603.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.

PR 18-JUN-2001; 2001US-00884441.
PR 17-JUL-2001; 2001US-00907969.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangor CS, Retter MW, Fanger GR, Hall P;
XX
XX WPI: 2003-897152/82.
DR P-PSDB; ADP08888, ADP08889.
XX
XX
PT Oncogenic nucleic acids useful for the prevention, diagnosis and
PT treatment of breast cancer.
XX
PS Example 2; SEQ ID NO 391; 399bp; English.
XX
XX The invention describes nucleic acids (I) and the polypeptides (II) they
XX encode. The nucleic acids (I) may be used for preventing, diagnosing and
XX treating diseases related to their aberrant expression i.e. breast
XX cancers. For example, (I) and (II) may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of (II) by expressing
XX inactive proteins or to supplement the patient's own production of (II).
XX Additionally, (I) may be used to produce (II), by inserting (I) into a
XX host cell and culturing the cell to express the protein (II). (I) And its
XX complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar nucleic acids in
XX samples, and therefore which patients may be in need of restorative
XX therapy. The host cell may also be used as antigens in the production of
XX antibodies against (II) and in assays to identify modulators of (II)'s
XX expression and activity. The anti-(II) antibodies, agonists and
XX antagonists may be used to regulate expression and activity and as
XX diagnostic agents for detecting the presence of (II) in samples (e.g. by
XX immunosay). This sequence represents a polynucleotide encoding a
XX secreted ovarian carcinoma antigen.
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 90.6%; Score 806.4; DB 10; Length 2627;
Best Local Similarity 91.9%; Pred. No. 1,9e-262;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

Qy 1 CAAGCTCTAGAGGCTTCTCCCTTCATCTCGCTGACAGCTTAAGACCTCAGTTTCAATA 60
Db 1721 CAAGCTCTAGAGGCTTCTCCCTTCATCTCGCTGACAGCTTAAGACCTCAGTTTCAATA 1780
Qy 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGATGATTTGCCCTCCATCTCCGGGGAAATGTC 120
Db 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGATGATTTGCCCTCCATCTCCGGGGAAATGTC 1840
Qy 121 TGAAGCAATTTTGTCTTACCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNNNN 180
Db 1841 TGAAGCAATTTTGTCTTACCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNNNN 1900
Qy 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
Db 1901 TACTGATTAAGGCCAGGAGTGTCTCAACCTCTCAATGATGACAGAGTCTCCCAT 1960
Qy 241 TACAACTACCCAAATCCGAAAGTCAACTGTGTGAGACTPAAGAAACCTGGTTTGAATA 300
Db 1961 TACAACTACCCAAATCCGAAAGTCAACTGTGTGAGACTPAAGAAACCTGGTTTGAATA 2020
Qy 301 GAAAGGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTCTCTCAATTAATGATTCATT 360
Db 2021 GAAAGGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTCTCTCAATTAATGATTCATT 2079
Qy 361 GGCAAATAGCATTTGTCTCTTTGGCTGCTGCTCAGCAGAGAGCCAGAACTATC 420
Db 2080 GGCAAATAGCATTTGTCTCTTTGGCTGCTGCTCAGCAGAGAGCCAGAACTATC 2139
Qy 421 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGA 480
Db 2140 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGA 2199

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OY 481 TGGATTATCTTACAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTACCCCTGCAAG 540
DB 2200 TGGATTATCTTACAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTACCCCTGCAAG 2259
OY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
OY 601 TCTCCAGACCCCTGCTGGCCCAATTCAAATTAAGCAACAAACATATACCTTCATGAA 660
DB 2320 TCTCCAGACCCCTGCTGGCCCAATTCAAATTAAGCAACAAACATATACCTTCATGAA 2379
OY 661 GCACACACAGACTTTTGAAGCAGACAGACATGACTGTTGAATGAGGCTTGAGAAATG 720
DB 2380 GCACACACAGACTTTTGAAGCAGACAGACATGACTGTTGAATGAGGCTTGAGAAATG 2439
OY 721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCCAACTCTTCATGTGTA 780
DB 2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCCAACTCTTCATGTGTA 2499
OY 781 ACCACTGCTCTGCTGAGACCTTGAGCCAGCGGTGACTGATTACATGTTTATAGAAAC 840
DB 2500 ACCACTGCTCTGCTGAGACCTTGAGCCAGCGGTGACTGATTACATGTTTATAGAAAC 2559
OY 841 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
DB 2560 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 2609
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RESULT 11

ADG46174
ID ADG46174 standard; cDNA; 2627 BP.

AC ADG46174;

DT 26-FEB-2004 (first entry)

DE Human ovarian carcinoma polynucleotide #387.

KM Human; ovarian carcinoma; gene; 88; OBE; ovarian cancer;
secreted tumour antigen; cyostatic; O772P.

OS Homo sapiens.

PN US2003165504-A1.

PD 04-SEP-2003.

PF 04-APR-2001; 2001US-00827271.

PR 17-DEC-1998; 98US-00215681.

PR 17-DEC-1998; 98US-00216003.

PR 23-JUN-1999; 99US-0038933.

PR 24-SEP-1999; 99US-00404879.

PR 17-JUL-2000; 2000US-00617747.

PR 10-AUG-2000; 2000US-00636801.

PR 20-SEP-2000; 2000US-00667857.

PA (RETT/) RETTER M W.

PA (FANG/) FANGER G R.

PI Retter MW, Fanger GR;

DR MPI, 2003-898035/82.

PT New isolated OBE or O772P polypeptides, useful for diagnosing,
preventing, treating and monitoring cancer, e.g. ovarian cancer,
stimulating the immune response in patient.

PS Example 2; SEQ ID NO 391; 290bp; English.

XX The invention relates to human ovarian carcinoma polypeptides, designated
OBE or O772P, and the polynucleotides encoding them. The invention also

CC relates to methods for inhibiting the development of cancer, e.g. ovarian
CC cancer in a patient, methods for stimulating and/or expanding T cells and
CC method for identifying secreted tumour antigens. The polypeptides,
CC compositions, antibodies to the polypeptides and methods are useful for
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC cancer. The composition is particularly useful for stimulating an immune
CC response in patient. This sequence represents a human ovarian carcinoma
CC polynucleotide of the invention.

XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 90.6%; Score 806.4; DB 10; Length 2627;

Best Local Similarity 91.9%; Pred. No. 1.9e-262;

Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

```
OY 1 CAAAGCTGAGAGCTTCTCCCTTCATCCCTGAGGAGACAGTACAGCTCAGTTTCAATA 60
DB 1721 CAAAGCTGAGAGCTTCTCCCTTCATCCCTGAGGAGACAGTACAGCTCAGTTTCAATA 1780
OY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTATTTGCCCCCAATCTCCGGGGAAATGTC 120
DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTATTTGCCCCCAATCTCCGGGGAAATGTC 1840
OY 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGGAGAGGATACAGNNNNNNNNNNNN 180
DB 1841 TGAAGACAATTTTGGTTACTCAATGAGGAGTGGAGAGGATACAGTCTACTACCAAC 1900
OY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
DB 1901 TAGTGATTAAGAGCCAGGAGATGCTGCTCAACCTCTACATGTACAGAGCTCTCCCAT 1960
OY 241 TACAATCAATCCCAATCCGAAGTGTCAACTGTGTAGAGTAAAGAAACCTGTGTTAGTA 300
DB 1961 TACAATCAATCCCAATCCGAAGTGTCAACTGTGTAGAGTAAAGAAACCTGTGTTAGTA 2020
OY 301 GAAAAGGGCCCTGGGAAAAGGGGAGCCAAACAATCTGTCTCTCTCTCACTTATGTCATT 360
DB 2021 GAAAAGGGCCCTGGGAAAAGGGGAGCCAAACAATCTGTCTCTCTCTCACTTATGTCATT 2079
OY 361 GGGAAATGAAGCATCTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 2080 GGGAAATGAAGCATCTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139
OY 421 GGGACACAGATTAATCTCTCAGTGAACAGAGTTGAACAAGCCTTAGGAAATGCTGTA 480
DB 2140 GGGACACAGATTAATCTCTCAGTGAACAGAGTTGAACAAGCCTTAGGAAATGCTGTA 2199
OY 481 TGGATTATCTTCAAGCTTGTGAGCTTGAAGTTTCTTCCCTCATTTACCTGCAAG 540
DB 2200 TGGATTATCTTCAAGCTTGTGAGCTTGAAGTTTCTTCCCTCATTTACCTGCAAG 2259
OY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
OY 601 TCTCCAGACCCCTGCTGGCCCAATTCAAATTAAGCAACAAACATATACCTTCATGAA 660
DB 2320 TCTCCAGACCCCTGCTGGCCCAATTCAAATTAAGCAACAAACATATACCTTCATGAA 2379
OY 661 GCACACACAGACTTTTGAAGCAGACAGACATGACTGTTGAATGAGGCTTGAGAAATG 720
DB 2380 GCACACACAGACTTTTGAAGCAGACAGACATGACTGTTGAATGAGGCTTGAGAAATG 2439
OY 721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCCAACTCTTCATGTGTA 780
DB 2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCCAACTCTTCATGTGTA 2499
OY 781 ACCACTGCTCTGCTGAGACCTTGAGCCAGCGGTGACTGATTACATGTTTATAGAAAC 840
DB 2500 ACCACTGCTCTGCTGAGACCTTGAGCCAGCGGTGACTGATTACATGTTTATAGAAAC 2559
OY 841 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
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XX WO2004053079-A2.
XX
XX 24-JUN-2004.
XX
XX 08-DEC-2003; 2003WO-US038855.
XX
XX 06-DEC-2002; 2002US-0431301P.
XX 06-DEC-2002; 2002US-0431321P.
XX 30-JUN-2003; 2003US-0484584P.
XX 07-NOV-2003; 2003US-0518607P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Turner LR, Sun Y, Liu S, Chen H;
XX
XX WPI; 2004-468850/44.
XX P-P8DB; ADP81235, ADP81236.
XX
XX New ovarian specific nucleic acid molecules and polypeptides useful for
XX diagnosing, preventing or treating ovarian cancer, for producing
XX transgenic animals or cells, or for research purposes.
XX
XX Claim 1; SEQ ID NO 109; 754bp; English.
XX
XX The invention relates to novel isolated nucleic acid molecules and
XX polypeptides present in normal and neoplastic ovarian cells. These
XX comprise a nucleic acid sequence encoding any of the 167 amino acid
XX sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
XX specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
XX the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
XX in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
XX further comprises: a method for determining the presence of a ovarian
XX specific nucleic acid (OSNA) in a sample; a vector comprising the above
XX nucleic acid molecule; a host cell comprising the vector; a method for
XX producing a polypeptide encoded by the nucleic acid molecule; a
XX polypeptide encoded by the nucleic acid molecule cited above; an antibody
XX or its fragment that specifically binds to the above polypeptide; a
XX method for determining the presence of an ovarian specific protein in a
XX sample; a method for diagnosing or monitoring the presence and metastases
XX of ovarian cancer in a patient; a kit for detecting a risk of cancer or
XX presence of cancer in a patient, the kit comprising a means for
XX determining the presence of the above nucleic acid molecule or
XX polypeptide; a method of treating a patient with ovarian cancer; and a
XX vaccine comprising the above polypeptide or nucleic acid encoding the
XX polypeptide. The isolated nucleic acid molecules and polypeptides have
XX cytostatic activity. The isolated polypeptides may be used to create a
XX vaccine. The isolated nucleic acid molecules and polypeptides can be used
XX for diagnosing or monitoring the presence and metastases of ovarian
XX cancer and treating ovarian cancer. This polynucleotide sequence
XX represents an ovarian specific gene of the invention.
XX
XX Sequence 2690 BP; 760 A; 611 C; 603 G; 716 T; 0 U; 0 Other;
XX
XX Query Match 90.6%; Score 806.4; DB 12; Length 2690;
XX Best Local Similarity 91.9%; Pred. No. 1.9e-262;
XX Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
XX
XX 1 CAAGCTCGAGGCTTCCTTCCTCCATCGCTGAGCAGCTAAGCCCAAGTTTCATTA 60
XX 1801 CAAGCTCGAGGCTTCCTTCCTCCATCGCTGAGCAGCTAAGCCCAAGTTTCATTA 1860
XX
XX 61 GCATCTAGAGAGAGTGGAGCTGAGTGGGTGATTTCCGCCCATCTCCGGGGAGATGTC 120
XX 1861 GCATCTAGAGAGAGTGGAGCTGAGTGGGTGATTTCCGCCCATCTCCGGGGAGATGTC 1920
XX
XX 121 TGAAGACAATTTTGGTTACCTCAATGAGGAGTGAGAGAGATACAGNNNNNNNNNN 180
XX 1921 TGAAGACAATTTTGGTTACCTCAATGAGGAGTGAGAGAGATACAGGTTACTACCAAC 1980
XX
XX 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
XX 1981 TAGTGATTAAGGCGAGGATGCTGCTCAACTCTCACTATGACAGACGTCTCCCAT 2040

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QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTGTGACAGACTAAGAAACCTGGTTTGAAGTA 300
DB 2041 TACAACCTACCCCAATCCGAAGTGTCACTGTGTGACAGACTAAGAAACCTGGTTTGAAGTA 2100
QY 301 GAAAAAGGCTGGGAAAGAGGGAGCCCAACAATGTGTCTGCTTCTCACTTAGTCAATT 360
DB 2101 GAAAAAGGCTGGGAAAGAGGGAGCCCAACAATGTGTCTGCTTCTCACTTAGTCAATT 2159
QY 361 GGGCAATATAGGATCTGTCTCTTGGGCTGCGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 2160 GGGCAATATAGGATCTGTCTCTTGGGCTGCGCTCAGACAGAGAGCCAGAACTCTATC 2219
QY 421 GGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGAGAAATGCTGA 480
DB 2220 GGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGAGAAATGCTGA 2279
QY 481 TGGGATTAATCTTCAGCTTGTGAGCTTTAGTTTCTTCCCTTCATCTACCTCGCAAG 540
DB 2280 TGGGATTAATCTTCAGCTTGTGAGCTTTAGTTTCTTCCCTTCATCTACCTCGCAAG 2339
QY 541 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
DB 2340 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2399
QY 601 TCTCCAGACCCCTGCTGCGCAAAATTCAAATTAAGCAACAAATATACCTTCATGAA 660
DB 2400 TCTCCAGACCCCTGCTGCGCAAAATTCAAATTAAGCAACAAATATACCTTCATGAA 2459
QY 661 GCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTAGAGCCCTTGAGGAATG 720
DB 2460 GCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTAGAGCCCTTGAGGAATG 2519
QY 721 AAGCTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCCACTCTCATGTGTTA 780
DB 2520 AAGCTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCCACTCTCATGTGTTA 2579
QY 781 ACCACTGCTTCTGAGACTTTGAGCCAGCGGTGACTGATTTAATGTTTATAGAAAAC 840
DB 2580 ACCACTGCTTCTGAGACTTTGAGCCAGCGGTGACTGATTTAATGTTTATAGAAAAC 2639
QY 841 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCTCT 890
DB 2640 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCTCT 2689

```

RESULT 14
AAD32519 standard; DNA; 3357 BP.

AAD32519;
18-JUN-2002 (first entry)

Human B7-H8 gene.

Human; B7-1like protein; inflammation; tissue damage; immune disorder;
Addison's disease; autoimmune haemolytic anaemia; autoimmune thyroiditis;
diabetes mellitus; Crohn's disease; multiple sclerosis; allergy; cancer;
rheumatoid arthritis; cardiovascular disorder; nervous system disorder;
myocardial ischaemia; ulcerative colitis; reproductive system disorder;
Alzheimer's disease; Parkinson's disease; endocrine disorder; hepatitis;
diabetes mellitus; Grave's disease; Paget's disease; liver disorder;
gastrointestinal disorder; irritable bowel syndrome; cerebral anoxia;
dysphagia; hepatomegaly; neurological disease; infectious disease;
epilepsy; gene therapy; B7-H8 protein; chromosome 1; gene; ds.

Homo sapiens.

Key Location/Qualifiers
CDS 419..1267
FT /*tag= a
FT /product= "Human B7-H8 protein"

21 / 1GHHGACMAAIIIGGIAACCAAGAGGGGAGIUGAGGAGGMAACAGIGCAAC

| Key | Location/Qualifiers |
|-----|---------------------|
| XX | |
| FH | |

| Result No. | Score | Query | | DB | ID | Description |
|------------|-------|-------|--------|----|---------------------|-------------------|
| | | Match | Length | | | |
| 1 | 806.4 | 90.6 | 2627 | 3 | US-09-404-879A-391 | Sequence 391, App |
| 2 | 806.4 | 90.6 | 2627 | 4 | US-09-667-857-391 | Sequence 391, App |
| 3 | 794.4 | 89.3 | 1567 | 3 | US-09-404-879A-74 | Sequence 74, App |
| 4 | 794.4 | 89.3 | 1567 | 4 | US-09-338-933-74 | Sequence 74, App |
| 5 | 794.4 | 89.3 | 1567 | 4 | US-09-215-681-74 | Sequence 74, App |
| 6 | 794.4 | 89.3 | 1567 | 4 | US-09-216-003A-74 | Sequence 74, App |
| 7 | 794.4 | 89.3 | 1567 | 4 | US-09-667-857-74 | Sequence 74, App |
| 8 | 446.6 | 50.2 | 461 | 3 | US-09-404-879A-27 | Sequence 27, App |
| 9 | 446.6 | 50.2 | 461 | 4 | US-09-338-933-27 | Sequence 27, App |
| 10 | 446.6 | 50.2 | 461 | 4 | US-09-215-681-27 | Sequence 27, App |
| 11 | 446.6 | 50.2 | 461 | 4 | US-09-216-003A-27 | Sequence 27, App |
| 12 | 446.6 | 50.2 | 461 | 4 | US-09-667-857-27 | Sequence 27, App |
| 13 | 364.8 | 41.0 | 695 | 3 | US-09-040-984-15 | Sequence 15, App |
| 14 | 364.8 | 41.0 | 695 | 3 | US-09-123-912-15 | Sequence 15, App |
| 15 | 364.8 | 41.0 | 695 | 3 | US-09-613-597-15 | Sequence 15, App |
| 16 | 364.8 | 41.0 | 695 | 4 | US-09-460-884A-15 | Sequence 15, App |
| 17 | 364.8 | 41.0 | 695 | 4 | US-09-542-615A-15 | Sequence 15, App |
| 18 | 364.8 | 41.0 | 695 | 4 | US-09-606-421B-15 | Sequence 15, App |
| 19 | 364.8 | 41.0 | 695 | 4 | US-09-221-107-15 | Sequence 15, App |
| 20 | 364.8 | 41.0 | 695 | 4 | US-09-466-196A-15 | Sequence 15, App |
| 21 | 364.8 | 41.0 | 695 | 4 | US-09-476-966A-15 | Sequence 15, App |
| 22 | 364.8 | 41.0 | 695 | 4 | US-09-630-940B-15 | Sequence 15, App |
| 23 | 364.8 | 41.0 | 695 | 4 | US-09-285-479-15 | Sequence 15, App |
| 24 | 52.4 | 5.9 | 59828 | 4 | US-09-949-016-16238 | Sequence 16238, F |
| 25 | 47.6 | 5.3 | 1082 | 2 | US-08-909-965C-12 | Sequence 12, App |
| 26 | 46.2 | 5.2 | 77661 | 4 | US-09-949-016-12770 | Sequence 12770, F |
| 27 | 46.2 | 5.2 | 77661 | 4 | US-09-949-016-13751 | Sequence 13751, F |

| | | | | | | | |
|------|------|-----|--------|---|----------------------|---|-----------------|
| C 28 | 45.2 | 5.1 | 6.01 | 4 | US-09-949-016-188942 | A | Sequence 88942 |
| C 29 | 44.4 | 4.9 | 162655 | 4 | US-09-949-016-112664 | A | Sequence 11264 |
| C 30 | 43 | 4.8 | 146601 | 4 | US-09-949-016-16151 | A | Sequence 16151 |
| C 31 | 41.2 | 4.6 | 112623 | 4 | US-09-949-016-14374 | A | Sequence 14374 |
| C 32 | 40.6 | 4.6 | 601 | 4 | US-09-949-016-160158 | A | Sequence 160158 |
| C 33 | 40.2 | 4.5 | 601 | 4 | US-09-949-016-43835 | A | Sequence 43835 |
| C 34 | 40.2 | 4.5 | 601 | 4 | US-09-949-016-43880 | A | Sequence 43880 |
| C 35 | 40.2 | 4.5 | 601 | 4 | US-09-949-016-52452 | A | Sequence 52452 |
| C 36 | 40.2 | 4.5 | 601 | 4 | US-09-949-016-52497 | A | Sequence 52497 |
| C 37 | 40.2 | 4.5 | 493164 | 4 | US-09-949-016-12985 | A | Sequence 12985 |
| C 38 | 40.2 | 4.5 | 493164 | 4 | US-09-949-016-12986 | A | Sequence 12986 |
| C 39 | 40.2 | 4.5 | 493164 | 4 | US-09-949-016-13262 | A | Sequence 13262 |
| C 40 | 40.2 | 4.5 | 493164 | 4 | US-09-949-016-13263 | A | Sequence 13263 |
| C 41 | 40.2 | 4.5 | 87863 | 4 | US-09-949-016-14402 | A | Sequence 14402 |
| C 42 | 39.8 | 4.5 | 82894 | 4 | US-09-949-016-15637 | A | Sequence 15637 |
| C 43 | 39.8 | 4.5 | 115814 | 4 | US-09-949-016-16205 | A | Sequence 16205 |
| C 44 | 39.6 | 4.4 | 178883 | 4 | US-09-949-016-12733 | A | Sequence 12733 |
| C 45 | 39.6 | 4.4 | 178884 | 4 | US-09-949-016-13039 | A | Sequence 13039 |

ALIGNMENTS

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RESULT 1
US-09-404-879A-391
; Sequence 391, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-404-879A-391

```

Query Match 90.6%; Score 806.4; DB 3; Length 2627;

Best Local Similarity 91.9%; Pred. No. 4.3e-246;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1

[illegible]

| | | | |
|----|------|------------------------------------------------------------|------|
| Db | 2080 | GGCAATATAGACATTCGTCTCTTTGGCTGCTGCCTCAGCACAGAGGCAAGAACTTATC | 2139 |
| QY | 421 | GGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCATGGAAATGCTGA | 480 |
| Db | 2140 | GGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCATGGAAATGCTGA | 2199 |
| QY | 481 | TGGATTAATCTTCAGCTGTTGAGCTTCTAAGTTCTTTCCCTCATTTACCTGCAAG | 540 |
| Db | 2200 | TGGATTAATCTTCAGCTGTTGAGCTTCTAAGTTCTTTCCCTCATTTACCTGCAAG | 2259 |
| QY | 541 | CCAAGTTCTGTAAAGAAATGCTCAGTCTTAGCTCAGTTTTCTTACCTGAATTAGA | 600 |
| Db | 2260 | CCAAGTTCTGTAAAGAAATGCTCAGTCTTAGCTCAGTTTTCTTACCTGAATTAGA | 2319 |
| QY | 601 | TCTCCAGACCCCTGCCTGCGCACAATTTCAATTAAGCAACAACATATACCTTCCATGA | 660 |
| Db | 2320 | TCTCCAGACCCCTGCCTGCGCACAATTTCAATTAAGCAACAACATATACCTTCCATGA | 2379 |
| QY | 661 | GCACACACAGACTTTTGAAGCAGAGACATAGACTGTTGAATTGAGCCCTTGAAGATG | 720 |
| Db | 2380 | GCACACACAGACTTTTGAAGCAGAGACATAGACTGTTGAATTGAGCCCTTGAAGATG | 2439 |
| QY | 721 | AAGCTTTAAGAGAAAAGAAATCTTTGTTCCAGCCCCCTCCACACCTTCAGTGTATA | 780 |
| Db | 2440 | AAGCTTTAAGAGAAAAGAAATCTTTGTTCCAGCCCCCTCCACACCTTCATGTGTATA | 2499 |
| QY | 781 | AACACTGCTTCTCTGAGCCTTGAAGCCACGGTACTGATTAACATGTTGTTATAGAAAC | 840 |
| Db | 2500 | AACACTGCTTCTCTGAGCCTTGAAGCCACGGTACTGATTAACATGTTGTTATAGAAAC | 2559 |
| QY | 841 | TGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAATATACATTTCTCT | 890 |
| Db | 2560 | TGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAATATACATTTCTCT | 2609 |

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RESULT 2
US-09-667-857-391
, Sequence 391, Application US/09667857
, Patent No. 6699664
, GENERAL INFORMATION:
, APPLICANT: Mitcham, Jennifer L.
, APPLICANT: King, Gordon E.
, APPLICANT: Algate, Paul A.
, APPLICANT: Retteer, Marc W.
, APPLICANT: Fanger, Gary Richard
, APPLICANT: Reed, Steven G.
, APPLICANT: Vedvick, Thomas S.
, APPLICANT: Carter, Patrick
, TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
, TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
, FILE REFERENCE: 210121.462C5
, CURRENT APPLICATION NUMBER: US/09/667,857
, CURRENT FILING DATE: 2000-09-20
, NUMBER OF SEQ ID NOS: 455
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 391
, LENGTH: 2627
, TYPE: DNA
, ORGANISM: Homo sapiens
, US-09-667-857-391

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| | Query Match | 90.6%; | Score 806.4; | DB 4; | Length 2627; |
|----|-----------------------|---------------------------------------------------------------|--------------------|----------------|--------------|
| | Best Local Similarity | 91.9%; | Pred. No.4.3e-246; | | |
| | Matches 818; | Conservative | 0; | Mismatches 71; | Indels 1; |
| | | | | Gaps | 1; |
| QY | 1 | CAAGCTCGAAGCTTCCTCTTCATCCTGCGTGAGGCTAAGACCTCAGTTTCATYA | 60 | | |
| Db | 1721 | CAAGCTCTGAGAGCTTCTCTTTCACCTCTGCGTGAGAGCTAAGACCTCAGTTTCANITA | 1780 | | |
| QY | 61 | GCATCTAAGACAGTGGAGCTCAGCTGGGGTGAATTTGGCCCCCATCTCCGGGGGAAATGTC | 120 | | |

[illegible]

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RESULT 3
US-09-404-879A--74
; Sequence 74, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
;

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ORGANISM: Homo sapien
US-09-404-879A-74

Query Match 89.3%; Score 794.4; DB 3; Length 1567;
Best Local Similarity 91.8%; Pred. No. 2.2e-242;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

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QY 1 CAAGCTCTGAGGCTTCTCTTCCATCCCTGCGAGCACTAAGACCTCAGTTTCAAT 60
DB 679 CAAGCTCTGAGGCTTCTCTTCCATCCCTGCGAGCACTAAGACCTCAGTTTCAAT 738
QY 61 GCATCTAGAGCACTGGAAGTCACTGAGGCTGATTTGCCCCCATCTCCGGGGAAATGTC 120
DB 739 GCATCTAGAGCACTGGAAGTCACTGAGGCTGATTTGCCCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGCAATTTTGGTTTACTCTCATGAGGAGTGAAGAGATACGNNNNNNNNNNNN 180
DB 799 TGAAGCAATTTT-GTTTACTCTCATGAGGAGTGAAGAGATACGTTACTACCAAC 857
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
DB 858 TAGTGATTAAGGCCAGAGGATGCTGCTCAACCTTCAATGATACAGAGCTCTCCCAT 917
QY 241 TACAATCACTCAATCCGAAGTGTCAACTGTGTCAGAGCTAAGAAACCTGGTTTGAATA 300
DB 918 TACAATCACTCAATCCGAAGTGTCAACTGTGTCAGAGCTAAGAAACCTGGTTTGAATA 977
QY 301 GAAAAGGCTTGGGAAAAGGGGAGCCAAATCTGTCTGCTTCTCTCATTAATGTCATT 360
DB 978 GAAAAGGCTT-GGAAAAGGGGAGCCAAATCTGTCTGCTTCTCTCATTAATGTCATT 1036
QY 361 GGGAAATAAGCAATCTGTCTTGGCTGCTGCTCAGACAGAGGCGCAAGCTCTATC 420
DB 1037 GGGAAATAAGCAATCTGTCTTGGCTGCTGCTCAGACAGAGGCGCAAGCTCTATC 1096
QY 421 GGGCAACAAGATTAACATCTCTCAGTAAACAGAGTTGAACAAGGCTTAAGGAAATGCTGA 480
DB 1097 GGGCAACAAGATTAACATCTCTCAGTAAACAGAGTTGAACAAGGCTTAAGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCACTGTTGAGCTTTGAAGCTTTCTTCCCTTCAATTCACCTGCAAG 540
DB 1157 TGGGATTAATCTTCACTGTTGAGCTTTGAAGCTTTCTTCCCTTCAATTCACCTGCAAG 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTGTAATTAGA 600
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTGTAATTAGA 1276
QY 601 TCTCCAGACCTGCTGCGCACAATTCAAATTAAAGCAACAACATATACCTTCCATGAA 660
DB 1277 TCTCCAGACCTTCTGCGCACAATTCAAATTAAAGCAACAACATATACCTTCCATGAA 1336
QY 661 GCAACACACAGACTTTGAAAGCAAGACCAATGACTCTGTAATTGAGGCTTGAAGAAATG 720
DB 1337 GCAACACACAGACTTTGAAAGCAAGACCAATGACTCTGTAATTGAGGCTTGAAGAAATG 1396
QY 721 AAGCTTTGAAGAAAGAAATACCTTGTTCACGCCCCCTTCCACACTCTTCAATGTGTA 780
DB 1397 AAGCTTTGAAGAAAGAAATACCTTGTTCACGCCCCCTTCCACACTCTTCAATGTGTA 1456
QY 781 ACCACTGCTTCTCTGAGACCTTGAAGCAAGTGAATGTAATCATGTTGTTAAGAAAC 840
DB 1457 ACCACTGCTTCTCTGAGACCTTGAAGCAAGTGAATGTAATCATGTTGTTAAGAAAC 1516
QY 841 TGAATTTAAGATTCTGATGTTCAAGAGATGTAATTAATTAATCAATTTCT 890
DB 1517 TGAATTTAAGATTCTGATGTTCAAGAGATGTAATTAATTAATCAATTTCT 1566
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RESULT 4
US-09-338-933-74
; Sequence 74, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-338-933-74

Query Match 89.3%; Score 794.4; DB 4; Length 1567;
Best Local Similarity 91.8%; Pred. No. 2.2e-242;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

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QY 1 CAAGCTCTGAGGCTTCTCTTCCATCCCTGCGAGCACTAAGACCTCAGTTTCAAT 60
DB 679 CAAGCTCTGAGGCTTCTCTTCCATCCCTGCGAGCACTAAGACCTCAGTTTCAAT 738
QY 61 GCATCTAGAGCACTGGAAGTCACTGAGGCTGATTTGCCCCCATCTCCGGGGAAATGTC 120
DB 739 GCATCTAGAGCACTGGAAGTCACTGAGGCTGATTTGCCCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGCAATTTTGGTTTACTCTCATGAGGAGTGAAGAGATACGNNNNNNNNNNNN 180
DB 799 TGAAGCAATTTT-GTTTACTCTCATGAGGAGTGAAGAGATACGTTACTACCAAC 857
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
DB 858 TAGTGATTAAGGCCAGAGGATGCTGCTCAACCTTCAATGATACAGAGCTCTCCCAT 917
QY 241 TACAATCACTCAATCCGAAGTGTCAACTGTGTCAGAGCTAAGAAACCTGGTTTGAATA 300
DB 918 TACAATCACTCAATCCGAAGTGTCAACTGTGTCAGAGCTAAGAAACCTGGTTTGAATA 977
QY 301 GAAAAGGCTTGGGAAAAGGGGAGCCAAATCTGTCTGCTTCTCTCATTAATGTCATT 360
DB 978 GAAAAGGCTT-GGAAAAGGGGAGCCAAATCTGTCTGCTTCTCTCATTAATGTCATT 1036
QY 361 GGGAAATAAGCAATCTGTCTTGGCTGCTGCTCAGACAGAGGCGCAAGCTCTATC 420
DB 1037 GGGAAATAAGCAATCTGTCTTGGCTGCTGCTCAGACAGAGGCGCAAGCTCTATC 1096
QY 421 GGGCAACAAGATTAACATCTCTCAGTAAACAGAGTTGAACAAGGCTTAAGGAAATGCTGA 480
DB 1097 GGGCAACAAGATTAACATCTCTCAGTAAACAGAGTTGAACAAGGCTTAAGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCACTGTTGAGCTTTGAAGCTTTCTTCCCTTCAATTCACCTGCAAG 540
DB 1157 TGGGATTAATCTTCACTGTTGAGCTTTGAAGCTTTCTTCCCTTCAATTCACCTGCAAG 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTGTAATTAGA 600
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTGTAATTAGA 1276
QY 601 TCTCCAGACCTGCTGCGCACAATTCAAATTAAAGCAACAACATATACCTTCCATGAA 660
DB 1277 TCTCCAGACCTTCTGCGCACAATTCAAATTAAAGCAACAACATATACCTTCCATGAA 1336
QY 661 GCAACACACAGACTTTGAAAGCAAGACCAATGACTCTGTAATTGAGGCTTGAAGAAATG 720
DB 1337 GCAACACACAGACTTTGAAAGCAAGACCAATGACTCTGTAATTGAGGCTTGAAGAAATG 1396
QY 721 AAGCTTTGAAGAAAGAAATACCTTGTTCACGCCCCCTTCCACACTCTTCAATGTGTA 780
DB 1397 AAGCTTTGAAGAAAGAAATACCTTGTTCACGCCCCCTTCCACACTCTTCAATGTGTA 1456
QY 781 ACCACTGCTTCTCTGAGACCTTGAAGCAAGTGAATGTAATCATGTTGTTAAGAAAC 840
DB 1457 ACCACTGCTTCTCTGAGACCTTGAAGCAAGTGAATGTAATCATGTTGTTAAGAAAC 1516
```

Db 1457 ACCACTGCTTCCTGAGACCTTGAGCCAGCGTAGCTGATTAATACATGTTGTTATAGAAAAC 1516
Qy 841 TGAATTTAGAGTTCTGATCGTTCAAGAGAAATGATTAATATACATTTCT 890
Db 1517 TGATTTAGAGTTCTGATCGTTCAAGAGAAATGATTAATATACATTTCT 1566

RESULT 5
US-09-215-681-74
; Sequence 74, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-215-681-74

Query Match 89.3%; Score 794.4; DB 4; Length 1567;
Best Local Similarity 91.8%; Pred. No. 2.2e-242;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

Qy 1 CAAGCTGAGGCTTCCTCTTCATCCGCTGAGACAGCTAAGACTCAGTTTCAATA 60
Db 679 CAAGCTGAGGCTTCCTCTTCATCCGCTGAGACAGCTAAGACTCAGTTTCAATA 738
Qy 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTCCGCCCATCTCCGGGGATGTC 120
Db 739 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTCCGCCCATCTCCGGGGATGTC 798
Qy 121 TGAAGCAATTTGGTTACCTCAATGAGAGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 799 TGAAGCAATTTT-GTTACTCAATGAGAGAGTGAAGAGATACAGTCTAATAACAAC 857
Qy 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
Db 858 TAGTGATAAAGGCCAGGAGTGTCTCAACTCTCAATGATAGAGACGTCTCCCAT 917
Qy 241 TACAACCTAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGTTTGAATA 300
Db 918 TACAACCTAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGTTTGAATA 977
Qy 301 GAAAAGGCGCTGGGAAAAGAGGGGAGCCAAATCTGTCTGCTTCTCACTAGTCAAT 360
Db 978 GAAAAGGCGCT-GGAAAAGGGGAGCCAAATCTGTCTGCTTCTCACTAGTCAAT 1036
Qy 361 GCGAATAAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAACTCTATC 420
Db 1037 GCGAATAAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAACTCTATC 1096
Qy 421 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCATATGGAAATGCTGA 480
Db 1097 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCATATGGAAATGCTGA 1156
Qy 481 TGGGATTAATCTTCACTGTTGAGCTTCTAAGTTCTTTCCCTTCAATCTACCTGCAAG 540
Db 1157 TGGGATTAATCTTCACTGTTGAGCTTCTAAGTTCTTTCCCTTCAATCTACCTGCAAG 1216
Qy 541 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTGA 600
Db 1217 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTGA 1276
Qy 601 TCTCCAGACCTGCTGGCCACAAATTAATTAAGCAACAAACATATATACCTTCATGA 660

Db 1277 TCTCAGACCCCTTCCTGGCCCAATTCAAATTAAGGCAACAAATATACCTTCATGA 1336
Qy 661 GCACACAGACTTTTGAAGCAAGACAAATGAGCTGTAATGAGGCTTGAAGAAATG 720
Db 1337 GCACACAGACTTTTGAAGCAAGACAAATGAGCTGTAATGAGGCTTGAAGAAATG 1396
Qy 721 AAGCTTGAAGAAAAGAAATCTTGTTCAGGCCCTTCACACTCTTCATGTGTA 780
Db 1397 AAGCTTGAAGAAAAGAAATCTTGTTCAGGCCCTTCACACTCTTCATGTGTA 1456
Qy 781 ACCACTGCTTCCTGAGACCTTGAGCCAGGCTGATGATTAATCATGTTGTTATGA 840
Db 1457 ACCACTGCTTCCTGAGACCTTGAGCCAGGCTGATGATTAATCATGTTGTTATGA 1516
Qy 841 TGAATTTAGAGTTCTGATCGTTCAAGAGAAATGATTAATATACATTTCT 890
Db 1517 TGATTTAGAGTTCTGATCGTTCAAGAGAAATGATTAATATACATTTCT 1566

RESULT 6

US-09-216-003A-74
; Sequence 74, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216,003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-216-003A-74

Query Match 89.3%; Score 794.4; DB 4; Length 1567;
Best Local Similarity 91.8%; Pred. No. 2.2e-242;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

Qy 1 CAAGCTGAGGCTTCCTCTTCATCCGCTGAGACAGCTAAGACTCAGTTTCAATA 60
Db 679 CAAGCTGAGGCTTCCTCTTCATCCGCTGAGACAGCTAAGACTCAGTTTCAATA 738
Qy 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTCCGCCCATCTCCGGGGATGTC 120
Db 739 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTCCGCCCATCTCCGGGGATGTC 798
Qy 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 799 TGAAGCAATTTT-GTTACTCAATGAGGAGTGAAGAGATACAGTCTAATAACAAC 857
Qy 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
Db 858 TAGTGATAAAGGCCAGGAGTGTCTCAACTCTCAATGATAGAGACGTCTCCCAT 917
Qy 241 TACAACCTAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGTTTGAATA 300
Db 918 TACAACCTAACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGTTTGAATA 977
Qy 301 GAAAAGGCGCTGGGAAAAGAGGGGAGCCAAATCTGTCTGCTTCTCACTAGTCAAT 360
Db 978 GAAAAGGCGCT-GGAAAAGGGGAGCCAAATCTGTCTGCTTCTCACTAGTCAAT 1036
Qy 361 GCGAATAAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAACTCTATC 420
Db 1037 GCGAATAAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAACTCTATC 1096
Qy 421 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCATATGGAAATGCTGA 480

| | | | |
|----|------|-----------------------------------------------------------|------|
| Db | 1097 | GGGCAACCGATACATCTCTCAGTGAACAGATTGACAAAGGCTATGGAAATGGCTGA | 1156 |
| Qy | 481 | TGGATTATCTTCAGCTTGTGAGCTTCMAAGTTTCCTCCCTCATCTCACCTGCAG | 540 |
| Db | 1157 | TGGATTATCTTCAGCTTGTGAGCTTCMAAGTTTCCTCCCTCATCTCACCTGCAG | 1216 |
| Qy | 541 | CCAACTCTGTAAAGAAATGCTGAGTTCTAGCTCAGCTTTTCTTACTGGAATTGA | 600 |
| Db | 1217 | CCAACTCTGTAAAGAAATGCTGAGTTCTAGCTCAGCTTTTCTTACTGGAATTGA | 1276 |
| Qy | 601 | TCTCCAGCCCTGCTGGCCCAATTCAAATTAAAGGCACAAACATATACCTTCATGAA | 660 |
| Db | 1277 | TCTCCAGCCCTGCTGGCCCAATTCAAATTAAAGGCACAAACATATACCTTCATGAA | 1336 |
| Qy | 661 | GCACACACAGACTTTTGAAGCAAGACAAATGACGTGTAATTGAGGCTTGAAGAAATG | 720 |
| Db | 1337 | GCACACACAGACTTTTGAAGCAAGACAAATGACGTGTAATTGAGGCTTGAAGAAATG | 1396 |
| Qy | 721 | AAGCTTTGAAGAAAAGATACTTGTGTTCCAGCCCCCTTCCCACTCTTCATGTGTTA | 780 |
| Db | 1397 | AAGCTTTGAAGAAAAGATACTTGTGTTCCAGCCCCCTTCCCACTCTTCATGTGTTA | 1456 |
| Qy | 781 | ACCACTGCTTCTGAGACCTTGAAGCCACGGTACTATTTACATGTTGTTATAGAAAAC | 840 |
| Db | 1457 | ACCACTGCTTCTGAGACCTTGAAGCCACGGTACTATTTACATGTTGTTATAGAAAAC | 1516 |
| Qy | 841 | TGATTTTGAAGTTTCGATGTTTCAAGAAATGATTTAAATATACATTTTCTT | 890 |
| Db | 1517 | TGATTTTGAAGTTTCGATGTTTCAAGAAATGATTTAAATATACATTTTCTT | 1566 |

RESULT 7
US-09-66

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: Sequence 74, Application US/09667857
: Patent No. 6699664
:
: GENERAL INFORMATION:
:   APPLICANT: Mitcham, Jennifer L.
:   APPLICANT: King, Gordon E.
:   APPLICANT: Algate, Paul A.
:   APPLICANT: Fling, Steven P.
:   APPLICANT: Retter, Marc W.
:   APPLICANT: Ranger, Gary Richard
:   APPLICANT: Reed, Steven G.
:   APPLICANT: Vedvick, Thomas S.
:   APPLICANT: Carter, Darick
:
:   TITLE OF INVENTION:  DIAGNOSIS AND METHODS FOR THE THERAPY AND
:   FILE REFERENCE: 210121.462C5
:   CURRENT APPLICATION NUMBER: US/09/667, 857
:   NUMBER OF SEQ ID NOS: 455
:   SOFTWARE: FastSeq for Windows Version 3.0
:   SEQ ID NO 74
:   LENGTH: 1567
:   TYPE: DNA
:   ORGANISM: Homo sapien
: US-09-667-857-74

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|---------------------------|-------|---------------------|-----------|--------------|
| Query Match | 89.3% | Score 794.4; | DB 4; | Length 1567; |
| Best Local Similarity | 91.8% | Pred. No. 2.2e-242; | | |
| Matches 817; Conservative | 0; | Mismatches 71; | Indels 2; | Gaps 2 |

QY CAAGCTCAGAGCCTCTCCTTCATCCGCGGTGACACTAAGACTCAGTTTCAATA 60
 Db CAAAGCTCAGAGCCTCTCCTTCATCCGCGGTGACACTAAGACTCAGTTTCAATA 738
 QY - 61 GCATCTAGACAGTGGGACTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGAAATGTC 120
 Db GCATCTAGACAGTGGGACTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGAAATGTC 798
 QY TGAAACAATTTGGTTACTCAATGAGGAGTGGAGAGATACGNNNNNNNNNNNNNN 180

| | | | | | |
|---|---|--|------|---------------------------------------------------------------|------|
| D | b | | 799 | TGAAACAATTTT-CTTAACCTCAATGAAGAGTGAGAGAGATACTAGTCGACTAACCAC | 857 |
| O | y | | 181 | NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT | 240 |
| D | b | | 858 | TAGTGATTAAGGCOCAGGAGTAGTCGTCAACTCCTCACATGTACAGAGCGTCCCCAT | 917 |
| O | y | | 241 | TACAACTAACCAAATCCGAAGTGTCACTGTGACAGACTAAGAAAACCTGGTTTTAGTA | 300 |
| D | b | | 918 | TACAACTAACCAAATCCGAAGTGTCACTGTGACAGACTAAGAAAACCTGGTTTTAGTA | 977 |
| O | y | | 301 | GAAAAAGGCCCTGGGAAAAGAAGGGAGCCAACAAATCTGTCTGCTCTCTCACTTAGTATT | 360 |
| D | b | | 978 | GAAAAAGGCCCT-GAAAAAGGGAGGCCAACAAATCTGTCTCTCTCTCACTTAGTATT | 1036 |
| O | y | | 361 | GGCAAATTAAGCATTTCTGTCTCTTGGGCTGTGCTCAGACAGAGAGCCAGAACTTATC | 420 |
| D | b | | 1037 | GGCAAATTAAGCATTTCTGTCTCTTGGGCTGTGCTCAGACAGAGAGCCAGAACTTATC | 1096 |
| O | y | | 421 | GGGCAACCAAGATTAATCTCTCACTGAAACAGAGTTGACAAAGGCTATGGGAAATGCTCGA | 480 |
| D | b | | 1097 | GGGCAACCAAGATTAATCTCTCACTGAAACAGAGTTGACAAAGGCTATGGGAAATGCTCGA | 1156 |
| O | y | | 481 | TGGGATTAATCTCAAGCTTTGAGCTCTTAAGTTCTTTCCCTCATTTCACTGACCTGCAAG | 540 |
| D | b | | 1157 | TGGGATTAATCTCAAGCTTTGAGCTCTTAAGTTCTTTCCCTCATTTCACTGACCTGCAAG | 1216 |
| O | y | | 541 | CCAAGTTCTGTAAAGAAATGCCCAGAGTCTAGCTCAGTTTTCTTACTGTAATTAGA | 600 |
| D | b | | 1217 | CCAAGTTCTGTAAAGAAATGCCCAGAGTCTAGCTCAGTTTTCTTACTGTAATTAGA | 1276 |
| O | y | | 601 | TCTCCAGACCTGCTGCGCCACAATTTCAATTAAAGCAACAACATTAACCTTCATGAA | 660 |
| D | b | | 1277 | TCTCCAGACCTGCTGCGCCACAATTTCAATTAAAGCAACAACATTAACCTTCATGAA | 1336 |
| O | y | | 661 | GCACAACAAGCTTTTAAAGCAAGCAATGAATGCTTGAATTGAAGCCTTGAGGATG | 720 |
| D | b | | 1337 | GCACAACAAGCTTTTAAAGCAAGCAATGAATGCTTGAATTGAAGCCTTGAGGATG | 1396 |
| O | y | | 721 | AAGCTTTGAAGGAAGAAATACTTTGTTTCAGAGCCCTTCCCACTCTTCATGTGTA | 780 |
| D | b | | 1397 | AAGCTTTGAAGGAAGAAATACTTTGTTTCAGAGCCCTTCCCACTCTTCATGTGTA | 1456 |
| O | y | | 781 | ACCACTGCTTCTGGAACCTTGAAGCAACGCTGACTGTATTACATGTTGTTATGAAGAAC | 840 |
| D | b | | 1457 | ACCACTGCTTCTGGAACCTTGAAGCAACGCTGACTGTATTACATGTTGTTATGAAGAAC | 1516 |
| O | y | | 841 | TGATTTTAGAGTTCTGATCGTTCAAGGAATGATTAATATACATTTTCTCT | 890 |
| D | b | | 1517 | TGATTTTAGAGTTCTGATCGTTCAAGGAATGATTAATATATACATTTTCTCT | 1566 |

RESULT 8

US-09-404-879A-27/c
; Sequence 27, Application US/09404879A

; Patent No. 6468546
: GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E
APPLICANT: Algate, Paul A

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
;
; TITLE OF INVENTION:

FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: U

CURRENT FILING DATE: 1999-09-24
NUMBER OF SEC. TO MOD. 303

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; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for windows Version 3.0.0

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; SEQ ID NO 27
; LENGTH: 461

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; TYPE: DNA
; ORGANISM: Homo sapiens

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| FEATURE: | NAME/KEY | WING | FEATURE |
|----------|----------|------|---------|
| ; | | | |

```

; NAME/KEY: INIBC_Leaui
; LOCATION: (1) ... (461)

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OTHER INFORMATION: n = A, T, C or G
US-09-404-879A-27

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|---------------------------|-------|---------------------|-----------|-------------|
| Query Match | 50.2% | Score 446.6; | DB 3; | Length 461; |
| Best Local Similarity | 98.9% | Pred. No. 7.1e-132; | | |
| Matches 457; Conservative | 2; | Mismatches 2; | Indels 1; | Gaps 1 |

| | | | |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 427 | CAGGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAAATGCTGATGGGAT | 486 |
| Db | 461 | CAGATTAACATCTCTCAGTGAACAGAGTTG - CAGGCCATATGGGAATGCTGATGGGAT | 403 |
| Qy | 487 | TATCTTCAGCTTGTTGAGCTTCTTAAGTTCTTCCCTTCATTTACCTCGCAAGCCAACT | 546 |
| Db | 402 | TATCTTCAGCTTGTTGAGCTTCTTAAGTTCTTCCCTTCATTTACCTCGCAAGCCAAAGT | 343 |
| Qy | 547 | TCTGTAAAGAAATGCGCTGAGTTCTTAGCTCAGGTTTCTTACCTGAAATTTAGATCTCCA | 606 |
| Db | 342 | TCTGTAAAGAAATGCGCTGAGTTCTTAGCTCAGGTTTCTTACCTGAAATTTAGATCTCCA | 283 |
| Qy | 607 | GACCTGCTGGCCACAATTTCAAATTTAAGGCCAACAAACATATACCTTCATGGAACAC | 666 |
| Db | 282 | GACCTGCTGGCCACAATTTCAAATTTAAGGCCAACAAACATATACCTTCATGGAACACAC | 223 |
| Qy | 667 | ACAGACTTTTGAAGCAAGGACATATGACTGTTGAATTTAGAGGCTTGAGGAATGAAGCTT | 726 |
| Db | 222 | ACAGACTTTTGAAGCAAGGACATATGACTGTTGAATTTAGAGGCTTGAGGAATGAAGCTT | 163 |
| Qy | 727 | TGAAGGAAAAAGATACCTTGTGTTCCAGCCGCCCTCCCACTCTTCATGTTAAACCACT | 786 |
| Db | 162 | TGAAGGAAAAAGATACCTTGTGTTCCAGCCGCCCTCCCACTCTTCATGTTAAACCACT | 103 |
| Qy | 787 | GCTTTCCTGGACCTTGAGACCAAGGTGACTGTATTAATGTTGTTATAGAAACTGATTT | 846 |
| Db | 102 | GCTTTCCTGGACCTTGAGACCAAGGTGACTGTATTAATGTTGTTATAGAAACTGATTT | 43 |
| Qy | 847 | TAGAGTTCTGATCGTTCAAGAGAAATTAATTAATATCATTTTC | 888 |
| Db | 42 | YAGAGTTCTGATCGTTCAAGAGAAATTAATTAATATCATTTTC 1 | |

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RESULT 9
US-09-338-933-27/c
; Sequence 27, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: fastSeq For Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-338-933-27

```

| | Query Match | Similarity | Score | DB | length |
|------------|-------------|--------------|-------|------------|--------|
| Best Local | 50.2% | 98.9% | 446.6 | 461 | |
| Matches | 457 | Conservative | 2 | Mismatches | 2 |
| | | | | Indels | 1 |
| | | | | Gaps | 1 |

| | | | |
|----|-----|--------------------------------------------------------------|-------|
| Db | 402 | TATCTTCAGCTTGTAGAGTTCTAAGTTCTTTCGNTCAATTACCTGAGCCAAAGT | 34.3 |
| OY | 547 | TCTGTAAAGAAATGCTGAGTTCAGTCTCAGGTTTCTTACTGAAATTTAATCTCCA | 6.66 |
| Db | 342 | TCTGTAAAGAAATGCTGAGTTCAGTCTCAGGTTTCTTACTGAAATTTAATCTCCA | 28.33 |
| OY | 607 | GACCTCGCCGCGCAATTCAAATTAAGGCAACAAATATACCTTCATGAAAGCACAC | 6.66 |
| Db | 282 | GACCTCTCTCGCGCAATTCAAATTAAGGCAACAAATATACCTTCATGAAAGCACAC | 22.33 |
| OY | 667 | ACAGACTTTTGAAGCAGGACAAATGACTGCTTGAATTAAGGCTTTGAAGATGAGCTT | 7.66 |
| Db | 222 | ACAGACTTTTGAAGCAGGACAAATGACTGCTTGAATTAAGGCTTTGAAGATGAGACTT | 16.33 |
| OY | 727 | TGAAGGAAAAGAAATCTTGTGTTTCAGGCCCTCCCACTCTTCATGATGTTAAACACT | 7.66 |
| Db | 162 | TGAAGGAAAAGAAATCTTGTGTTTCAGGCCCTCCCACTCTTCATGATGTTAAACACT | 10.3 |
| OY | 787 | GCCCTTCTGAGACCTTGAGACACGGTGACTGATTTACATGTTGTTATAGAAAACTGATTT | 84.6 |
| Db | 102 | GCCCTTCTGAGACCTTGAGACACGGTGACTGATTTACATGATGTTATAGAAAACTGATTT | 4.3 |
| OY | 847 | TAGAATTCATGATGCTTCAAGAGAAATGATTAATTAATACATTTTC | 8.88 |
| Db | 42 | YAGAGTTCTGATGCTTCAAGAGAAATGATTAATTAATACATTTTC 1 | |

```

RESULT 10
US-09-215-681-27/C
; Sequence 27, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ. ID NOS: 310
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-215-681-27

```

| Query Match | 50.2% | Score 446.6 | DB 4 | Length 461 |
|-------------|-------|--------------------------------------------------------------|----------|------------|
| Similarity | 98.9% | Pred. No. 7.1e-132 | | |
| Best Local | 57.1 | Mismatches 2 | Indels 1 | Gaps 1 |
| Matches | 457 | Conservative 2 | | |
| QY | 427 | CAGATAACATCTCTCAGTGAACAGAGTTGCAAGGCGCTATGGAAATGCTGATGGAT | 486 | |
| DB | 461 | CAGATATACATCTCTCAGTGAACAGAGTTG-CAAGGCGCTATGGAAAGCGCTGATGGGAT | 403 | |
| QY | 487 | TATCTCAGCTGTGGTGGACCTCTAAGTTCTTTCCCTCATTTCAACCGCGAAGCAAGT | 546 | |
| DB | 402 | TATCTTCAAGCTGTGGTGGACCTCTAAGTTCTTTCCCTCATTTCAACCGCGAAGCAAGT | 343 | |
| QY | 547 | TCTGTAAAGAAATGCGCTGAGTTCTAGCTCAGGTTTTCTTACTCTGAATTTAGATCTCCA | 606 | |
| DB | 342 | TCTGTAAAGAAATGCGCTGAGTTCTAGCTCAGGTTTTCTTACTCTGAATTTAGATCTCCA | 283 | |
| QY | 607 | GACCTGCTGTGGCCACATTTCAATTAAAGCAACAAATATACTTCCATGAAACACAC | 666 | |
| DB | 282 | GACCTTCTGTGGCCACATTTCAATTAAAGCAACAAATATACTTCCATGAAACACAC | 223 | |

QY 667 ACAGACTTTTGAAGAAGACATGACTCTGTAATTGAGGCTTGAGGAATGAGCTT 726
|
|
|
Db 222 ACAGACTTTTGAAGAAGACATGACTCTGTAATTGAGGCTTGAGGAATGAGCTT 163
|
|
|
QY 727 TGAAGGAAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCAATGTTAACCACT 786
|
|
|
Db 162 TGAAGGAAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCAATGTTAACCACT 103
|
|
|
QY 787 GCCTTCTGACCTTGAGGACGAGCTGATATATACATCTGTTATAGAAAATGATTT 846
|
|
|
Db 102 GCCTTCTGACCTTGAGGACGAGCTGATATATACATCTGTTATAGAAAATGATTT 43
|
|
|
QY 847 TAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTTC 888
|
|
|
Db 42 YAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTTC 1

RESULT 11
US-09-216-003A-27/c
; Sequence 27, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216,003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (367)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-216-003A-27

Query Match 50.2%; Score 446.6; DB 4; Length 461;
Best Local Similarity 98.9%; Pred. No. 7,1e-132;
Matches 457; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGATGGAT 486
|
|
|
Db 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAAGGCTTATGGAAATGCTGATGGAT 403
|
|
|
QY 487 TATCTTACCTGTTTGAAGCTTTCTAAAGTTTCTTCCCTTCACTTACCTGCAAGCCAGT 546
|
|
|
Db 402 TATCTTACCTGTTTGAAGCTTTCTAAAGTTTCTTCCCTTCACTTACCTGCAAGCCAGT 343
|
|
|
QY 547 TCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 606
|
|
|
Db 342 TCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283
|
|
|
QY 607 GACCTGCTGGCCCAATTTCAATTTAAGCAACAAACATATACCTTCATGAAGACAC 666
|
|
|
Db 282 GACCTGCTGGCCCAATTTCAATTTAAGCAACAAACATATACCTTCATGAAGACAC 223
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|
|
QY 667 ACAGACTTTTGAAGAAGACATGACTGCTGTAATTGAGGCTTGAGGAATGAGCTT 726
|
|
|
Db 222 ACAGACTTTTGAAGAAGACATGACTGCTGTAATTGAGGCTTGAGGAATGAGCTT 163
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|
|
QY 727 TGAAGGAAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCAATGTTAACCACT 786
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|
|
Db 162 TGAAGGAAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCAATGTTAACCACT 103
|
|
|
QY 787 GCCTTCTGACCTTGAGGACGAGCTGATATATACATCTGTTATAGAAAATGATTT 846
|
|
|
Db 102 GCCTTCTGACCTTGAGGACGAGCTGATATATACATCTGTTATAGAAAATGATTT 43

QY 847 TAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTTC 888
|
|
|
Db 42 YAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTTC 1

RESULT 12
US-09-667-857-27/c
; Sequence 27, Application US/09667857
; Patent No. 6696664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Rling, Steven P.
; APPLICANT: Rafter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-667-857-27

Query Match 50.2%; Score 446.6; DB 4; Length 461;
Best Local Similarity 98.9%; Pred. No. 7,1e-132;
Matches 457; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGATGGAT 486
|
|
|
Db 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAAGGCTTATGGAAATGCTGATGGAT 403
|
|
|
QY 487 TATCTTACCTGTTTGAAGCTTTCTAAAGTTTCTTCCCTTCACTTACCTGCAAGCCAGT 546
|
|
|
Db 402 TATCTTACCTGTTTGAAGCTTTCTAAAGTTTCTTCCCTTCACTTACCTGCAAGCCAGT 343
|
|
|
QY 547 TCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 606
|
|
|
Db 342 TCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283
|
|
|
QY 607 GACCTGCTGGCCCAATTTCAATTTAAGCAACAAACATATACCTTCATGAAGACAC 666
|
|
|
Db 282 GACCTGCTGGCCCAATTTCAATTTAAGCAACAAACATATACCTTCATGAAGACAC 223
|
|
|
QY 667 ACAGACTTTTGAAGAAGACATGACTGCTGTAATTGAGGCTTGAGGAATGAGCTT 726
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|
|
Db 222 ACAGACTTTTGAAGAAGACATGACTGCTGTAATTGAGGCTTGAGGAATGAGCTT 163
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|
|
QY 727 TGAAGGAAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCAATGTTAACCACT 786
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|
|
Db 162 TGAAGGAAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCAATGTTAACCACT 103
|
|
|
QY 787 GCCTTCTGACCTTGAGGACGAGCTGATATATACATCTGTTATAGAAAATGATTT 846
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Db 102 GCCTTCTGACCTTGAGGACGAGCTGATATATACATCTGTTATAGAAAATGATTT 43
|
|
|
QY 847 TAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTTC 888
|
|
|
Db 42 YAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTTC 1

RESULT 13
US-09-040-984-15
; Sequence 15, Application US/09040984
; Patent No. 6210883
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF LUNG CANCER
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PastSEO for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,984
; FILING DATE: 18-MAR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-282-6031
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-040-984-15
Query Match 41.0%; Score 364.8; DB 3; Length 695;
Best Local Similarity 77.4%; Pred. No. 1e-105;
Matches 486; Conservative 0; Mismatches 131; Indels 11; Gaps 7;
QY 238 CATTCACCTACCTCCGATCCGAGTGTCACTGTCTCAGAGCAAGAAACCCGTGTTTGA 297
DB 61 CATTCACCTACCTCCGATCCGAGTGTCACTGTCTCAGAGCAAGAAACCCGTGTTTGA 120
QY 238 GTAGAAAAGGCGCTGGGAAAGAGGGAGCAACAATCTGTCTGCTTCTCACTTAATGTC 357
DB 121 TTTAAAAAGGCGCT--GAAAAAGGGAGGCCAANATCTGTCTGCTTCTCACTTAATGTC 178
QY 358 ATTGGCAATTAAGCAATTCTGTCTTTGGCTGCTGCTGCTCAGACAGAGAGCCAGACTCT 417
DB 179 NTTGGCAATTAAGCAATTCTGTCTTTGGCTGCTGCTGCTCAGACAGAGAGCCAGACTCT 238
QY 418 ATCGGGCAACGAGATAAATCTCTGAGTAACAGAGATTGCAAGAGCCATATGGGAATGCC 477
DB 239 ATCTNGGC--CCAGGATTAATCTCTCNCATTAACNAATTAAGCAGGCGGGAATATGCC 297
QY 478 TGATGGATTATCTTCAGCTGTGTTGAGCTTCTTAAGTTCTTCCCTTCAATTCACCTGTC 537
DB 238 NGATGGATTATCTTCAGCTGTGTTGAGCTTCTTAAGTTCTTCCCTTCAATTCACCTGTC 357
QY 538 AAGCCAGTTCTGTAAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTT 597
DB 358 CAGCCNAGTTCTGTAAAGAGAAATGCGNAGATTGCAACCCGGTTTCTTACTCNGAATTT 417
QY 598 AGATCTCAGACCCGCGCTGGGCAATTCAAAT--AAGGCAACAACAATATACCTTCCA 656
DB 418 AGATCTCAGACCCGCGCTGGGCAATTCAAATTAATTAAGCAGACGACGATTAATCTTCCA 477

QY 657 TGAAGCACACAGACCTTTTGAAGCAGACAAATGACTGTGTTGAATTTAGGCGCTTGAGG 716
DB 478 TTAATNCAC--CCACATTTTGAAGCCAGCAATGACTGCTTAATTAAGAGGAGGTTGAAG 536
QY 717 AATGAGCTTTGAAGAGAAAGATATCTTTGTTTTCAGGCCCCCTTCCACACTCTTCAATG 776
DB 537 GAANAA--CTTTGAAGAGAAAAAACTTTGTTTCGGGCCCTT---CCAACTCTTCTGT 591
QY 777 GTTAACGACGCTTCTCTGG--ACCTTGGAGCCAGGTGATTAATACATGTTGTTATAG 835
DB 592 GTTANACCTGCTCTTCTTGNAAACCTGTGAAGCCCGNAGACGTGTACATGTTGTTCTAN 651
QY 836 AAAACTGATTTTGAAGTTCTGATCGTTG 863
DB 652 NAAACGACGCTTAATTAATTCATCTTCC 679
RESULT 14
US-09-123-912-15
; Sequence 15, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: 09/040,802
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (105)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (172)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (176)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (179)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (189)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (203)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (212)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (219)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (221)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (229)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (231)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (238)

[illegible]

[illegible]

Best Local Similarity 91.9%; Pred. No. 2.9e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

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QY 1 CAAGCTGAGAGCTTCTCCTTCCATCTCGCTGAGAGCTTAAGACCTCAGTTTTCATA 60
Db 1 CAAGCTGAGAGCTTCTCCTTCCATCTCGCTGAGAGCTTAAGACCTCAGTTTTCATA 60
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
Db 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
QY 121 TGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 121 TGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
QY 121 TGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 121 TGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
Db 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
QY 181 TAGTGAATTAAGGCCAGGAGATCTGCTCAACTCTCAATGATACAGAGCTCTCCCAT 240
Db 181 TAGTGAATTAAGGCCAGGAGATCTGCTCAACTCTCAATGATACAGAGCTCTCCCAT 240
QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
Db 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
Db 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
QY 301 GAAAAGGGCTTGGGAAAAGAGGGGAGCCAAATCTGCTCTCTCTCTCTCTCTCTCT 360
Db 301 GAAAAGGGCTTGGGAAAAGAGGGGAGCCAAATCTGCTCTCTCTCTCTCTCTCTCT 360
QY 301 GAAAAGGGCTTGGGAAAAGAGGGGAGCCAAATCTGCTCTCTCTCTCTCTCTCTCT 360
Db 301 GAAAAGGGCTTGGGAAAAGAGGGGAGCCAAATCTGCTCTCTCTCTCTCTCTCTCT 360
QY 361 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 361 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 361 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 361 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 421 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 421 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 421 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 421 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAACTTCTTCTCTCTCTCTCTCTCT 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAACTTCTTCTCTCTCTCTCTCTCT 540
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAACTTCTTCTCTCTCTCTCTCTCT 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAACTTCTTCTCTCTCTCTCTCTCT 540
QY 541 CCAAGTTCTGTAAGGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 600
Db 541 CCAAGTTCTGTAAGGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 600
QY 541 CCAAGTTCTGTAAGGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 600
Db 541 CCAAGTTCTGTAAGGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 600
QY 601 TCTCCAGACCTCTGCTGAGCCATCAATTTAAGGCAACCAATATACCTTCCATGAA 660
Db 601 TCTCCAGACCTCTGCTGAGCCATCAATTTAAGGCAACCAATATACCTTCCATGAA 660
QY 601 TCTCCAGACCTCTGCTGAGCCATCAATTTAAGGCAACCAATATACCTTCCATGAA 660
Db 601 TCTCCAGACCTCTGCTGAGCCATCAATTTAAGGCAACCAATATACCTTCCATGAA 660
QY 661 GCACACACAGACTTTTGAAGCAGACATGATGCTTGAATTTGAAGCTTGAAGATG 720
Db 661 GCACACACAGACTTTTGAAGCAGACATGATGCTTGAATTTGAAGCTTGAAGATG 720
QY 661 GCACACACAGACTTTTGAAGCAGACATGATGCTTGAATTTGAAGCTTGAAGATG 720
Db 661 GCACACACAGACTTTTGAAGCAGACATGATGCTTGAATTTGAAGCTTGAAGATG 720
QY 721 AAGCTTTGAAGGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780
Db 721 AAGCTTTGAAGGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780
QY 721 AAGCTTTGAAGGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780
Db 721 AAGCTTTGAAGGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780
QY 781 ACCACTGCTCTCTGAGACCTTGAAGCAGAGTGAATTTAATGATTTTGAAGAAAC 840
Db 781 ACCACTGCTCTCTGAGACCTTGAAGCAGAGTGAATTTAATGATTTTGAAGAAAC 840
QY 781 ACCACTGCTCTCTGAGACCTTGAAGCAGAGTGAATTTAATGATTTTGAAGAAAC 840
Db 781 ACCACTGCTCTCTGAGACCTTGAAGCAGAGTGAATTTAATGATTTTGAAGAAAC 840
QY 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGATTTAATATCATTTTCT 890
Db 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGATTTAATATCATTTTCT 890
QY 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGATTTAATATCATTTTCT 890
Db 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGATTTAATATCATTTTCT 890
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RESULT 2

US-09-850-178-6
; Sequence 6, Application US/09850178
; Patent No. US20020034749A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colipits, Tracey L.

```
; APPLICANT: Friedman, Paula N.  
; APPLICANT: Russell, John C.  
; APPLICANT: Granados, Edward N.  
; APPLICANT: Hodges, Steven C.  
; APPLICANT: Klass, Michael R.  
; APPLICANT: Kralovich, Jon D.  
; APPLICANT: Roberts-Rapp, Lisa  
; APPLICANT: Stoupe, Stephen D.  
; APPLICANT: Gordon, Julian  
; TITLE OF INVENTION: REAGENTS AND METHODS OF THE BREAST  
; TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST  
; FILE REFERENCE: 6251.US.P1  
; CURRENT FILING DATE: 2001-05-07  
; PRIOR APPLICATION NUMBER: US 08/972,376  
; PRIOR FILING DATE: 1997-11-18  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 6  
; LENGTH: 893  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-850-178-6
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Query Match 90.6%; Score 806.4; DB 9; Length 893;
Best Local Similarity 91.9%; Pred. No. 2.9e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

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QY 1 CAAGCTGAGAGCTTCTCCTTCCATCTCGCTGAGAGCTTAAGACCTCAGTTTTCATA 60
Db 1 CAAGCTGAGAGCTTCTCCTTCCATCTCGCTGAGAGCTTAAGACCTCAGTTTTCATA 60
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
Db 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
Db 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
QY 121 TGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 121 TGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
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Db 121 TGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
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Db 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
QY 181 TAGTGAATTAAGGCCAGGAGATCTGCTCAACTCTCAATGATACAGAGCTCTCCCAT 240
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QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
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QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
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QY 301 GAAAAGGGCTTGGGAAAAGAGGGGAGCCAAATCTGCTCTCTCTCTCTCTCTCTCT 360
Db 301 GAAAAGGGCTTGGGAAAAGAGGGGAGCCAAATCTGCTCTCTCTCTCTCTCTCTCT 360
QY 361 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 361 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 361 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 361 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 421 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 421 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 421 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 421 GGGCAATTAAGCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAACTTCTTCTCTCTCTCTCTCTCT 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAACTTCTTCTCTCTCTCTCTCTCT 540
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAACTTCTTCTCTCTCTCTCTCTCT 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAACTTCTTCTCTCTCTCTCTCTCT 540
QY 541 CCAAGTTCTGTAAGGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 600
Db 541 CCAAGTTCTGTAAGGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 600
QY 541 CCAAGTTCTGTAAGGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 600
Db 541 CCAAGTTCTGTAAGGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 600
QY 601 TCTCCAGACCTCTGCTGAGCCATCAATTTAAGGCAACCAATATACCTTCCATGAA 660
Db 601 TCTCCAGACCTCTGCTGAGCCATCAATTTAAGGCAACCAATATACCTTCCATGAA 660
QY 601 TCTCCAGACCTCTGCTGAGCCATCAATTTAAGGCAACCAATATACCTTCCATGAA 660
Db 601 TCTCCAGACCTCTGCTGAGCCATCAATTTAAGGCAACCAATATACCTTCCATGAA 660
QY 661 GCACACACAGACTTTTGAAGCAGACATGATGCTTGAATTTGAAGCTTGAAGATG 720
Db 661 GCACACACAGACTTTTGAAGCAGACATGATGCTTGAATTTGAAGCTTGAAGATG 720
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Db 660 GCACACAGACTTTTGAAGCAAGACATGACTGTTGAATGAGGCTTGAGGAATG 719
Qy 721 AACCTTGAAGAAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 780
Db 720 AACCTTGAAGAAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 779
Qy 781 AACCTTGAAGAAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 840
Db 780 AACCTTGAAGAAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 839
Qy 841 TGAATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 890
Db 840 TGAATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 889

RESULT 3
US-09-778-320-207
Sequence 207, Application US/09778320
Patent No. US20010034052A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778,320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 207
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-778-320-207

Query Match 90.6%; Score 806.4; DB 9; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
Qy 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGCAAGCACTTCAATTA 60
Db 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGCAAGCACTTCAATTA 1780
Qy 61 GATCTAGAGCACTGAGCACTGAGGCTGAGTATTTGCCCCCATCTCCGGGGAATGTC 120
Db 1781 GATCTAGAGCACTGAGCACTGAGGCTGAGTATTTGCCCCCATCTCCGGGGAATGTC 1840
Qy 121 TGAAGCAATTTTGTCTTACCTCAATGAGGAGTGAGAGATACANNNNNNNNNNNN 180
Db 1841 TGAAGCAATTTTGTCTTACCTCAATGAGGAGTGAGAGATACAGTGTACTACCAAC 1900
Qy 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
Db 1901 TAGTGATTAAGGCCAGGAGATGCTGCTCAACTCTTACATGTACAGAGCTCTCCCAT 1960
Qy 241 TACCACTACCAATCCGAGTGTCACTGTGTCAAGCACTTAAGAAACCTGTTTGAAGTA 300
Db 1961 TACCACTACCAATCCGAGTGTCACTGTGTCAAGCACTTAAGAAACCTGTTTGAAGTA 2020
Qy 301 GAAAAGGCGCTGGAAGAGAGGAGCCAAATCTGTCTGCTCTCTCAATTAATGTCAT 360
Db 2021 GAAAAGGCGCT-GAAAAGAGGAGAGCCAAATCTGTCTGCTCTCTCAATTAATGTCAT 2079
Qy 361 GGAATTAAGCAATCTGTCTCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 420
Db 2080 GGAATTAAGCAATCTGTCTCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2139

Qy 421 GGGCAGGATTAATCATCTCTCAGTGAAGAGTTGACAAGGCTTATGGAAATGCTCTGA 480
Db 2140 GGGCAGGATTAATCATCTCTCAGTGAAGAGTTGACAAGGCTTATGGAAATGCTCTGA 2199
Qy 481 TGGGATTAATCTTCAAGTTGTGAGCTTGAAGTTTCTTCCCTTCAATTAATGTCATG 540
Db 2200 TGGGATTAATCTTCAAGTTGTGAGCTTGAAGTTTCTTCCCTTCAATTAATGTCATG 2259
Qy 541 CCAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAAGTTTCTTACTGTGAATTTAGA 600
Db 2260 CCAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAAGTTTCTTACTGTGAATTTAGA 2319
Qy 601 TCTCCAGACCCCTGCTGGCCAAATTCATTAAGGCAACAAATATACCTTCCATGAA 660
Db 2320 TCTCCAGACCCCTGCTGGCCAAATTCATTAAGGCAACAAATATACCTTCCATGAA 2379
Qy 661 GCACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTTGAGGCTTGAGGAATG 720
Db 2380 GCACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTTGAGGCTTGAGGAATG 2439
Qy 721 AACCTTGAAGAAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 780
Db 2440 AACCTTGAAGAAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 2499
Qy 781 AACCTTGAAGAAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 840
Db 2500 AACCTTGAAGAAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 2559
Qy 841 TGAATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 890
Db 2560 TGAATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 2609

RESULT 4
US-09-910-689-207
Sequence 207, Application US/09910689
Patent No. US20020081609A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C6
CURRENT APPLICATION NUMBER: US/09/910,689
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 207
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-910-689-207

Query Match 90.6%; Score 806.4; DB 9; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
Qy 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGCAAGCACTTCAATTA 60
Db 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGCAAGCACTTCAATTA 1780
Qy 61 GATCTAGAGCACTGAGCACTGAGGCTGAGTATTTGCCCCCATCTCCGGGGAATGTC 120
Db 1781 GATCTAGAGCACTGAGCACTGAGGCTGAGTATTTGCCCCCATCTCCGGGGAATGTC 1840
Qy 121 TGAAGCAATTTTGTCTTACCTCAATGAGGAGTGAGAGATACAGNNNNNNNNNNNN 180

[illegible]

RESULT 5
US-09-884-441-391

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Sequence 391, Application US/09884441
Patent No. US20020119158A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 391
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-884-441-391

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| | Matches | 818; | Conservative | 0; | Mismatches | 71; | Indels | 1; | Gaps | 1 |
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| QY | 1 | CAAGCTGAGGCTTCTCTTTCATCTCGCTGAGCAGCTAAGACCTCAAGTTTCAATA | 60 | | | | | | | |
| Db | 1721 | CAAGCTCGAAGCTTCTCTTTCATCTCGCTGAGCAGCTAAGACCTCAAGTTTCAATA | 1780 | | | | | | | |
| QY | 61 | GCATCTGAGAGTGGGACTCAGCTGGGGGTATTTGCGCCCATCTCGGGGGGAATGTC | 120 | | | | | | | |
| Db | 1781 | GCATCTGAGAGTGGGACTCAGCTGGGGGTATTTGCGCCCATCTCGGGGGGAATGTC | 1844 | | | | | | | |
| QY | 121 | TGAAGACAAATTTGGTTAACTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNNNN | 180 | | | | | | | |
| Db | 1841 | TGAAGACAAATTTGGTTAACTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC | 1900 | | | | | | | |
| QY | 181 | NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN | 240 | | | | | | | |
| Db | 1901 | TAGTGATTAAGGCGAGGATGTGCTCAACCTCTACATGTACAGAGCTCTCCCAT | 1966 | | | | | | | |
| QY | 241 | TACAATATCCCAATCCGAAGTGTCACTGTGTCAAGATAAGAAACCTGTGTTTGAATA | 300 | | | | | | | |
| Db | 1961 | TACAATATCCCAATCCGAAGTGTCACTGTGTCAAGATAAGAAACCTGTGTTTGAATA | 2020 | | | | | | | |
| QY | 301 | GAAAAGGCGCTGGGAAAAGAGGGAGCCAACAATCTGTCTCTTCTCTCACTTAAGTCA | 360 | | | | | | | |
| Db | 2021 | GAAAAGGCGCTGGGAAAAGAGGGAGCCAACAATCTGTCTCTTCTCTCACTTAAGTCA | 2079 | | | | | | | |
| QY | 361 | GGCAATTAAGCAATCTGTCTCTTGGCTGTGCTCAGACAGAGAGCAGAACTATATC | 420 | | | | | | | |
| Db | 2080 | GGCAATTAAGCAATCTGTCTCTTGGCTGTGCTCAGACAGAGAGCAGAACTATATC | 2139 | | | | | | | |
| QY | 421 | GGGCAACCAAGATTAATCTCTCACTGAAACAAGTTGACAAGGCTATGGGAAATGCCGTA | 480 | | | | | | | |
| Db | 2140 | GGGCAACCAAGATTAATCTCTCACTGAAACAAGTTGACAAGGCTATGGGAAATGCCGTA | 2199 | | | | | | | |
| QY | 481 | TGGGATTAATCTTCAAGCTTGTGAGGCTTCAAGTTTCTTCCCTTCAATCTACCTCGAAG | 540 | | | | | | | |
| Db | 2200 | TGGGATTAATCTTCAAGCTTGTGAGGCTTCAAGTTTCTTCCCTTCAATCTACCTCGAAG | 2255 | | | | | | | |
| QY | 541 | CCAAATCTGTAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCGAATTTAGA | 600 | | | | | | | |
| Db | 2260 | CCAAATCTGTGTAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCGAATTTAGA | 2319 | | | | | | | |
| QY | 601 | TCTCCAGAACCTGCTGGCCCAATTTCAATTAAGGCAACAACATATACCTTCATGAA | 660 | | | | | | | |
| Db | 2320 | TCTCCAGAACCTTCTGGCCCAATTTCAATTAAGGCAACAACATATACCTTCATGAA | 2379 | | | | | | | |
| QY | 661 | GCACACACAGCTTTTGAAGCAAGGCAATGACGTGTAATTGAGGCTTGGAGAAATG | 720 | | | | | | | |
| Db | 2380 | GCACACACAGCTTTTGAAGCAAGGCAATGACGTGTAATTGAGGCTTGGAGAAATG | 2433 | | | | | | | |
| QY | 721 | AAGCTTGAAGGAAAAGATATCTTGTGTTCCAGGCCCTTCCCACTCTTCATGTGTATA | 780 | | | | | | | |
| Db | 2440 | AAGCTTGAAGGAAAAGATATCTTGTGTTCCAGGCCCTTCCCACTCTTCATGTGTATA | 2499 | | | | | | | |
| QY | 781 | ACCACTGCTTCTTGACCTTGAAGCCACGGTACTGTATTAATATGTTTATAGAAAAC | 840 | | | | | | | |
| Db | 2500 | ACCACTGCTTCTTGACCTTGAAGCCACGGTACTGTATTAATATGTTTATAGAAAAC | 2555 | | | | | | | |
| QY | 841 | TGATTTTAAAGATTCGTATCGTTCAAGAAAGATTAATAATATCAATTTCTT | 890 | | | | | | | |
| Db | 2560 | TGATTTTAAAGATTCGTATCGTTCAAGAAAGATTAATAATATCAATTTCTT | 2609 | | | | | | | |

RESULT 6
US-09-907-969-391

Sequence 391, Application US/09907966
Publication No. US20030091580A1
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.

| | | | |
|----|------|----------------------------------------------------------------|------|
| Qy | 121 | TGAAGACAAATTTGGTTACCTTCATAGAGGAGTGAGAGAGATACAGNNNNNNNNNNNNNN | 180 |
| Db | 1841 | TGAAGACAAATTTGGTTACTCTCAATGAGGAGTGAGAGAGATACAGTCTACTACCAAC | 1900 |
| Qy | 181 | NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN | 240 |
| Db | 1901 | TAGTGATTAAGGCCAGGAGTGCTGCTCAACCTCTCATCATGTACAGAGCGTCTCCCAT | 1960 |
| Qy | 241 | TACAACATCCAAATCCGAAGTGTCAACTGTGTACAGACTAAGAAACCCTGGTTTGAATA | 300 |
| Db | 1961 | TACAACATCCCAATCCGAAGTGTCAACTGTGTACAGACTAAGAAACCCTGGTTTGAATA | 2020 |
| Qy | 301 | GAAAAGGCGCTGGGAAAGAGGAGACCNAACAAATCTGTCTGCTTTCACATTAAGTCATT | 360 |
| Db | 2021 | GAAAAGGCGCT-GGAAAGAGGAGAGCCAAACAAATCTGTCTGCTTTCACATTAAGTCATT | 2079 |
| Qy | 361 | GGCAAAATGAGCAATCTGTCTCTTTGGCTGTGCTCCACACAGAGAGCCAAATCTATC | 420 |
| Db | 2080 | GGCAAAATGAGCAATCTGTCTCTTTGGCTGTGCTCCACACAGAGAGCCAAATCTATC | 2139 |
| Qy | 421 | GGGCAACCGAGTAACATCTCTCAGTGAAACAGAGTTGACAAAGGCGCTATGGGAAATGCCGA | 480 |
| Db | 2140 | GGGCAACCGAGTAACATCTCTCAGTGAAACAGAGTTGACAAAGGCGCTATGGGAAATGCCGA | 2199 |
| Qy | 481 | TGGGATTAATCTTCAGCTGTGTGAGTTCTAAGTTTCTTCCCTTCATTTACCTGCAAG | 540 |
| Db | 2200 | TGGGATTAATCTTCAGCTGTGTGAGTTCTAAGTTTCTTCCCTTCATTTACCTGCAAG | 2259 |
| Qy | 541 | CCAAGTCTGTAAAGAAATCCTGAGTTCAGCTCAGGTTTTCTTACTGAAATTTAGA | 600 |
| Db | 2260 | CCAAGTCTGTAAAGAAATCCTGAGTTCAGCTCAGGTTTTCTTACTGAAATTTAGA | 2319 |
| Qy | 601 | TCTCCAGACCTCGCTGCGCCACATTCAAATTAAGGCAACAAACATATACTTCATGAA | 660 |
| Db | 2320 | TCTCCAGACCTCTTCTGCGCCAAATTCAAATTAAGGCAACAAACATATACTTCATGAA | 2379 |
| Qy | 661 | GCAACACACAGCTTTTGAAGCAAGAACAAATGACTGTTGAATTAGGCGCTTGAGAAATG | 720 |
| Db | 2380 | GCAACACACAGCTTTTGAAGCAAGAACAAATGACTGTTGAATTAGGCGCTTGAGAAATG | 2439 |
| Qy | 721 | AAAGCTTGAAGAAAAGATATCTTTGTTCCAGCCCTCTCCACACTCTTCATGTGTTA | 780 |

541 CCGAAGTTCATTGTTAAAGAGAAATGCGCTGGAGTTCATTAGCTTCAAGTCTTCTCTCTTAACTTCTGAAATTTTACGA 600

| | | | |
|----|--------------------------------------------------------------------|---------------------------------------------------------------|--------------|
| | RESULT | 7 | |
| | US-09-827-271-391 | | |
| | ; Sequence 391, Application US/09827271 | | |
| | ; Publication No. US20030165504A1 | | |
| | ; GENERAL INFORMATION: | | |
| | ; APPLICANT: Retter, Marc W. | | |
| | ; APPLICANT: Patger, Gary R. | | |
| | ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND | | |
| | ; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER | | |
| | ; FILE REFERENCE: 210121.462C6 | | |
| | ; CURRENT APPLICATION NUMBER: US/09/827,271 | | |
| | ; CURRENT FILING DATE: 2001-04-04 | | |
| | ; NUMBER OF SEQ ID NOS: 461 | | |
| | ; SOFTWARE: FastSeq for Windows Version 3.0 | | |
| | ; SEQ ID NO 391 | | |
| | ; LENGTH: 2627 | | |
| | ; TYPE: DNA | | |
| | ; ORGANISM: Homo sapiens | | |
| | US-09-827-271-391 | | |
| | Query March | 90.6%; Score 806.4; DB 10; | Length 2627; |
| | Best Local Similarity | 91.9%; Pred. No. 5.4e-260; | |
| | Matches 818; Conservative | 0; Mismatches 71; Indels | 1; Gaps 1; |
| Dy | 1 | CAAGCTGTGAGGCTTCTCCCTTTCCATCTTGCGTGAACAGTAAGACTCAGTTTTTCATA | 60 |
| Dy | 1721 | CAGGCTGTGAGGCTTCTCCCTTTCCATCTTGCGTGAACAGTAAGACTCAGTTTTTCATA | 1780 |
| Dy | 61 | GCACTTGAAGACAGTGGGACCTCACAGTGGGATTTGGCCCCCATCTCGGGGAAATGTC | 120 |
| Dy | 1781 | GCACTTGAAGACAGTGGGACCTCACAGTGGGATTTGGCCCCCATCTCGGGGAAATGTC | 1840 |
| Dy | 121 | TGAAGAACAATTTTGTTTACCCTCAATGAGGAGTGGAAGAGATACAGNNNNNNNNNNNN | 180 |
| Dy | 1841 | TGAAGAACAATTTTGTTTACCCTCAATGAGGAGTGGAAGAGATACAGTGTCTACTACCAAC | 1900 |
| Dy | 181 | NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN | 240 |
| Dy | 1901 | TAGTGATTAAGGCCAGAGGATGCTGTCAACCTCTAACATGTAACAGACGTCTCCCAT | 1960 |
| Dy | 241 | TACAACTACCCAATCCGAAGTGCACACTGTGTGACAGACTTAAGAAACCTGTGTTGAGTA | 300 |
| Dy | 1961 | TACAACTACCCAATCCGAAGTGCACACTGTGTGACAGACTTAAGAAACCTGTGTTGAGTA | 2020 |
| Dy | 301 | GAAAAGGGGCTGGAAAAAGAGGGAGCCAAATCTGTCTGCTCTCCACATAGTCATT | 360 |
| Dy | 2021 | GAAAAGGGGCT -GAAAAGGGGAGCCAAATCTGTCTGCTCTCTCACATTAGTCATT | 2079 |
| Dy | 2080 | GGAATAAAGCATTTCTGTCTTTTGGCTGTGCTCAGACACAGAGCCGAACTCTATC | 2139 |
| Dy | 361 | GGAATAAAGCATTTCTGTCTTTTGGCTGTGCTCAGACACAGAGCCGAACTCTATC | 420 |
| Dy | 421 | GGGACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAGGCTTATGGAAATGCTCTGA | 480 |
| Dy | 2140 | GGGACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAGGCTTATGGAAATGCTCTGA | 2199 |
| Dy | 481 | TGGAGTTATCTTACGCTGTGTGAGCTTCTTAAGTTCTTTCCCTTCACTTCAACCTCAG | 540 |
| Dy | 2200 | TGGAGTTATCTTACGCTGTGTGAGCTTCTTAAGTTCTTTCCCTTCACTTCAACCTCAG | 2259 |
| Dy | 541 | CCAAGTTCTGTAAAGAAATGCTGAGTTCTTAGCTCAGGTTTTTCTTACTGTAATTTAGA | 600 |

Db 2260 CCAAGTTCGTGAAGAAATGCGTAGTTCTAGCTCAGGTTTCTTACTGTGAATTTAGA 2319
Qy 601 TCTCCAGACCTGCTGCGCAATTCATTAAGGCAACAACATATACCTTCCATGAA 660
Db 2320 TCTCCAGACCTTCTGCGCAATTCATTAAGGCAACAACATATACCTTCCATGAA 2379
Qy 661 GCACACAGACCTTTTGAAGCAAGCAATGCTGTTGAATGAGGCTTTGAGGAATG 720
Db 2380 GCACACAGACCTTTTGAAGCAAGCAATGCTGTTGAATGAGGCTTTGAGGAATG 2439
Qy 721 AAGCTTTGAAGAAAGAAATACTTTGTTCCAGCCCCCTTCCACACCTTCATGTTA 780
Db 2440 AAGCTTTGAAGAAAGAAATACTTTGTTCCAGCCCCCTTCCACACCTTTGATGTTA 2499
Qy 781 ACCACTGCTTCTGAGACCTTGAGCCAGGTCGATGTTATCATGTTTATGAAAC 840
Db 2500 ACCACTGCTTCTGAGACCTTGAGCCAGGTCGATGTTATCATGTTTATGAAAC 2559
Qy 841 TGATTTAGAGTTCTGATGTTCAAGAGAAATGATTAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATGTTCAAGAGAAATGATTAATATACATTTCT 2609

RESULT 8

US-10-010-742-207
; Sequence 207, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yudi
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tongrong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-742-207

Query Match 90.6%; Score 806.4; DB 13; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

Qy 1 CAAGCTCGAGGCTTCTCTTCATCTCGGCGGAGCACTAAGACCTGATTTCAATA 60
Db 1721 CAAGCTCGAGGCTTCTCTTCATCTCGGCGGAGCACTAAGACCTGATTTCAATA 1780
Qy 61 GCATCTAGAGCAGTGGAGCTCACTGCGGTGATTTGCCCCCATCTCCGGGGAGATGTC 120
Db 1781 GCATCTAGAGCAGTGGAGCTCACTGCGGTGATTTGCCCCCATCTCCGGGGAGATGTC 1840
Qy 121 TGAAGACAATTTTGTGTTACCTCAATGAGGAGTGAAGAGATPACAGNNNNNNNNNN 180
Db 1841 TGAAGACAATTTTGTGTTACCTCAATGAGGAGTGAAGAGATPACAGNNNNNNNNNN 1900
Qy 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
Db 1901 TAGTGATTAAGGCCAGGAGTCTGCTCAACTCTTACCATGTAAGAGCGTCTCCCAT 1960

Qy 241 TACAATCAACCAATCCGAAGTGTCACTGTGTCAAGACTTAAGAAACCTGGTTTGAGTA 300
Db 1961 TACAATCAACCAATCCGAAGTGTCACTGTGTCAAGACTTAAGAAACCTGGTTTGAGTA 2020
Qy 301 GAAAAGGCGCTGGGAAAGAGGGAGCCAAACAATCTGTCTGCTTCTTCAATTAAGTCAAT 360
Db 2021 GAAAAGGCGCTGGGAAAGAGGGAGCCAAACAATCTGTCTGCTTCTTCAATTAAGTCAAT 2079
Qy 361 GGGCAATTAAGATCTGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 2080 GGGCAATTAAGATCTGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2139
Qy 421 GGGCAACGAGATTAATCTCTCACTGAGAAACAAGTTGAACAAGGCTTATGGAAATGCTGTA 480
Db 2140 GGGCAACGAGATTAATCTCTCACTGAGAAACAAGTTGAACAAGGCTTATGGAAATGCTGTA 2199
Qy 481 TGGGATTAATCTTCACTGCTTGTGAGGCTTGAAGTTCTTCCCTTCAATCTACCTGCAAG 540
Db 2200 TGGGATTAATCTTCACTGCTTGTGAGGCTTGAAGTTCTTCCCTTCAATCTACCTGCAAG 2259
Qy 541 CCAAGTTCGTGAAGAAATGCTGAGTTCTTCTAGCTCAGGTTTCTTACTGTGAATTTAGA 600
Db 2260 CCAAGTTCGTGAAGAAATGCTGAGTTCTTCTAGCTCAGGTTTCTTACTGTGAATTTAGA 2319
Qy 601 TCTCCAGACCTGCTGCGCAATTCATTAAGGCAACAACATATACCTTCCATGAA 660
Db 2320 TCTCCAGACCTTCTGCGCAATTCATTAAGGCAACAACATATACCTTCCATGAA 2379
Qy 661 GCACACAGACCTTTTGAAGCAAGCAATGACTGCTTGAATGAGGCTTTGAGGAATG 720
Db 2380 GCACACAGACCTTTTGAAGCAAGCAATGACTGCTTGAATGAGGCTTTGAGGAATG 2439
Qy 721 AAGCTTTGAAGAAAGAAATACTTTGTTCCAGCCCCCTTCCACACCTTTCATGTTA 780
Db 2440 AAGCTTTGAAGAAAGAAATACTTTGTTCCAGCCCCCTTCCACACCTTTCATGTTA 2499
Qy 781 ACCACTGCTTCTGAGACCTTGAGCCAGGTCGATGTTATCATGTTTATGAAAC 840
Db 2500 ACCACTGCTTCTGAGACCTTGAGCCAGGTCGATGTTATCATGTTTATGAAAC 2559
Qy 841 TGATTTAGAGTTCTGATGTTCAAGAGAAATGATTAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATGTTCAAGAGAAATGATTAATATACATTTCT 2609

RESULT 9

US-10-198-053-391
; Sequence 391, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-053-391

Query Match 90.6%; Score 806.4; DB 15; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

Qy 1 CAAGCTCGAGGCTTCTCTTCATCTCGGCGGAGCACTAAGACCTGATTTCAATA 60
|||||

Db 2560 TGATTTAGAGTTCTGATCGTTCAAGAGAAAGATTAAATATACATTCT 2609

RESULT 11

US-10-717-296-207

Sequence 207, Application US/10717296

Publication No. US20040142361A1

GENERAL INFORMATION:

APPLICANT: Dillion, Davin C.

APPLICANT: Jiang, Yuhui

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.491C8

CURRENT APPLICATION NUMBER: US/10/717,296

CURRENT FILING DATE: 2003-11-19

NUMBER OF SEQ ID NOS: 313

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 207

LENGTH: 2627

TYPE: DNA

ORGANISM: Homo sapiens

US-10-717-296-207

Query Match 90.6%; Score 806.4; DB 18; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCTCGAGGCTCTCTCTCCATCCGCGTGAAGAGCTTAAGACCTCAGTTTCATA 60

Db 1721 CAAGCTCGAGGCTCTCTCTCCATCCGCGTGAAGAGCTTAAGACCTCAGTTTCATA 1780

QY 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 120

Db 1781 GCATCTAGAGCAGTGGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 1840

QY 121 TGAAGACAATTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180

Db 1841 TGAAGACAATTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 1900

QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240

Db 1901 TAGTGATTAAGAGCCAGGAGTCTGCTCAACCTCTACCATGTATACAGACGCTCCCAT 1960

QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGCTAAGAAAACCTGTTTGAAGTA 300

Db 1961 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGCTAAGAAAACCTGTTTGAAGTA 2020

QY 301 GAAAAGGCTTGGGAAAAGGGGAGCCAAACAATCTGTCTGCTTCTCTCACTTAATGCTATT 360

Db 2021 GAAAAGGCTTGGGAAAAGGGGAGCCAAACAATCTGTCTGCTTCTCTCACTTAATGCTATT 2079

QY 361 GGCATAATAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 420

Db 2080 GGCATAATAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 2139

QY 421 GGCACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGAAATGCTGA 480

Db 2140 GGCACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGAAATGCTGA 2199

QY 481 TGGGATTAATCTTCACTGTTGAAGCTTCTTAAGTTCTTTCCCTCATTTCACTCCTGCAAG 540

Db 2200 TGGGATTAATCTTCACTGTTGAAGCTTCTTAAGTTCTTTCCCTCATTTCACTCCTGCAAG 2259

QY 541 CCAAGTTCTGTAAGAGAAATGCTGAGTTTCAAGTCTCAGGTTTCTTACTCTGAATTTGA 600

Db 2260 CCAAGTTCTGTAAGAGAAATGCTGAGTTTCAAGTCTCAGGTTTCTTACTCTGAATTTGA 2319

QY 601 TCTCCAGACCTGCTGGCCCAATTAATTAAGGCAACAACATATACCTTCATGAA 660

Db 2320 TCTCCAGACCTGCTGGCCCAATTAATTAAGGCAACAACATATACCTTCATGAA 2379

QY 661 GCACACACAGCTTTTGAAGAGAGACATGATGCTTGAATTGAGGCTTTGAGAAATG 720

Db 2380 GCACACACAGCTTTTGAAGAGCAAGACATGACTCTGTAATTGAGGCTTTGAGAAATG 2439

QY 721 AAGCTTGAAGAAAAGAAATCTTGTTCACGCCCTTCCACACACTCTTCATGATGTTA 780

Db 2440 AAGCTTGAAGAAAAGAAATCTTGTTCACGCCCTTCCACACACTCTTCATGATGTTA 2499

QY 781 ACCACTGCTTCTGAGACTTTGAGCCAGCGGTGACTGATTAATGATTTGTAAGAAAAC 840

Db 2500 ACCACTGCTTCTGAGACTTTGAGCCAGCGGTGACTGATTAATGATTTGTAAGAAAAC 2559

QY 841 TGATTTAGAGTTCTGATCGTTCAAGAGAAATTAATATACATTCT 890

Db 2560 TGATTTAGAGTTCTGATCGTTCAAGAGAAATTAATATACATTCT 2609

RESULT 12

US-10-860-790-391

Sequence 391, Application US/10860790

Publication No. US20050031634A1

GENERAL INFORMATION:

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary R.

APPLICANT: Hill, Paul

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C11

CURRENT APPLICATION NUMBER: US/10/860,790

CURRENT FILING DATE: 2004-06-02

NUMBER OF SEQ ID NOS: 624

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 391

LENGTH: 2627

TYPE: DNA

ORGANISM: Homo sapiens

US-10-860-790-391

Query Match 90.6%; Score 806.4; DB 19; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCTCGAGGCTTCTCTCTCCATCCGCGTGAAGAGCTTAAGACCTCAGTTTCATA 60

Db 1721 CAAGCTCGAGGCTTCTCTCTCCATCCGCGTGAAGAGCTTAAGACCTCAGTTTCATA 1780

QY 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 120

Db 1781 GCATCTAGAGCAGTGGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 1840

QY 121 TGAAGACAATTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180

Db 1841 TGAAGACAATTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 1900

QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240

Db 1901 TAGTGATTAAGAGCCAGGAGTCTGCTCAACCTCTACCATGTATACAGACGCTCCCAT 1960

QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGCTAAGAAAACCTGTTTGAAGTA 300

Db 1961 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGCTAAGAAAACCTGTTTGAAGTA 2020

QY 301 GAAAAGGCTTGGGAAAAGGGGAGCCAAACAATCTGTCTGCTTCTCTCACTTAATGCTATT 360

Db 2021 GAAAAGGCTTGGGAAAAGGGGAGCCAAACAATCTGTCTGCTTCTCTCACTTAATGCTATT 2079

QY 361 GGCATAATAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 420

Db 2080 GGCATAATAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 2139

QY 421 GGCACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGAAATGCTGA 480

Db 2140 GGCACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGAAATGCTGA 2199

| | | | |
|----|------|---------------------------------------------------------------|------|
| OY | 481 | TGGGATATATCTTCAAGCTTTGAGCTTCATAGTTCTTCCCTCATCTCAACCGCAGAAG | 540 |
| Db | 2200 | TGGGATTAATTCTTCAAGCTTTGAGCTTCAAAGTTCTTCCCTCATCTCAACCGCAGAAG | 2259 |
| OY | 541 | CCAAGTTCTGTAAAGAAATGCCTGAGTTCTAGCTCAGATTCTTACTCTGAATTTAGA | 600 |
| Db | 2260 | CCAAGTTCTGTAAAGAAATGCCTGAGTTCTAGCTCAGATTCTTACTCTGAANTTTAGA | 2319 |
| OY | 601 | TCTCCACAACCCTGCTGGCCACATTCAAATTTAAGGCAACAACATATACCTTCATGAA | 660 |
| Db | 2320 | TCTCCAGACCCCTTCTGCGCAAAATTCAAATTTAAGGCAACAACATATACCTTCATGAA | 2379 |
| OY | 661 | GCACACACAGACTTTTGAAGCAAGSACATGACGTGTAATTGAGGCCCTTGAGGAATG | 720 |
| Db | 2380 | GCACACACAGACTTTTGAAGCAAGSACATGACGTGTAATTGAGGCCCTTGAGGAATG | 2439 |
| OY | 721 | AAGCTTTGAAGAAAAGATACTTTGTTTCCAGCCCCCTCCACACTCTTCATGTGTTA | 780 |
| Db | 2440 | AAGCTTTGAAGAAAAGATACTTTGTTTCCAGCCCCCTCCACACTCTTCATGTGTTA | 2499 |
| OY | 781 | ACCACTGCTTCTCTGAGACTTTGAGCCACGSGTAGCTGTATTAACATGTTGTTATGAAAAA | 840 |
| Db | 2500 | ACCACTGCTTCTCTGAGACTTTGAGCCACGSGTAGCTGTATTAACATGTTGTTATGAAAAA | 2559 |
| OY | 841 | TGATTTTGAAGTTCTGATCTTCAAGAGAAATGATTAATATACATTTCTT | 890 |
| Db | 2560 | TGATTTTGAAGTTCTGATCTTCAAGAGAAATGATTAATATACATTTCTT | 2609 |

RESULT 13
US-10-023-339-2

```

Sequence 2, Application US/100233339
Publication No. US20030208058A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: B7-Like Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: P1124P1
CURRENT APPLICATION NUMBER: US/10/023,339
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: PCT/US01/20917
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 3357
TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-339-2

```

| | | | | |
|---------------------------|-------|--------------------|----------|-------------|
| Query Match | 90.6% | Score 806.4 | DB 17 | Length 3357 |
| Best Local Similarity | 91.9% | Pred. No. 6.3e-260 | | |
| Matches 818, Conservative | 0 | Mismatches 71 | Indels 1 | Gaps 1 |

[illegible]

| | | | |
|----|------|---------------------------------------------------------------|------|
| QY | 241 | TACAACTAACCAATCCGAAGTGCACATGAGTACAGACTAAGAAACCTCGTTTTGAGTA | 300 |
| Db | 2297 | TACAACTAACCAATCCGAAGTGCACATGAGTACAGACTAAGAAACCTCGTTTTGAGTA | 2356 |
| QY | 301 | GAAGAGGCGCTGGGAAAGAGGGAGCCACAAATCTGTCTGCTTCTCAATTAAGTCAT | 360 |
| Db | 2357 | GAAGAGGCGCT - GGAAAGAGGGAGGCGCAACAAATCTGTCTGCTTCTCAATTAAGTCAT | 2415 |
| QY | 361 | GGCAAAATPAAGATTCTGTCTCTTTGGCTGTGCTGCCTCAGCAACAGAGCCGAAATCTATC | 420 |
| Db | 2416 | GGCAAAATPAAGATTCTGTCTCTTTGGCTGTGCTGCCTCAGCAACAGAGCCGAAATCTATC | 2475 |
| QY | 421 | GGGACACGAGTAACATCTCTCAGTGAACAGAGTTGACAAGGCGTATGGGAAATGCGCTGA | 480 |
| Db | 2476 | GGGACACGAGTAACATCTCTCAGTGAACAGAGTTGACAAGGCGTATGGGAAATGCGCTGA | 2535 |
| QY | 481 | TGGATTATCTCTCAGCTTGTGAGCTTCTAAGTTCTTCTCCCTTCAATTCACCTGCAAG | 540 |
| Db | 2536 | TGGATTATCTCTCAGCTTGTGAGCTTCTAAGTTCTTCTCCCTTCAATTCACCTGCAAG | 2595 |
| QY | 541 | CCAAGTCTGTAGAGAGAAATGCCGAGTCTAGCTCAGTTTCTTAAGTCTGAATTAGA | 600 |
| Db | 2596 | CCAAGTCTGTAGAGAGAAATGCCGAGTCTAGCTCAGTTTCTTAAGTCTGAATTAGA | 2655 |
| QY | 601 | TCTCCAGACCCCTGCTGGCCACAATTCAAATTAAGGCACAAACATTAACCTTCCATGAA | 660 |
| Db | 2656 | TCTCCAGACCCCTGCTGGCCACAATTCAAATTAAGGCACAAACATTAACCTTCCATGAA | 2715 |
| QY | 661 | GCACACACACACTTTTGAAGCAAGACACATGACTGTTGAATTGAGGCTTGAAGAAATG | 720 |
| Db | 2716 | GCACACACACACTTTTGAAGCAAGACACATGACTGTTGAATTGAGGCTTGAAGAAATG | 2775 |
| QY | 721 | AAGCTTTGAAGGAAAAAATACTATTGTTTCCAGCCCCCTCCACACACTCTTCATGTGTGA | 780 |
| Db | 2776 | AAGCTTTGAAGGAAAAAATACTATTGTTTCCAGCCCCCTCCACACACTCTTCATGTGTGA | 2835 |
| QY | 781 | ACCACTGCTTCTGTGACCTTGGAGCCACGGTGAATGTATTAATGTTTGAATGAAGAAC | 840 |
| Db | 2836 | ACCACTGCTTCTGTGACCTTGGAGCCACGGTGAATGTATTAATGTTTGAATGAAGAAC | 2895 |
| QY | 841 | TGATTTTAGAGTCTGATCGTTTCAAGAAATGATTAATTAACATTTTCC | 890 |
| Db | 2896 | TGATTTTAGAGTCTGATCGTTTCAAGAAATGATTAATTAATTAACATTTTCC | 2945 |

RESULT 14
US-09-896-738-1

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Sequence 1, Application US/09896738
Patent No. US20020165347A1
GENERAL INFORMATION:
APPLICANT: Fox, Michael
APPLICANT: Sullivan, John K.
APPLICANT: Pang, Mei
TITLE OF INVENTION: B7-like Molecules and Uses Thereof
FILE REFERENCE: 00-513-A
CURRENT APPLICATION NUMBER: US/09/896, 738
PRIORITY FILING DATE: 2001-06-29
PRIORITY APPLICATION NUMBER: 60/215, 645
PRIORITY FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2603
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (53) .. (901)
US-09-896-738-1

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| Query Match | 90.6% | Score | 806; | DB | 9; | Length | 2603; |
| Best Local Similarity | 91.8% | Pred. No. | 7.4e-250; | | | | |
| Matches | 817; | Conservative | 1; | Mismatches | 71; | Indels | 1; |
| | | | | Gaps | | | 1; |

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| Db | 2418 | AGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTTA | 2477 |
| Qy | 781 | ACCACTGCGCTTCTCTGACCTTTGAGCCAGCGTGACTGTATTACATGTTGTTATAGAAAC | 840 |
| Db | 2478 | ACCACTGCGCTTCTCTGAGCCTTGGAGCCACGCTGATTTACATGTTGTTATAGAAAC | 2537 |
| Qy | 841 | TGATTTTAGAGTTCGTGATCGTTCAGAGAAATGATTAAATATACATTTCCT | 890 |
| Db | 2538 | TGATTTTAGAGTTCGTGATCGTTCAGAGAAATGATTAAATATACATTTCCT | 2587 |

Search completed: May 31, 2005, 10:07:43
 Job time : 613.64 secs

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Db 1570 CAAGCTCTGAGGCTTCTCTTCATCCTGCGTGACAGCTAAGACCTCAGTTTCAATA 1629

[illegible]

JOURNAL
 COMMENT
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30346592.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 742.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CSODI039AD11Nf1ac=742.r.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI039IG21"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA
 was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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 Best Local Similarity 85.7%; Pred. No.1.5e-190;
 Matches 746; Conservative 25; Mismatches 90; Indels 9; Gaps 7;
 Oy 2 AAGCTTGAGGCTTCCTCTTCATCTCTGCGTGACACGTAAAGCTCAAGTTTCAATAG 61
 Db AAGCTGAGGCTTCCTCTTCAGTCTCTGCGTGAMAGATGACCTCAAGTTTCAATAG 810
 Oy 62 CATCTAAGACAGTGGGACTCAGCTGGGGGTATTTGGCCCC-ATCCGGGGGAATGTC 120
 Db CATCTGAGGCTTCCTCTTCAGTCTCTGCGTGAMAGATGACCTCAAGTTTCAATAG 810
 Oy 809 CATGTTGAGGCTTCCTCTTCAGTCTCTGCGTGAMAGATGACCTCAAGTTTCAATAG 750
 Db 121 TGAAGACAAATTTGGTGA-CTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNN 178
 Oy 749 TTAATACAAATTTGGTGA-CTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNN 690
 Db 179 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 238
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 Db 299 TAGAAAAGGGCTTGGGAAAGGGGAGCCAAACAATGTCTGGTCTTCAATTAAGTCA 358
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 Oy 450 TCGGGACACAGGATTAACATCTCTCAAGT-ACAAGATTG--ACAAGCTTAAGGAAATG 391
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 Oy 390 AACTGATGGGATTAATCTTCAAGCTTGTGAGC-CTCTAAGTTCTTTCCTCAATTCAC 331
 Db 534 CTGCAACCAAGTTCTGTTAAGAAATGCTGAGTTTACCTCAGTTTCTTACTCTGA 593
 Oy 330 CKGCAACCAAGTTCTGTTAAGAAATGCTGAGTTTACCTCAGTTTCTTACTCTGA 271
 Db 594 ATTATGATCTTCAGACCTGCTGGCCACAATTCAAATTAAAGCAACAAATATTAACCTT 653

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Db 270 ATTAGATCTCCAGACCTTCTCGGCCCAATTCAATTAGGCAACAAATATACCTT 211
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Db 210 CCATGAGCACACAGACCTTTTGAAGCAAGCAATGACTGTTGAATGAGGCTTG 151
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QY 774 TGTGTACCACTGCTTCTCGGCCCAATTGAGCAAGCAATGACTGTTGAT 833
Db 90 TGTGTACCACTGCTTCTCGGCCCAATTGAGCAAGCAATGACTGTTGAT 31
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RESULT 3

CB241729/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CB241729 691 bp mRNA linear EST 12-FEB-2003
 UI-CF-FNO-afz-p-01-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
 CB241729
 CB241729.1 GI:28363373
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 691)
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 8889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 618-691. >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 PolyA+es.

FEATURES

source

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-afz-p-01-0-UI"
 /tissue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-FNO is a subtracted cDNA library derived from two
 normalized human lung epithelial cell libraries (EN1 and
 DU1) The library was subtracted according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:

ORIGIN

bento-soares@uiowa.edu
 TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_LIB=UI-CF-FNO
 TAG_SEQ=GAGCTGTAGGC"

Query Match 71.8%; Score 639.4; DB 6; Length 691;
 Best Local Similarity 99.7%; Pred. No. 7.6e-181;
 Matches 651; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 238 CATTACACTACCAATCCGAAATGTCATCTGTGTGAGCACTAAGAAACCTGGTTTGA 297
Db 670 CATTACACTACCAATCCGAAATGTCATCTGTGTGAGCACTAAGAAACCTGGTTTGA 611
QY 298 GTGAAAAGGCGCTGGGAAAAGAGGAGCCAAATCTGTCTCTCTCTCAATTATGTC 357
Db 610 GTGAAAAGGCGCT -GGAAAAGAGGAGCCAAATCTGTCTCTCTCTCAATTATGTC 552
QY 358 ATTGCAAAATTAAGCATTTGTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
Db 551 ATTGCAAAATTAAGCATTTGTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
QY 418 ATGCGGACACAGATTAACATCTCTCACTGAGCAAGATTGACAGAGGCTTAAGGAAATGCC 477
Db 491 ATGCGGACACAGATTAACATCTCTCACTGAGCAAGATTGACAGAGGCTTAAGGAAATGCC 432
QY 478 TGTGAGGATTAATCTGTAGCTTGTGAGCTTCTTAAGTTCTTTCCCTTCAATCTTCCCTGC 537
Db 431 TGTGAGGATTAATCTGTAGCTTGTGAGCTTCTTAAGTTCTTTCCCTTCAATCTTCCCTGC 372
QY 538 AAGCCAAATGCTGTAGAGAAATAGCTGAGTTCTTACCTGAGTTCTTACTGTAATTT 597
Db 371 AAGCCAAATGCTGTAGAGAAATAGCTGAGTTCTTACTGAGTTCTTACTGTAATTT 312
QY 598 AGATCTCCAGACCTTCTGCGCACAATTCATTAATTAAGCAACAAATATACCTTCAT 657
Db 311 AGATCTCCAGACCTTCTGCGCACAATTCATTAATTAAGCAACAAATATACCTTCAT 252
QY 658 GAAGCACACACAGACTTTTGAAGCAAGCAATGCTGTTGAATGAGGCTTGAAGA 717
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QY 718 ATGAGCTTTGAAGGAAAGAAATATCTTGTTCAGGCCCCCTCCACACTCTTCATGTC 777
Db 191 ATGAGCTTTGAAGGAAAGAAATATCTTGTTCAGGCCCCCTCCACACTCTTCATGTC 132
QY 778 TTACCACTGCTTCTGAGACCTTGAGCCACGCTGATGTTATCATGTTGTTATAGAA 837
Db 131 TTACCACTGCTTCTGAGACCTTGAGCCACGCTGATGTTATCATGTTGTTATAGAA 72
QY 838 AACTGATTTTGAAGCTTGTGATGTTCAAGAGAAATGATTAATATACATTTCTCT 890
Db 71 AACTGATTTTGAAGCTTGTGATGTTCAAGAGAAATGATTAATATACATTTCTCT 19

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RESULT 4

BU632767/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BU632767 700 bp mRNA linear EST 23-SEP-2002
 UI-H-FBI-bdy-k-03-0-UI.s1 NCI CGAP FBI Homo sapiens cDNA clone
 BU632767
 BU632767.1 GI:23300022
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 700)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
 Tissue Procurement: James Martin
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 623-700, >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 PolyA=yes.

FEATURES

source

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FEI-bdy-k-03-0-UI"
 /tissue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_1ib="NCI CGAP FE1"
 /note="Organ: Chondrosarcoma; Vector: pTV73-Pac
 (Pharmacia) with a modified polylinker; Site 1: EcoR I;
 Site 2: Not I; NCI CGAP FE1 is a normalized cDNA library
 derived from a pool of mRNA obtained from 3 cell lines
 from grade II chondrosarcoma tissues. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pTV73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 CGCTACGGAC. The cell lines were provided by Dr James
 Martin from the University of Iowa.
 TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
 TAG_Lib=UI-H-FEI
 TAG_SEQ=CGCTACGGAC"

ORIGIN

Query Match 71.8%; Score 639.4; DB 5; Length 700;
 Best Local Similarity 99.7%; Pred. No. 7.6e-181;
 Matches 651; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Db
 238 CATTCACTACCTACCCATCCGAAGTGCACCTGTGCAGACTTAAGAAACCTGGTTTGA 297
 675 CATTCACTACCTACCCATCCGAAGTGCACCTGTGCAGACTTAAGAAACCTGGTTTGA 616
 238 GTAGAAAAGGGCCTGGGAAAAGAGGAGCAACAATCTGTCTGCTTCTCCTCATTTATGTC 357
 615 GTAGAAAAGGGCCT-GGAAAAGGGGAGCAACAATCTGTCTGCTTCTCCTCATTTATGTC 557
 358 ATTGGCAATTAAGCATTTCTGTTCTTTGGCTGCTGCTTCAAGACACAGAGAGCCAGACTCT 417
 556 ATTGGCAATTAAGCATTTCTGTTCTTTGGCTGCTGCTTCAAGACACAGAGAGCCAGACTCT 497
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 496 ATCGGGGACCCAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTATGGGAATGCC 437
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 436 TGATGGGATTAATCTTCAGCTTGTGAGCTTCAAGTTCTTTCCCTTCAATTCACCTGTC 377
 538 AAGCCAAAGTTCTGTAAAGAGAAATGCCCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATT 597
 376 AAGCCAAAGTTCTGTAAAGAGAAATGCCCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATT 317
 598 AGATCTCCAGACCCGCGCTGGCACAATTCAAATTAAGGCAACAACATATCCTTCAT 657
 316 AGATCTCCAGACCCGCTGGCACAATTCAAATTAAGGCAACAACATATCCTTCAT 257

FEATURES

source

Db
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 256 GAAGCACAACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTGAGGCTTTGAGCA 197
 718 ATGAAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCCAACTTTATGTC 777
 196 ATGAAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCCAACTTTATGTC 137
 778 TTAACTGCTGCTTCTGCTGAGCCTTGGAGCCACGGTACTGATTAATCATGTTTATGAA 837
 136 TTAACTGCTGCTTCTGCTGAGCCTTGGAGCCACGGTACTGATTAATCATGTTTATGAA 77
 838 AACTGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTCT 890
 76 AACTGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTCT 24
 RESULT 5
 CA314865/c
 LOCUS
 DEFINITION
 UI-CF-FN0-afi-e-12-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
 UI-CF-FN0-afi-e-12-0-UI 3', mRNA sequence.
 ACCESSION
 CA314865
 VERSION
 CA314865.1 GI:24532963
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 651)
 AUTHORS
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL
 Genome Res. 6 (9), 791-806 (1996)
 MEDLINE
 97044477
 PUBMED
 8889548
 COMMENT
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.regen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 PolyA=yes.

Location/Qualifiers

1..691

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FN0-afi-e-12-0-UI"
 /tissue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (TI phage resistant)"
 /clone_1ib="UI-CF-FN0"
 /note="Organ: Lung; Vector: pTV73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-FN0 is a subcloned cDNA library derived from two
 normalized Human Lung epithelial cell libraries (EN1 and
 DUL) The library was subcloned according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@uiowa.edu
 TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_SEQ=

ORIGIN

TAG LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

Query Match 71.7%; Score 638.4; DB 6; Length 691;
Best Local Similarity 99.5%; Pred. No. 1.5e-180;
Matches 650; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 238 CATTACAACTACCAATCCCAATGTCATCTGTCTGTCAGAGCTAAGAAACCTGGTTTGA 297
DB 670 CATTACAACTACCAATCCCAATGTCATCTGTCTGTCAGAGCTAAGAAACCTGGTTTGA 611
QY 298 GTAGAAAAGGCGCTGGGAAAAGAGGAGCAACAATCTGTCTGCTTCTCTACATTAGTC 357
DB 610 GTAGAAAAGGCGCT-GGAAAAGGAGGAGCAACAATCTGTCTGCTTCTCTACATTAGTC 552
QY 358 ATTGGCAATTAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAAGAGCCAGAACTCT 417
DB 551 ATTGGCAATTAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAAGAGCCAGAACTCT 492
QY 418 ATGGGCAACCAAGATTAACATCTCTCACTGAACAGAGTTGACAGGCTATGGAAATGCC 477
DB 491 ATGGGCAACCAAGATTAACATCTCTCACTGAACAGAGTTGACAGGCTATGGAAATGCC 432
QY 478 TGATGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCACTTACCCTGC 537
DB 431 TGATGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCACTTACCCTGC 372
QY 538 AAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTT 597
DB 371 AAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTT 312
QY 598 AGATCTCCAGACCCCTGCTGCGCAATTAAGGCAACAATTAACCTTACCTCCAT 657
DB 311 AGATCTCCAGACCCCTGCTGCGCAATTAAGGCAACAATTAACCTTACCTCCAT 252
QY 658 GAAGCACACACAGACTTTTGAAGCAAGACATGACTGTTGAATGAGGCTTGAAGA 717
DB 251 GAAGCACACACAGACTTTTGAAGCAAGACATGACTGTTGAATGAGGCTTGAAGA 192
QY 718 ATGAAAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCTTCCACACTCTTCAATG 777
DB 191 ATGAAAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCTTCCACACTCTTCAATG 132
QY 778 TTACCACTGCTCTCTGAGACCTTGAAGCCAGCGTGAATTAATGTTGTTATAGAA 837
DB 131 TTAAACACCTGCTCTCTGAGACCTTGAAGCCAGCGTGAATTAATGTTGTTATAGAA 72
QY 838 AACTGATTTTAAGTCTGATGCTTCAAGAAATGAATTAATATACATTTCT 890
DB 71 AACTGATTTTAAGTCTGATGCTTCAAGAAATGAATTAATATACATTTCT 19

RESULT 6
CA133445/c 737 bp mRNA 1linear EST 04-NOV-2002
LOCUS UI-CF-FNO-aeY-b-10-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
DEFINITION UI-CF-FNO-aeY-b-10-0-UI 3', mRNA sequence.
ACCESSION CA133445
VERSION CA133445.1 GI:24531543
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 737)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery
MEDLINE Genome Res. 6 (9), 791-806 (1996)
PUBMED 97044477
COMMENT Contact: McCray, PB

McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 618-737, >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-aeY-b-10-0-UI"
/issue_type="Human Lung Epithelial cells"
/lab_host="PH108 (Life Technologies) (T1 phage resistant)"
/clone_1ib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DN1). The library was subtracted according to
Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial cells Tissue nos 359-368
TAG LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 71.7%; Score 638.4; DB 6; Length 737;
Best Local Similarity 99.5%; Pred. No. 1.5e-180;
Matches 650; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 238 CATTACAACTACCAATCCCAATGTCATCTGTCTGTCAGAGCTAAGAAACCTGGTTTGA 297
DB 670 CATTACAACTACCAATCCCAATGTCATCTGTCTGTCAGAGCTAAGAAACCTGGTTTGA 611
QY 298 GTAGAAAAGGCGCTGGGAAAAGAGGAGCAACAATCTGTCTGCTTCTCTACATTAGTC 357
DB 610 GTAGAAAAGGCGCT-GGAAAAGGAGGAGCAACAATCTGTCTGCTTCTCTACATTAGTC 552
QY 358 ATTGGCAATTAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAAGAGCCAGAACTCT 417
DB 551 ATTGGCAATTAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAAGAGCCAGAACTCT 492
QY 418 ATGGGCAACCAAGATTAACATCTCTCACTGAACAGAGTTGACAGGCTATGGAAATGCC 477
DB 491 ATGGGCAACCAAGATTAACATCTCTCACTGAACAGAGTTGACAGGCTATGGAAATGCC 432
QY 478 TGATGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCACTTACCCTGC 537
DB 431 TGATGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCACTTACCCTGC 372
QY 538 AAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTT 597
DB 371 AAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTT 312
QY 598 AGATCTCCAGACCCCTGCTGCGCAATTAAGGCAACAATTAACCTTACCTCCAT 657
DB 311 AGATCTCCAGACCCCTGCTGCGCAATTAAGGCAACAATTAACCTTACCTCCAT 252
QY 658 GAAGCACACACAGACTTTTGAAGCAAGACATGACTGTTGAATGAGGCTTGAAGA 717

Db 251 GAAGCACACAGACTTTTGAAGACAGACATGACTGCTGAATTGAGGCTTGAGGA 192
QY 718 ATGAAGCTTTGAAGAAAAAATACCTTTGTTCCAGCCCCCTTCCACACTCTCATGTG 777
Db 191 ATGAAGCTTTGAAGAAAAAATACCTTTGTTCCAGCCCCCTTCCACACTCTCATGTG 132
QY 778 TTAACCACTGCTTCTTGAGACCTTGAGCAGCGTACTGTAATTAATGTTGTAAGAA 837
Db 131 TTAACCACTGCTTCTTGAGACCTTGAGCAGCGTACTGTAATTAATGTTGTAAGAA 72
QY 838 AACCTATTTTGAAGTTGATGCTTCAAGAGAAATGATTAATATCATTTCTT 890
Db 71 AACTGATTTTGAAGTTGATGCTTCAAGAGAAATGATTAATATCATTTCTT 19

RESULT 7
BU608696/c 691 bp mRNA linear EST 21-FEB-2003

LOCUS UI-CF-FN0-aeg-c-07-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
DEFINITION UI-CF-FN0-aeg-c-07-0-UI 3', mRNA sequence.

ACCESSION BU608696
VERSION BU608696.1 GI:23274911

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 691)
Normalizaton and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: McCray, PB

University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171

Email: paul.mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).

The following repetitive elements were found in this cDNA
sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source

Location/Qualifiers
1..691
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FN0-aeg-c-07-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="PHIOB (Life technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FN0"
/note="Organ: Lung; Vector: pTT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-FN0 is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI1) The library was subtracted according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG LIB=UI-CF-FN0
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 71.3%; Score 634.6; DB 5; Length 691;
Best Local Similarity 99.2%; Pred. No. 2.1e-179;
Matches 648; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 238 CATTACAACTACCCATCCGAAGTGTCACTGTGTGACGACTAAGAAACCTGGTTTGA 297
Db 670 CATACAAACTACCCATCCGAAGTGTCACTGTGTGACGACTAAGAAACCTGGTTTGA 611
QY 298 GTAGAAAAGGGGCTGGGAAAGAGGGGAGCCAACAATCGTGTGCTTCTCCTACATTAAGC 357
Db 610 GTAGAAAAGGGGCTGGGAAAGAGGGGAGCCAACAATCGTGTGCTTCTCCTACATTAAGC 552
QY 358 ATTGGCAATTAAGCAATTCGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCT 417
Db 551 ATTGGCAATTAAGCAATTCGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCT 492
QY 418 ATCGGGGACCAAGATTAATCTCTCAAGTGAACAGAGTTGACAAAGGCTTAGGAAATGCC 477
Db 491 ATCGGGGACCAAGATTAATCTCTCAAGTGAACAGAGTTGACAAAGGCTTAGGAAATGCC 432
QY 478 TGATGGATTAATCTCTCAAGTGAACAGAGTTGACAAAGGCTTAGGAAATGCC 537
Db 431 TGATGGATTAATCTCTCAAGTGAACAGAGTTGACAAAGGCTTAGGAAATGCC 372
QY 538 AAGCCAACTCTGTAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTGAATTT 597
Db 371 AAGCCAACTCTGTAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTGAATTT 312
QY 598 AGATTCACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
Db 311 AGATTCACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
QY 658 GAAGCACACAGACTTTTGAAGACAGACATGACTGCTGAATTGAGGCTTGAGGA 717
Db 251 GAAGCACACAGACTTTTGAAGACAGACATGACTGCTGAATTGAGGCTTGAGGA 192
QY 718 ATGAAGCTTTGAAGAAAAAATACCTTTGTTCCAGCCCCCTTCCACACTCTCATGTG 777
Db 191 ATGAAGCTTTGAAGAAAAAATACCTTTGTTCCAGCCCCCTTCCACACTCTCATGTG 132
QY 778 TTAACCACTGCTTCTTGAGACCTTGAGCAGCGTACTGTAATTAATGTTGTAAGAA 837
Db 131 TTAACCACTGCTTCTTGAGACCTTGAGCAGCGTACTGTAATTAATGTTGTAAGAA 72
QY 838 AACCTATTTTGAAGTTGATGCTTCAAGAGAAATGATTAATATCATTTCTT 890
Db 71 AACTGATTTTGAAGTTGATGCTTCAAGAGAAATGATTAATATCATTTCTT 19

RESULT 8
CB852239/c 660 bp mRNA linear EST 22-APR-2003

LOCUS UI-CF-FN0-aef-m-01-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
DEFINITION UI-CF-FN0-aef-m-01-0-UI 3', mRNA sequence.

ACCESSION CB852239
VERSION CB852239.1 GI:30047206

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homindae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 660)
Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: McCray, PB

University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.regen.com) or from Open Biosystems (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1. 660
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-aff-m-01-0-UI"
 /issue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-FNO is a subcloned CDNA library derived from two normalized Human lung epithelial cell libraries (BN1 and DN1). The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu
 TAG_SEQ=None found"

ORIGIN

Query Match 70.6%; Score 628.4; DB 6; Length 660;
 Best Local Similarity 99.5%; Pred. No. 1.5e-177;
 Matches 640; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

248 ACCCATCCGAAGTGTCACTGTGTCAGACTAGAAACCTGGTTTGTAGTAAAG 307
 660 ACCCATCCGAAGTGTCACTGTGTCAGACTAGAAACCTGGTTTGTAGTAAAG 601
 308 GCGTGGAAAGAGGGAGCCCAAAATCTGTCTCTCTCCTCATTAGTATGGCAAT 367
 600 GCGT-GGAAAGAGGGAGCCCAAAATCTGTCTCTCTCCTCATTAGTATGGCAAT 542
 368 AAGCATTTCTCTCTTTGGTGTGCTGTGTCAGACAGAGAGCCGAATCTATGGGACC 427
 541 AAGCATTTCTCTCTTTGGTGTGCTGTGTCAGACAGAGAGCCGAATCTATGGGACC 482
 428 AAGATTAACATCTCTCAGTGAACAGAGTGAAGGCTATGGAAATGCTGATGGGATT 487
 481 AAGATTAACATCTCTCAGTGAACAGAGTGAAGGCTATGGAAATGCTGATGGGATT 422
 488 ATCTTCAGCTTTGTGAGCTTCTAAGTTTCTTCTTCCTTCACTTACCTGCAAGCAAGT 547
 421 ATCTTCAGCTTTGTGAGCTTCTAAGTTTCTTCTTCCTTCACTTACCTGCAAGCAAGT 362
 548 CTGTAGAAGAAATGCTGAGTCTTACTGAGTTTCTTACTGTAATTAATCTTCAG 607
 361 CTGTAGAAGAAATGCTGAGTCTTACTGAGTTTCTTACTGTAATTAATCTTCAG 302
 608 ACCCTGCTGGCAGCAATCAATTAAGGCAAAACATTAACCTTCCATGAAGCAGACA 667
 301 ACCCTGCTGGCAGCAATCAATTAAGGCAAAACATTAACCTTCCATGAAGCAGACA 242
 668 CAGACTTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGAAGCAATGACTTT 727
 241 CAGACTTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGAAGCAATGACTTT 182
 728 GAAGGAAAGAAATATCTTTGTTTCCAGCCCTCCCAACATCTTCAATGTTTAAACAC 787
 181 GAAGGAAAGAAATATCTTTGTTTCCAGCCCTCCCAACATCTTCAATGTTTAAACAC 122
 788 CTTCTGTGACCTTGGAGCAGGTGACTGTATTACATGTTTATAGAAACCTGATTTT 847

Db 121 CCTCTGAGCCTTGGAGCAGGTGACTGTATTACATGTTTATAGAAACCTGATTTT 62
 848 AGAGTTCTGATCGTTCAAGAGATGATTTAATATACATTTCTT 890
 61 AGAGTTCTGATCGTTCAAGAGATGATTTAATATACATTTCTT 19

RESULT 9

CA426580/c 660 bp mRNA linear EST 07-NOV-2002
 LOCUS UI-H-FEI-beh-p-14-0-UI.s1 NCI CGAP FEI Homo sapiens CDNA clone
 DEFINITION UI-H-FEI-beh-p-14-0-UI 3', mRNA sequence.
 ACCESSION CA426580
 VERSION CA426580.1 GI:24789306
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 660)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabds-r@mail.nih.gov

JOURNAL

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1. 660
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FEI-beh-p-14-0-UI"
 /issue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI-CGAP_FEI"
 /note="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FEI is a normalized CDNA library derived from a pool of mRNA obtained from 3 cell lines from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGTACGAGC. The cell lines were provided by Dr James Martin from the University of Iowa.
 TAG TISSUE=human grade 2 chondrosarcoma cell line pool
 TAG_LIB=UI-H-FEI
 TAG_SEQ=CGTACGAGC"

ORIGIN

Query Match 69.9%; Score 621.8; DB 6; Length 660;
 Best Local Similarity 99.4%; Pred. No. 1.5e-175;
 Matches 634; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

253 ATCCGAAGTGTCACTGTGTCAGACTAGAAACCTGGTTTGTAGTAAAGGCGCTG 312
 660 ATCCGAAGTGTCACTGTGTCAGACTAGAAACCTGGTTTGTAGTAAAGGCGCTG 602

313 GGAAGAGGAGGAGCAAAATCTGTCTCTCTCACTAGTATGTCATTTGGCAATTAAGCA 372
601 GGAAGAGGAGGAGCAAAATCTGTCTCTCTCTCACTAGTATGTCATTTGGCAATTAAGCA 542
373 TTCTGTCTCTTTGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 432
541 TTCTGTCTCTTTGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 482
433 AACATCTCTCACTGAAACAGATTTGACAGGCTCTATGGGAAAGCCCTGATGGATTAATCT 492
481 AACATCTCTCACTGAAACAGATTTGACAGGCTCTATGGGAAAGCCCTGATGGATTAATCT 422
493 CAGCTTGTGAGCTCTAAGTTCTTTCCCTCATTTCTACCTCTGAGCAAGCTTCTGTA 552
421 CAGCTTGTGAGCTCTAAGTTCTTTCCCTCATTTCTACCTCTGAGCAAGCTTCTGTA 362
553 AGAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 612
361 AGAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 302
613 GCTGCGCCCAATTCATAATTAAGCAACAAATATACCTTCATGAGCAACACAGAC 672
301 TCTGCGCCCAATTCATAATTAAGCAACAAATATACCTTCATGAGCAACACAGAC 242
673 TTTTGAAGCAAGCAATGACTGCTGATTTGAGGCTTGAAGCAATGAGCTTGAAGG 732
241 TTTTGAAGCAAGCAATGACTGCTGATTTGAGGCTTGAAGCAATGAGCTTGAAGG 182
733 AAAAGATATCTTTGTTTCCAGCCCTCTTCCACACTCTTCAATGTTTGAACACTGCTTC 792
181 AAAAGATATCTTTGTTTCCAGCCCTCTTCCACACTCTTCAATGTTTGAACACTGCTTC 122
793 CTGAGCTTTGAGCCACGCTGACTGATTAACATGTTTGAATTAAGCAATGAGT 852
121 CTGAGCTTTGAGCCACGCTGACTGATTAACATGTTTGAATTAAGCAATGAGT 62
853 TCTGATCGTTCAAGAGATGATTAATATATACCTTCT 890
61 TCTGATCGTTCAAGAGATGATTAATATATACCTTCT 24

RESULT 10
CA312678/c 679 bp mRNA linear EST 04-NOV-2002
LOCUS UI-CF-FN0-afl-m-11-0-UI-s1 UI-CF-FN0 Homo sapiens cDNA clone
DEFINITION UI-CF-FN0-afl-m-11-0-UI 3', mRNA sequence.
ACCESSION CA312678.1 GI:24530776
VERSION CA312678.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 679)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL MEDLINE 9704477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research

Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes

FEATURES
source
Location/Qualifiers
1..679
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FN0-afl-m-11-0-UI"
/isue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: pRT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FN0 is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI1) The library was subtracted according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-FN0
TAG_SEQ=CTGCTCAGT"

ORIGIN
Query Match 69.1%; Score 615.4; DB 6; Length 679;
Best Local Similarity 97.4%; Pred. No. 1.3e-173;
Matches 636; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

238 CATTCAACATCCCAATCCGAAGTGTCACTGTCTGAGCAAGCAAACTGTGTTTGA 297
670 CATTCAAGTACCAATCCGAAGTGTCACTGTCTGAGCAAGCAAACTGTGTTTGA 611
238 GTAGAAAAGGCTTGGGAAAGGGAGCCCAAAATCTGTCTGTTCTTCAATTATGTC 357
610 GCAGAAAAGGGGCTTGGGAAAGGGAGCCCAAAATCTGTCTGTTCTTCAATTATGTC 552
358 ATTGGCAATATAGCAATTTCTGTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 417
551 ATTGGCAATATATAGCAATTTCTGTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 492
418 ATTCGGCAACAGGATTAATATATATATATATATATATATATATATATATATATATATAT 477
491 ATTCGGCAACAGGATTAATATATATATATATATATATATATATATATATATATATATAT 432
478 TGATGGATTAATCTTCACTGTTGAGCTTCTTAAATTTCTTCTTCTTCTTCTTCTTCTTCT 537
431 TGATGGATTAATCTTCACTGTTGAGCTTCTTAAATTTCTTCTTCTTCTTCTTCTTCTTCT 372
538 AAGCCAGTTCTGTAAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 597
371 AAGCCAGTTCTGTAAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 312
538 AGATCTCCAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
311 AGATCTCCAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
658 GAAGCAACACAGATCTTTGAAAGCAAGCAATGATCTGTTGAATTTGAGGCTTGAAGA 717
251 GAAGCAACACAGATCTTTGAAAGCAAGCAATGATCTGTTGAATTTGAGGCTTGAAGA 192
718 ATGAAGCTTTGAAGAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCAATG 777
191 ATGAAGCTTTGAAGAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCAATG 132
778 TTAACCACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
131 TTAACCACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 72
838 AACTGATTTGAGTCTGATCTGTTCAAGAGATGATTAATATATATATATATATATATATAT 890

Db 71 AACTGATTGAGTCTGATCGTTCAAGAGATGATTAATATACATTCTT 19

RESULT 11
CA503188/c 594 bp mRNA linear EST 14-NOV-2002
LOCUS UI-CF-FNO Homo sapiens cDNA clone
DEFINITION UI-CF-FNO-afp-p-10-0-UI 3', mRNA sequence.
CA503188
ACCESSION CA503188.1 GI:24994142
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Bernaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
Seq primer: M13 FORWARD
POLY=Yes.
FEATURES
source Location/Qualifiers
1..594
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-afp-p-10-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Score 1; Site 2: Not 1; UI-CF-FNO is a subtracted cDNA library derived from two normalized human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

ORIGIN
Query Match 63.6%; Score 566.4; DB 6; Length 594;
Best Local Similarity 99.0%; Pred. No. 7e-159; Indels 0; Gaps 0;
Matches 570; Conservative 0; Mismatches 6;

Db 315 AAAGAGGGGAGCCAAATCTGTCTTCTTCTTCAATTAAGTGGCAATTAAGCATT 374
|||||
Db 594 AAAGAGGGGAGCCAAATCTGTCTTCTTCTTCAATTAAGTGGCAATTAAGCATT 535
|||||
QY 375 CTGTCTTTTGGTGTCTGCTGACGACAGAGACCGAACTATATGGGGACAGATTA 434
|||||
Db 534 CTGTCTCAATGCTGTGCTGCTGACGACAGAGACCGAACTATATGGGGACAGATTA 475
|||||
QY 435 CATCTCAAGTAAAGAGTTGACAAAGGCTTATGGGAATGCTGATGGATTATCTTCA 494
|||||

Db 474 CATCTCAAGTAAAGAGTTGACAAAGGCTTATGGGAATGCTGATTAATCTTCA 415
|||||

QY 495 GCTTGTGAGCTTCTTAAGTTCTTCTTCTTCAATTAAGTGGCAATTAAGCATT 554
|||||

Db 414 GCTTGTGAGCTTCTTAAGTTCTTCTTCTTCAATTAAGTGGCAATTAAGCATT 355
|||||

QY 555 AGAATGCTGAGTTCTTACGTTCTTCTTCTTCAATTAAGTGGCAATTAAGCATT 614
|||||

Db 354 AGAATGCTGAGTTCTTACGTTCTTCTTCTTCAATTAAGTGGCAATTAAGCATT 295
|||||

QY 615 CTGGCCAACTTCAATTAAGGCAACAAATTAAGTGGCAATTAAGCATT 674
|||||

Db 294 CTGGCCAACTTCAATTAAGGCAACAAATTAAGTGGCAATTAAGCATT 235
|||||

QY 675 TTGAAGCAAGCAATTAAGTGGCAATTAAGTGGCAATTAAGCATT 734
|||||

Db 234 TTGAAGCAAGCAATTAAGTGGCAATTAAGTGGCAATTAAGCATT 175
|||||

QY 735 AAGAAATCTTGTGTTTCAAGCCCTTCCGACACTCTTCAATTAAGTGGCAATTAAGCATT 794
|||||

Db 174 AAGAAATCTTGTGTTTCAAGCCCTTCCGACACTCTTCAATTAAGTGGCAATTAAGCATT 115
|||||

QY 795 GGACCTTGAAGCAGCTGATGATTAATTAAGTGGCAATTAAGCATT 854
|||||

Db 114 GGACCTTGAAGCAGCTGATGATTAATTAAGTGGCAATTAAGCATT 55
|||||

QY 855 TGATCGTTCAAGAGATTAATTAATTAAGTGGCAATTAAGCATT 890
|||||

Db 54 TGATCGTTCAAGAGATTAATTAATTAAGTGGCAATTAAGCATT 19
|||||

RESULT 12
A1684143 556 bp mRNA linear EST 16-DEC-1999
LOCUS tx79904.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2275830 3',
DEFINITION mRNA sequence.
A1684143
ACCESSION A1684143
VERSION A1684143.1 GI:4895437
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 556)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher Miskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 2042 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 417.
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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2275830"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut1"
/note="Organ: uterus; Vector: pCMV-Sport6; Site 1: SalI;

ORIGIN

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

Query Match 61.8%; Score 550.4; DB 1; Length 556;

Best Local Similarity 99.8%; Pred. No. 4.5e-154;

Matches 551; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 339 CTGCTTCCCATAGTATGATGAGCAATATACATTTCTCTTGGCTGCTGCTG 398
DB 556 CTGCTTCCCATAGTATGATGAGCAATATACATTTCTCTTGGCTGCTGCTG 497
OY 399 CACAGAGAGCCAGAACTCTATCGGGGACAGAGATTAATCTCTCACTGA 458
DB 496 CACAGAGAGCCAGAACTCTATCGGGGACAGAGATTAATCTCTCACTGA 437
OY 459 AAGGCTTATGGGAATGCTGATGGGATTAATCTCTCACTGTTGAGCTTAA 518
DB 436 AAGGCTTATGGGAATGCTGATGGGATTAATCTCTCACTGTTGAGCTTAA 377
OY 519 TCCCTTCAATTCACCTGCAAGCCAAAGTCTGTAAGAGAAATGCTGAGTT 578
DB 376 TCCCTTCAATTCACCTGCAAGCCAAAGTCTGTAAGAGAAATGCTGAGTT 317
OY 579 GTTTTCTTACTGATTTAGATCTTCAGACCCCTGCTGCAATTCATTAAGGA 638
DB 316 GTTTTCTTACTGATTTAGATCTTCAGACCCCTGCTGCAATTCATTAAGGA 257
OY 639 ACAAACATATACCTTCCATGAGACACACAGACTTTTGAAGCAAGACATG 698
DB 256 ACAAACATATACCTTCCATGAGACACACAGACTTTTGAAGCAAGACATG 197
OY 699 TGAATTTGAGGCTTGAAGATGAGCTTGAAGAAAGATACCTTGTTCAGCCC 758
DB 136 TGAATTTGAGGCTTGAAGATGAGCTTGAAGAAAGATACCTTGTTCAGCCC 137
OY 759 TTCCACACTCTTCAATGTTTAAACCACTGCTCTGCACTTGAAGCCAGGTA 818
DB 136 TTCCACACTCTTCAATGTTTAAACCACTGCTCTGCACTTGAAGCCAGGTA 77
OY 819 ATTACATGTTGTTATAGAAACTGATTTTGAAGTTTGAATGATTAATTA 878
DB 76 ATTACATGTTGTTATAGAAACTGATTTTGAAGTTTGAATGATTAATTA 17
OY 879 TATACATTTCT 890
DB 16 TATACATTTCT 5

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RESULT 13
LOCUS CD632169 568 bp mRNA linear EST 12-JAN-2004
DEFINITION 56084071H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD632169
VERSION CD632169.1 GI:40280436
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
TITLE Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)

JOURNAL COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
Source 1..568
Location/Qualifiers

ORIGIN

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

Query Match 61.8%; Score 549.6; DB 6; Length 568;

Best Local Similarity 99.3%; Pred. No. 7.9e-154;

Matches 552; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY 335 CTGCTGCTTCTCATATGATGAGCAATATACATTTCTCTTGGCTGCTGCT 394
DB 11 CAGTGTGCTTCTCATATGATGAGCAATATACATTTCTCTTGGCTGCTGCT 70
OY 395 TCAGCAGAGAGCCAGAACTCTATCGGGGACAGAGATTAATCTCTCACTGA 454
DB 71 TCAGCAGAGAGCCAGAACTCTATCGGGGACAGAGATTAATCTCTCACTGA 130
OY 455 TGACAGAGCCATATGGGAATGCTGATGGGATTAATCTCTCACTGTTAGCT 514
DB 131 TGACAGAGCCATATGGGAATGCTGATGGGATTAATCTCTCACTGTTAGCT 190
OY 515 TCTTCCCTTCAATTCACCTGCAAGCCAAAGTCTGTAAGGAATGCTGAGTT 574
DB 191 TCTTCCCTTCAATTCACCTGCAAGCCAAAGTCTGTAAGGAATGCTGAGTT 250
OY 575 TCAGGTTTCTTACTGATTTAGATCTTCAGACCCCTGCTGCAATTCATTAAG 634
DB 251 TCAGGTTTCTTACTGATTTAGATCTTCAGACCCCTGCTGCAATTCATTAAG 310
OY 635 GGCACAAACATATACCTTCCATGAGACACACAGACTTTTGAAGCAAGACAT 694
DB 311 GGCACAAACATATACCTTCCATGAGACACACAGACTTTTGAAGCAAGACAT 370
OY 695 TGCTTGAATGAGGCTTGAAGATGAGCTTGAAGAAAGATACCTTGTTCAGCC 754
DB 371 TGCTTGAATGAGGCTTGAAGATGAGCTTGAAGAAAGATACCTTGTTCAGCC 430
OY 755 CCCCTTCCCACTCTTCAATGTTTAAACCACTGCTCTGCACTTGAAGCCAGGTA 814
DB 431 CCCCTTCCCACTCTTCAATGTTTAAACCACTGCTCTGCACTTGAAGCCAGGTA 490
OY 815 CTGATTTACATGTTTATAGAAACTGATTTTGAAGTTTGAATGATTAATTA 874
DB 491 CTGATTTACATGTTTATAGAAACTGATTTTGAAGTTTGAATGATTAATTA 550
OY 875 TAAATATACATTTCT 890
DB 551 TAAATATACATTTCT 566

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RESULT 14
LOCUS CD632170/c 560 bp mRNA linear EST 12-JAN-2004
DEFINITION 56084071J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD632170
VERSION CD632170.1 GI:40280437
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
TITLE Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)

JOURNAL COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
Source 1..568
Location/Qualifiers

FEATURES
source 1.560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/notes="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 61.0%; Score 542.6; DB 6; Length 560;
Best Local Similarity 99.3%; Pred. No. 1e-151;
Matches 545; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

335 CTGTGCTTCCACATTTAGTGGCAATAGCATCTCTCTTTGGCTGCC 394
549 CAGTGTCTTCTCACTTGTGATGGCAATAGCATCTCTCTTTGGCTGCC 490
395 TCAGCAGAGAGCCAGAACTCTATCGGCACGAGTAACTCTCACTGAAGAGT 454
489 TCAGCAGAGAGCCAGAACTCTATCGGCACGAGTAACTCTCACTGAAGAGT 430
455 TCAGCAGAGCCATGGGAATGCTGATGGATATCTTCACTTTGAGCTTTAAGT 514
429 TCAGCAGAGCCATGGGAATGCTGATGGATATCTTCACTTTGAGCTTTAAGT 370
515 TCTTCCCTTCACTTCACTGAGCAGATCTGTAAGAGAAATGCTGAGTCTAGC 574
369 TCTTCCCTTCACTTCACTGAGCAGATCTGTAAGAGAAATGCTGAGTCTAGC 310
575 TCAGTCTTCTTCACTGATTTAGATCTCAGACCCCTGCGCAATTCGAAATTA 634
309 TCAGTCTTCTTCACTGATTTAGATCTCAGACCCCTGCGCAATTCGAAATTA 250
635 GGCACAAACATATACCTTCATGAGACACACAGACCTTTGAAAGCAATGAC 694
249 GGCACAAACATATACCTTCATGAGACACACAGACCTTTGAAAGCAATGAC 190
695 TGCTTAATTTAGAGCCCTGAGAAAGAGTGTGAAGAAAGAAATGCTTTGCTCAGC 754
189 TGCTTAATTTAGAGCCCTGAGAAAGAGTGTGAAGAAAGAAATGCTTTGCTCAGC 130
755 CCCCTTCCACACTCTTCACTGATTTAAACCACTGCTTCTGACCTTGAAGCCAGGTGA 814
129 CCCCTTCCACACTCTTCACTGATTTAAACCACTGCTTCTGACCTTGAAGCCAGGTGA 70
815 CTGTATTAATGTTGTTATAGAAACTGATTTAGAGTCTGATTCGTAAGAAATGAT 874
69 CTGTATTAATGTTGTTATAGAAACTGATTTAGAGTCTGATTCGTAAGAAATGAT 10
875 TAAATATAC 883
9 TAAATATAC 1

RESULT 15
BM982674 557 bp mRNA linear EST 21-FEB-2003
LOCUS BM982674
DEFINITION UI-CF-EN1-acq-n-01-0-UI-s1 UI-CF-EN1 Homo sapiens cDNA clone
VERSION UI-CF-EN1-acq-n-01-0-UI-3', mRNA sequence.
ACCESSION BM982674
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 8889548

COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source 1.557
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="UI-CF-EN1-acq-n-01-0-UI"
/issue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
/dev_stage="Adult"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
TAG_TISSUE=human Lung Epithelial Cell lines untreated LPS 6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN
Query Match 59.6%; Score 530.8; DB 5; Length 557;
Best Local Similarity 99.6%; Pred. No. 3.6e-148;
Matches 532; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

357 CATTGGCAATAAAGCATCTGTCCTTTGGCTGCTGCTCAGACAGAGCCAGAACTC 416
557 CATTGGCAATAAAGCATCTGTCCTTTGGCTGCTGCTCAGACAGAGCCAGAACTC 498
417 TATCGGCAACAGATTAACATCTCTCAGGAAACAGGTTGACAAAGCCCTATGGAAATGC 476
497 TATCGGCAACAGATTAACATCTCTCAGGAAACAGGTTGACAAAGCCCTATGGAAATGC 438
477 CTGATGGAGTATATCTTCACTGAGCTTGAAGTTCCTTCCCTTCACTTCACTGAGT 536
437 CTGATGGAGTATATCTTCACTGAGCTTGAAGTTCCTTCCCTTCACTTCACTGAGT 378
537 CAAGCCAAATCTGTAGAAGAAATGCTGAGTTTGAAGTTCCTTCACTGAGT 596
377 CAAGCCAAATCTGTAGAAGAAATGCTGAGTTTGAAGTTCCTTCACTGAGT 318
597 TAGATTTCAAGACCTGCTGCGCAATTTCAATTAAGGCAACAACTATACCTTCCA 656
317 TAGATTTCAAGACCTGCTGCGCAATTTCAATTAAGGCAACAACTATACCTTCCA 258
657 TGAAGCACACAGACTTTTGAAGCAAGCAATGATGCTTGAATTTAGGCTTGAAG 716

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Db      257 TGAAGCACACACAGACTTTGAAAGCAAGACATGACTGCTGAATTGAGGCTTGAGG 198
Oy      717 AATGAAGCTTTGAAGGAAAAAGATACTTTGTTCCAGCCCCCTTCCACACTCTTCATGT 776
Db      197 AATGAAGCTTTGAAGGAAAAAGATACTTTGTTCCAGCCCCCTTCCACACTCTTCATGT 138
Oy      777 GTTAACCACTGCTTCTCTGAGCCTTGAGCCACGGGTGACTGTATTACATGTTGTTATAGA 836
Db      137 GTTAACCACTGCTTCTCTGAGCCTTGAGCCACGGGTGACTGTATTACATGTTGTTATAGA 78
Oy      837 AAACGTATTTAGAGTCTGATCGTTCAGAGAGATGATTAATAATATACATTTCCT 890
Db      77 AAACGTATTTAGAGTCTGATCGTTCAGAGAGATGATTAATAATATACATTTCCT 24
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